

PATENT APPLICATION

**INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN
IMMUNODEFICIENCY VIRUS-1 USING PEPTIDE AND NUCLEIC ACID
COMPOSITIONS**

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CROSS-REFERENCES TO RELATED APPLICATIONS

10 *WJ* This application is a Continuation-In-Part ("CIP") of U.S.S.N. 09/189,702, filed
11/10/98, which is a CIP of U.S.S.N 08/205,713 filed 3/4/94, which is a CIP of abandoned
U.S.S.N. 08/159,184 filed 11/29/93, which is a CIP of abandoned U.S.S.N. 08/073,205 filed
6/4/93 which is a CIP of abandoned U.S.S.N 08/027,146 filed 3/5/93. The present
application is also related to U.S.S.N. 09/226,775, which is a CIP of abandoned U.S.S.N.
15 08/815,396, which claims benefit of abandoned U.S.S.N. 60/013,113. Furthermore, the
present application is related to U.S.S.N. 09/017,735, which is a CIP of abandoned U.S.S.N.
08/589,108; U.S.S.N. 08/454,033; and U.S.S.N. 08/349,177. The present application is also
related to U.S.S.N. 09/017,524, U.S.S.N. 08/821,739, which claims benefit of abandoned
U.S.S.N. 60/013,833; and U.S.S.N. 08/347,610, which is a CIP of U.S.S.N. 08/159,339,
20 which is a CIP of abandoned U.S.S.N. 08/103,396, which is a CIP of abandoned U.S.S.N.
08/027,746, which is a CIP of abandoned U.S.S.N. 07/926,666. The present application is
also related to U.S.S.N. 09/017,743, which is a CIP of abandoned U.S.S.N. 08/590,298; and
U.S.S.N. 08/452,843, which is a CIP of U.S.S.N. 08/344,824, which is a CIP of abandoned
U.S.S.N. 08/278,634. The present application is also related to PCT application 99/12066
25 filed 5/28/99 which claims benefit of provisional U.S.S.N. 60/087,192; U.S.S.N. 09/009,953,
which is a CIP of abandoned U.S.S.N. 60/036,713; and abandoned U.S.S.N. 60/037,432. In
addition, the present application is related to U.S.S.N. 09/098,584; U.S.S.N. 09/239,043;
U.S.S.N. 60/117,486; U.S.S.N. 09/350,401; U.S.S.N. 09/357,737; and U.S.S.N. 09/390,061.
All of the above applications are incorporated herein by reference.

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FEDERALLY SPONSORED RESEARCH AND DEVELOPMENT

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I. BACKGROUND OF THE INVENTION

Acquired immunodeficiency syndrome (AIDS) caused by infection with human immunodeficiency virus-1 (HIV-1) represents a major world health problem. Estimates indicate that about 16,000 people worldwide are infected with HIV each day.

5 The development of anti-viral drugs has been a major advancement in reducing viral loads in HIV infected patients. Highly active retroviral therapy (HAART) has been shown to reduce viremia to nearly undetectable levels. However, current drug therapies are not practicable as a long term solution to the HIV epidemic. HAART therapy is severely limited due to poor tolerance for the drugs and the emergence of drug-resistant virus. Moreover, replication competent HIV persists in the lymphoid tissue of patients
10 who have responded to HAART, thus serving as a reservoir of virus. Lastly, current anti-retroviral drug therapies have little impact upon the global epidemic: almost 90% of the world's HIV infected population resides within countries lacking financial resources for these drugs. Thus, a need exists for an efficacious vaccine to both prevent and treat HIV
15 infection.

Virus-specific, human leukocyte antigen (HLA) class I-restricted cytotoxic T lymphocytes (CTL) are known to play a major role in the prevention and clearance of virus infections *in vivo* (Oldstone *et al.*, *Nature* 321:239, 1989; Jamieson *et al.*, *J. Virol.* 61:3930, 1987; Yap *et al.*, *Nature* 273:238, 1978; Lukacher *et al.*, *J. Exp. Med.* 160:814,
20 1994; McMichael *et al.*, *N. Engl. J. Med.* 309:13, 1983; Sethi *et al.*, *J. Gen. Virol.* 64:443, 1983; Watari *et al.*, *J. Exp. Med.* 165:459, 1987; Yasukawa *et al.*, *J. Immunol.* 143:2051, 1989; Tigges *et al.*, *J. Virol.* 66:1622, 1993; Reddenhase *et al.*, *J. Virol.* 55:263, 1985; Quinnan *et al.*, *N. Engl. J. Med.* 307:6, 1982). HLA class I molecules are expressed on the surface of almost all nucleated cells. Following intracellular processing of antigens,
25 epitopes from the antigens are presented as a complex with the HLA class I molecules on the surface of such cells. CTL recognize the peptide-HLA class I complex, which then results in the destruction of the cell bearing the HLA-peptide complex directly by the CTL and/or via the activation of non-destructive mechanisms *e.g.*, the production of
interferon, that inhibit viral replication.

30 While immune correlates of protective immunity against HIV infection are not well defined, there is a growing body of evidence that suggests CTL are important in controlling HIV infection. HIV-specific CTL responses can be detected early in infection and the appearance of the responses corresponds to the time in infection at which initial viremia is reduced (Pantaleo *et al.*, *Nature* 370:463, 1994; Walker *et al.*, *Proc. Natl.*

Acad. Sci. 86:9514, 1989). In addition, HIV replication in infected lymphocytes can be inhibited by incubation with autologous CTL (*see, e.g., Tsubota et al., J. Exp. Med.* 169:1421, 1989). These data are supported by recent studies that indicate CTL are required for controlling viral replication in a SIV/rhesus animal model (Schmitz *et al., Science* 283:857, 1999), and additionally supported by studies that demonstrate that CTL exert selective pressure on HIV populations as evidenced by the eventual predominance of viruses with amino acid replacements in those regions of the virus to which CTL responses are directed (*see, e.g., Borrow et al., Nature Med.* 3:205-211, 1997; Price *et al., Proc. Nat. Acad. Sci.* 94:12890-1895, 1997; Koenig *et al., Nature Med.* 1:330-336, 1995; and Haas *et al., J. Immunol.* 157:4212-4221, 1996)

Virus-specific T helper lymphocytes are also known to be critical for maintaining effective immunity in chronic viral infections. Historically, HTL responses were viewed as primarily supporting the expansion of specific CTL and B cell populations; however, more recent data indicate that HTL may directly contribute to the control of virus replication. For example, a decline in CD4⁺ T cells and a corresponding loss in HTL function characterize infection with HIV (Lane *et al., New Engl. J. Med.* 313:79, 1985). Furthermore, studies in HIV infected patients have also shown that there is an inverse relationship between virus-specific HTL responses and viral load, suggesting that HTL play a role in viremia (*see, e.g., Rosenberg et al., Science* 278:1447, 1997).

A fundamental challenge in the development of an efficacious HIV vaccine is the heterogeneity observed in HIV. The virus, like other retroviruses, rapidly mutates during replication resulting in the generation of virus that can escape anti-viral therapy and immune recognition (Borrow *et al., Nature Med.* 3:205, 1997). In addition, HIV can be classified into a variety of subtypes that exhibit significant sequence divergence (*see, e.g., Lukashov et al., AIDS* 12:S43, 1998). In view of the heterogeneous nature of HIV, and the heterogeneous immune response observed with HIV infection, induction of a multi-specific cellular immune response directed simultaneously against multiple HIV epitopes appears to be important for the development of an efficacious vaccine against HIV. There is a need to establish such vaccine embodiments which elicit immune responses of sufficient breadth and vigor to prevent and/or clear HIV infection.

The epitope approach, as we have described, may represent a solution to this challenge, in that it allows the incorporation of various antibody, CTL and HTL epitopes, from various proteins, in a single vaccine compositions. Such a composition may

simultaneously target multiple dominant and subdominant epitopes and thereby be used to achieve effective immunization in a diverse population.

The information provided in this section is intended to disclose the presently understood state of the art as of the filing date of the present application. Information is included in this section which was generated subsequent to the priority date of this application. Accordingly, information in this section is not intended, in any way, to delineate the priority date for the invention.

II. SUMMARY OF THE INVENTION

This invention applies our knowledge of the mechanisms by which antigen is recognized by T cells, for example, to develop epitope-based vaccines directed towards HIV. More specifically, this application communicates our discovery of specific epitope pharmaceutical compositions and methods of use in the prevention and treatment of HIV infection.

Upon development of appropriate technology, the use of epitope-based vaccines has several advantages over current vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The epitopes for inclusion in an epitope-based vaccine may be selected from conserved regions of viral or tumor-associated antigens, which thereby reduces the likelihood of escape mutants. Furthermore, immunosuppressive epitopes that may be present in whole antigens can be avoided with the use of epitope-based vaccines.

An additional advantage of an epitope-based vaccine approach is the ability to combine selected epitopes (CTL and HTL), and further, to modify the composition of the epitopes, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches.

Another major benefit of epitope-based immune-stimulating vaccines is their safety. The possible pathological side effects caused by infectious agents or whole protein antigens, which might have their own intrinsic biological activity, is eliminated.

An epitope-based vaccine also provides the ability to direct and focus an immune response to multiple selected antigens from the same pathogen. Thus, patient-by-patient variability in the immune response to a particular pathogen may be alleviated by inclusion

of epitopes from multiple antigens from the pathogen in a vaccine composition. In the case of HIV, epitopes derived from multiple strains may also be included. A "pathogen" may be an infectious agent or a tumor associated molecule.

One of the most formidable obstacles to the development of broadly efficacious epitope-based immunotherapeutics, however, has been the extreme polymorphism of HLA molecules. To date, effective non-genetically biased coverage of a population has been a task of considerable complexity; such coverage has required that epitopes be used that are specific for HLA molecules corresponding to each individual HLA allele. Impractically large numbers of epitopes would therefore have to be used in order to cover ethnically diverse populations. Thus, there has existed a need for peptide epitopes that are bound by multiple HLA antigen molecules for use in epitope-based vaccines. The greater the number of HLA antigen molecules bound, the greater the breadth of population coverage by the vaccine.

Furthermore, as described herein in greater detail, a need has existed to modulate peptide binding properties, *e.g.*, so that peptides that are able to bind to multiple HLA antigens do so with an affinity that will stimulate an immune response. Identification of epitopes restricted by more than one HLA allele at an affinity that correlates with immunogenicity is important to provide thorough population coverage, and to allow the elicitation of responses of sufficient vigor to prevent or clear an infection in a diverse segment of the population. Such a response can also target a broad array of epitopes. The technology disclosed herein provides for such favored immune responses.

In a preferred embodiment, epitopes for inclusion in vaccine compositions of the invention are selected by a process whereby protein sequences of known antigens are evaluated for the presence of motif or supermotif-bearing epitopes. Peptides corresponding to a motif- or supermotif-bearing epitope are then synthesized and tested for the ability to bind to the HLA molecule that recognizes the selected motif. Those peptides that bind at an intermediate or high affinity *i.e.*, an IC_{50} (or a K_D value) of 500 nM or less for HLA class I molecules or an IC_{50} of 1000 nM or less for HLA class II molecules, are further evaluated for their ability to induce a CTL or HTL response. Immunogenic peptide epitopes are selected for inclusion in vaccine compositions.

Supermotif-bearing peptides may additionally be tested for the ability to bind to multiple alleles within the HLA supertype family. Moreover, peptide epitopes may be analogued to modify binding affinity and/or the ability to bind to multiple alleles within an HLA supertype.

The invention also includes embodiments comprising methods for monitoring or evaluating an immune response to HIV in a patient having a known HLA-type. Such methods comprise incubating a T lymphocyte sample from the patient with a peptide composition comprising an HIV epitope that has an amino acid sequence described in Tables VII to Table XX which binds the product of at least one HLA allele present in the patient, and detecting for the presence of a T lymphocyte that binds to the peptide. A CTL peptide epitope may, for example, be used as a component of a tetrameric complex for this type of analysis.

An alternative modality for defining the peptide epitopes in accordance with the invention is to recite the physical properties, such as length; primary structure; or charge, which are correlated with binding to a particular allele-specific HLA molecule or group of allele-specific HLA molecules. A further modality for defining peptide epitopes is to recite the physical properties of an HLA binding pocket, or properties shared by several allele-specific HLA binding pockets (*e.g.* pocket configuration and charge distribution) and reciting that the peptide epitope fits and binds to the pocket or pockets.

As will be apparent from the discussion below, other methods and embodiments are also contemplated. Further, novel synthetic peptides produced by any of the methods described herein are also part of the invention.

III. BRIEF DESCRIPTION OF THE FIGURES

Figure 1: Figure 1 provides a graph of total frequency of genotypes as a function of the number of PF candidate epitopes bound by HLA-A and B molecules, in an average population.

Figure 2: Figure 2 illustrates the position of peptide epitopes in an experimental model minigene construct.

IV. DETAILED DESCRIPTION OF THE INVENTION

The peptide epitopes and corresponding nucleic acid compositions of the present invention are useful for stimulating an immune response to HIV by stimulating the production of CTL or HTL responses. The peptide epitopes, which are derived directly or indirectly from native HIV protein amino acid sequences, are able to bind to HLA molecules and stimulate an immune response to HIV. The complete sequence of the HIV proteins to be analyzed can be obtained from Genbank. Peptide epitopes and analogs thereof can also be readily determined from sequence information that may subsequently

primary, secondary and tertiary peptide structure, and charge, that together form a site recognized by an immunoglobulin, T cell receptor or HLA molecule. Throughout this disclosure epitope and peptide are often used interchangeably. It is to be appreciated, however, that isolated or purified protein or peptide molecules larger than and comprising an epitope of the invention are still within the bounds of the invention.

"Human Leukocyte Antigen" or "HLA" is a human class I or class II Major Histocompatibility Complex (MHC) protein (*see, e.g., Stites, et al., IMMUNOLOGY, 8TH ED., Lange Publishing, Los Altos, CA (1994).*

An "HLA supertype or family", as used herein, describes sets of HLA molecules grouped on the basis of shared peptide-binding specificities. HLA class I molecules that share somewhat similar binding affinity for peptides bearing certain amino acid motifs are grouped into HLA supertypes. The terms HLA superfamily, HLA supertype family, HLA family, and HLA xx-like molecules (where xx denotes a particular HLA type), are synonyms.

Throughout this disclosure, results are expressed in terms of "IC₅₀'s." IC₅₀ is the concentration of peptide in a binding assay at which 50% inhibition of binding of a reference peptide is observed. Given the conditions in which the assays are run (*i.e.,* limiting HLA proteins and labeled peptide concentrations), these values approximate K_D values. Assays for determining binding are described in detail, *e.g.,* in PCT publications WO 94/20127 and WO 94/03205. It should be noted that IC₅₀ values can change, often dramatically, if the assay conditions are varied, and depending on the particular reagents used (*e.g.,* HLA preparation, *etc.*). For example, excessive concentrations of HLA molecules will increase the apparent measured IC₅₀ of a given ligand.

Alternatively, binding is expressed relative to a reference peptide. Although as a particular assay becomes more, or less, sensitive, the IC₅₀'s of the peptides tested may change somewhat, the binding relative to the reference peptide will not significantly change. For example, in an assay run under conditions such that the IC₅₀ of the reference peptide increases 10-fold, the IC₅₀ values of the test peptides will also shift approximately 10-fold. Therefore, to avoid ambiguities, the assessment of whether a peptide is a good, intermediate, weak, or negative binder is generally based on its IC₅₀, relative to the IC₅₀ of a standard peptide.

Binding may also be determined using other assay systems including those using: live cells (*e.g., Ceppellini et al., Nature 339:392, 1989; Christnick et al., Nature 352:67, 1991; Busch et al., Int. Immunol. 2:443, 1990; Hill et al., J. Immunol. 147:189, 1991; del*

Guercio *et al.*, *J. Immunol.* 154:685, 1995), cell free systems using detergent lysates (*e.g.*, Cerundolo *et al.*, *J. Immunol.* 21:2069, 1991), immobilized purified MHC (*e.g.*, Hill *et al.*, *J. Immunol.* 152, 2890, 1994; Marshall *et al.*, *J. Immunol.* 152:4946, 1994), ELISA systems (*e.g.*, Reay *et al.*, *EMBO J.* 11:2829, 1992), surface plasmon resonance (*e.g.*,
 5 Khilko *et al.*, *J. Biol. Chem.* 268:15425, 1993); high flux soluble phase assays (Hammer *et al.*, *J. Exp. Med.* 180:2353, 1994), and measurement of class I MHC stabilization or assembly (*e.g.*, Ljunggren *et al.*, *Nature* 346:476, 1990; Schumacher *et al.*, *Cell* 62:563, 1990; Townsend *et al.*, *Cell* 62:285, 1990; Parker *et al.*, *J. Immunol.* 149:1896, 1992).

As used herein, "high affinity" with respect to HLA class I molecules is defined as
 10 binding with an IC_{50} , or K_D value, of 50 nM or less; "intermediate affinity" is binding with an IC_{50} or K_D value of between about 50 and about 500 nM. "High affinity" with respect to binding to HLA class II molecules is defined as binding with an IC_{50} or K_D value of 100 nM or less; "intermediate affinity" is binding with an IC_{50} or K_D value of between about 100 and about 1000 nM.

15 The terms "identical" or percent "identity," in the context of two or more peptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues that are the same, when compared and aligned for maximum correspondence over a comparison window, as measured using a sequence comparison algorithm or by manual alignment and visual inspection.

20 An "immunogenic peptide" or "peptide epitope" is a peptide that comprises an allele-specific motif or supermotif such that the peptide will bind an HLA molecule and induce a CTL and/or HTL response. Thus, immunogenic peptides of the invention are capable of binding to an appropriate HLA molecule and thereafter inducing a cytotoxic T cell response, or a helper T cell response, to the antigen from which the immunogenic
 25 peptide is derived.

The phrases "isolated" or "biologically pure" refer to material which is substantially or essentially free from components which normally accompany the material as it is found in its native state. Thus, isolated peptides in accordance with the invention preferably do not contain materials normally associated with the peptides in their *in situ*
 30 environment.

"Major Histocompatibility Complex" or "MHC" is a cluster of genes that plays a role in control of the cellular interactions responsible for physiologic immune responses. In humans, the MHC complex is also known as the HLA complex. For a detailed

description of the MHC and HLA complexes, see, Paul, FUNDAMENTAL IMMUNOLOGY, 3RD ED., Raven Press, New York, 1993.

The term "motif" refers to the pattern of residues in a peptide of defined length, usually a peptide of from about 8 to about 13 amino acids for a class I HLA motif and from about 6 to about 25 amino acids for a class II HLA motif, which is recognized by a particular HLA molecule. Peptide motifs are typically different for each protein encoded by each human HLA allele and differ in the pattern of the primary and secondary anchor residues.

A "negative binding residue" or "deleterious residue" is an amino acid which, if present at certain positions (typically not primary anchor positions) in a peptide epitope, results in decreased binding affinity of the peptide for the peptide's corresponding HLA molecule.

Def's
The term "peptide" is used interchangeably with "oligopeptide" in the present specification to designate a series of residues, typically L-amino acids, connected one to the other, typically by peptide bonds between the α -amino and carboxyl groups of adjacent amino acids. The preferred CTL-inducing peptides of the invention are 13 residues or less in length and usually consist of between about 8 and about 11 residues, preferably 9 or 10 residues. The preferred HTL-inducing oligopeptides are less than about 50 residues in length and usually consist of between about 6 and about 30 residues, more usually between about 12 and 25, and often between about 15 and 20 residues.

"Pharmaceutically acceptable" refers to a non-toxic, inert, and/or physiologically compatible composition.

A "primary anchor residue" is an amino acid at a specific position along a peptide sequence which is understood to provide a contact point between the immunogenic peptide and the HLA molecule. One to three, usually two, primary anchor residues within a peptide of defined length generally defines a "motif" for an immunogenic peptide. These residues are understood to fit in close contact with peptide binding grooves of an HLA molecule, with their side chains buried in specific pockets of the binding grooves themselves. In one embodiment, for example, the primary anchor residues are located at position 2 (from the amino terminal position) and at the carboxyl terminal position of a 9-residue peptide epitope in accordance with the invention. The primary anchor positions for each motif and supermotif are set forth in Table 1. For example, analog peptides can be created by altering the presence or absence of particular

residues in these primary anchor positions. Such analogs are used to modulate the binding affinity of a peptide comprising a particular motif or supermotif.

“Promiscuous recognition” is where a distinct peptide is recognized by the same T cell clone in the context of various HLA molecules. Promiscuous recognition or binding is synonymous with cross-reactive binding.

A “protective immune response” or “therapeutic immune response” refers to a CTL and/or an HTL response to an antigen derived from an infectious agent or a tumor antigen, which prevents or at least partially arrests disease symptoms or progression. The immune response may also include an antibody response which has been facilitated by the stimulation of helper T cells.

The term “residue” refers to an amino acid or amino acid mimetic incorporated into an oligopeptide by an amide bond or amide bond mimetic.

A “secondary anchor residue” is an amino acid at a position other than a primary anchor position in a peptide which may influence peptide binding. A secondary anchor residue occurs at a significantly higher frequency amongst bound peptides than would be expected by random distribution of amino acids at one position. The secondary anchor residues are said to occur at “secondary anchor positions.” A secondary anchor residue can be identified as a residue which is present at a higher frequency among high or intermediate affinity binding peptides, or a residue otherwise associated with high or intermediate affinity binding. For example, analog peptides can be created by altering the presence or absence of particular residues in these secondary anchor positions. Such analogs are used to finely modulate the binding affinity of a peptide comprising a particular motif or supermotif.

A “subdominant epitope” is an epitope which evokes little or no response upon immunization with whole antigens which comprise the epitope, but for which a response can be obtained by immunization with an isolated peptide, and this response (unlike the case of cryptic epitopes) is detected when whole protein is used to recall the response *in vitro* or *in vivo*.

A “supermotif” is a peptide binding specificity shared by HLA molecules encoded by two or more HLA alleles. Preferably, a supermotif-bearing peptide is recognized with high or intermediate affinity (as defined herein) by two or more HLA antigens.

“Synthetic peptide” refers to a peptide that is not naturally occurring, but is man-made using such methods as chemical synthesis or recombinant DNA technology.

The nomenclature used to describe peptide compounds follows the conventional practice wherein the amino group is presented to the left (the N-terminus) and the carboxyl group to the right (the C-terminus) of each amino acid residue. When amino acid residue positions are referred to in a peptide epitope they are numbered in an amino to carboxyl direction with position one being the position closest to the amino terminal end of the epitope, or the peptide or protein of which it may be a part. In the formulae representing selected specific embodiments of the present invention, the amino- and carboxyl-terminal groups, although not specifically shown, are in the form they would assume at physiologic pH values, unless otherwise specified. In the amino acid structure formulae, each residue is generally represented by standard three letter or single letter designations. The L-form of an amino acid residue is represented by a capital single letter or a capital first letter of a three-letter symbol, and the D-form for those amino acids having D-forms is represented by a lower case single letter or a lower case three letter symbol. Glycine has no asymmetric carbon atom and is simply referred to as "Gly" or G. Symbols for the amino acids are shown below.

Single Letter Symbol	Three Letter Symbol	Amino Acids
A	Ala	Alanine
C	Cys	Cysteine
D	Asp	Aspartic Acid
E	Glu	Glutamic Acid
F	Phe	Phenylalanine
G	Gly	Glycine
H	His	Histidine
I	Ile	Isoleucine
K	Lys	Lysine
L	Leu	Leucine
M	Met	Methionine
N	Asn	Asparagine
P	Pro	Proline
Q	Gln	Glutamine
R	Arg	Arginine
S	Ser	Serine
T	Thr	Threonine
V	Val	Valine
W	Trp	Tryptophan
Y	Tyr	Tyrosine

IV.B. Stimulation of CTL and HTL responses

5 The mechanism by which T cells recognize antigens has been delineated during the past ten years. Based on our understanding of the immune system we have developed efficacious peptide epitope vaccine compositions that can induce a therapeutic or prophylactic immune response to HIV in a broad population. For an understanding of the value and efficacy of the claimed compositions, a brief review of immunology-related technology is provided.

10 A complex of an HLA molecule and a peptidic antigen acts as the ligand recognized by HLA-restricted T cells (Buus, S. *et al.*, *Cell* 47:1071, 1986; Babbitt, B. P. *et al.*, *Nature* 317:359, 1985; Townsend, A. and Bodmer, H., *Annu. Rev. Immunol.* 7:601,

1989; Germain, R. N., *Annu. Rev. Immunol.* 11:403, 1993). Through the study of single amino acid substituted antigen analogs and the sequencing of endogenously bound, naturally processed peptides, critical residues that correspond to motifs required for specific binding to HLA antigen molecules have been identified and are described herein and are set forth in Tables I, II, and III (see also, e.g., Southwood, *et al.*, *J. Immunol.* 160:3363, 1998; Rammensee, *et al.*, *Immunogenetics* 41:178, 1995; Rammensee *et al.*, SYFPEITHI, access via web at : <http://134.2.96.221/scripts.hlaserver.dll/home.htm>; Sette, A. and Sidney, J. *Curr. Opin. Immunol.* 10:478, 1998; Engelhard, V. H., *Curr. Opin. Immunol.* 6:13, 1994; Sette, A. and Grey, H. M., *Curr. Opin. Immunol.* 4:79, 1992; Sinigaglia, F. and Hammer, J. *Curr. Biol.* 6:52, 1994; Ruppert *et al.*, *Cell* 74:929-937, 1993; Kondo *et al.*, *J. Immunol.* 155:4307-4312, 1995; Sidney *et al.*, *J. Immunol.* 157:3480-3490, 1996; Sidney *et al.*, *Human Immunol.* 45:79-93, 1996; Sette, A. and Sidney, J. *Immunogenetics*, in press, 1999).

Furthermore, x-ray crystallographic analysis of HLA-peptide complexes has revealed pockets within the peptide binding cleft of HLA molecules which accommodate, in an allele-specific mode, residues borne by peptide ligands; these residues in turn determine the HLA binding capacity of the peptides in which they are present. (See, e.g., Madden, D.R. *Annu. Rev. Immunol.* 13:587, 1995; Smith, *et al.*, *Immunity* 4:203, 1996; Fremont *et al.*, *Immunity* 8:305, 1998; Stern *et al.*, *Structure* 2:245, 1994; Jones, E.Y. *Curr. Opin. Immunol.* 9:75, 1997; Brown, J. H. *et al.*, *Nature* 364:33, 1993; Guo, H. C. *et al.*, *Proc. Natl. Acad. Sci. USA* 90:8053, 1993; Guo, H. C. *et al.*, *Nature* 360:364, 1992; Silver, M. L. *et al.*, *Nature* 360:367, 1992; Matsumura, M. *et al.*, *Science* 257:927, 1992; Madden *et al.*, *Cell* 70:1035, 1992; Fremont, D. H. *et al.*, *Science* 257:919, 1992; Saper, M. A., Bjorkman, P. J. and Wiley, D. C., *J. Mol. Biol.* 219:277, 1991.)

Accordingly, the definition of class I and class II allele-specific HLA binding motifs, or class I or class II supermotifs allows identification of regions within a protein that have the potential of binding particular HLA antigen(s).

The present inventors have found that the correlation of binding affinity with immunogenicity, which is disclosed herein, is an important factor to be considered when evaluating candidate peptides. Thus, by a combination of motif searches and HLA-peptide binding assays, candidates for epitope-based vaccines have been identified. After determining their binding affinity, additional confirmatory work can be performed to select, amongst these vaccine candidates, epitopes with preferred characteristics in terms of population coverage, antigenicity, and immunogenicity.

Various strategies can be utilized to evaluate immunogenicity, including:

- 1) Evaluation of primary T cell cultures from normal individuals (*see, e.g.,* Wentworth, P. A. *et al.*, *Mol. Immunol.* 32:603, 1995; Celis, E. *et al.*, *Proc. Natl. Acad. Sci. USA* 91:2105, 1994; Tsai, V. *et al.*, *J. Immunol.* 158:1796, 1997; Kawashima, I. *et al.*, *Human Immunol.* 59:1, 1998); This procedure involves the stimulation of peripheral blood lymphocytes (PBL) from normal subjects with a test peptide in the presence of antigen presenting cells *in vitro* over a period of several weeks. T cells specific for the peptide become activated during this time and are detected using, *e.g.*, a ^{51}Cr -release assay involving peptide sensitized target cells.
- 2) Immunization of HLA transgenic mice (*see, e.g.,* Wentworth, P. A. *et al.*, *J. Immunol.* 26:97, 1996; Wentworth, P. A. *et al.*, *Int. Immunol.* 8:651, 1996; Alexander, J. *et al.*, *J. Immunol.* 159:4753, 1997); In this method, peptides in incomplete Freund's adjuvant are administered subcutaneously to HLA transgenic mice. Several weeks following immunization, splenocytes are removed and cultured *in vitro* in the presence of test peptide for approximately one week. Peptide-specific T cells are detected using, *e.g.*, a ^{51}Cr -release assay involving peptide sensitized target cells and target cells expressing endogenously generated antigen.
- 3) Demonstration of recall T cell responses from immune individuals who have effectively been vaccinated, recovered from infection, and/or from chronically infected patients (*see, e.g.,* Rehmann, B. *et al.*, *J. Exp. Med.* 181:1047, 1995; Doolan, D. L. *et al.*, *Immunity* 7:97, 1997; Bertoni, R. *et al.*, *J. Clin. Invest.* 100:503, 1997; Threlkeld, S. C. *et al.*, *J. Immunol.* 159:1648, 1997; Diepolder, H. M. *et al.*, *J. Virol.* 71:6011, 1997); In applying this strategy, recall responses are detected by culturing PBL from subjects that have been naturally exposed to the antigen, for instance through infection, and thus have generated an immune response "naturally", or from patients who were vaccinated against the infection. PBL from subjects are cultured *in vitro* for 1-2 weeks in the presence of test peptide plus antigen presenting cells (APC) to allow activation of "memory" T cells, as compared to "naive" T cells. At the end of the culture period, T cell activity is detected using assays for T cell activity including ^{51}Cr release involving peptide-sensitized targets, T cell proliferation, or lymphokine release.

The following describes the peptide epitopes and corresponding nucleic acids of the invention.

IV.C. Binding Affinity of Peptide Epitopes for HLA Molecules

As indicated herein, the large degree of HLA polymorphism is an important factor to be taken into account with the epitope-based approach to vaccine development. To address this factor, epitope selection encompassing identification of peptides capable of binding at high or intermediate affinity to multiple HLA molecules is preferably utilized, most preferably these epitopes bind at high or intermediate affinity to two or more allele-specific HLA molecules.

CTL-inducing peptides of interest for vaccine compositions preferably include those that have an IC_{50} or binding affinity value for class I HLA molecules of 500 nM or better (*i.e.*, the value is ≤ 500 nM). HTL-inducing peptides preferably include those that have an IC_{50} or binding affinity value for class II HLA molecules of 1000 nM or better, (*i.e.*, the value is $\leq 1,000$ nM). For example, peptide binding is assessed by testing the capacity of a candidate peptide to bind to a purified HLA molecule *in vitro*. Peptides exhibiting high or intermediate affinity are then considered for further analysis. Selected peptides are tested on other members of the supertype family. In preferred embodiments, peptides that exhibit cross-reactive binding are then used in cellular screening analyses or vaccines.

As disclosed herein, higher HLA binding affinity is correlated with greater immunogenicity. Greater immunogenicity can be manifested in several different ways. Immunogenicity corresponds to whether an immune response is elicited at all, and to the vigor of any particular response, as well as to the extent of a population in which a response is elicited. For example, a peptide might elicit an immune response in a diverse array of the population, yet in no instance produce a vigorous response. In accordance with these principles, close to 90% of high binding peptides have been found to be immunogenic, as contrasted with about 50% of the peptides which bind with intermediate affinity. Moreover, higher binding affinity peptides lead to more vigorous immunogenic responses. As a result, less peptide is required to elicit a similar biological effect if a high affinity binding peptide is used. Thus, in preferred embodiments of the invention, high affinity binding epitopes are particularly useful.

The relationship between binding affinity for HLA class I molecules and immunogenicity of discrete peptide epitopes on bound antigens has been determined for the first time in the art by the present inventors. The correlation between binding affinity and immunogenicity was analyzed in two different experimental approaches (*see, e.g.*,

Sette, *et al.*, *J. Immunol.* 153:5586-5592, 1994). In the first approach, the immunogenicity of potential epitopes ranging in HLA binding affinity over a 10,000-fold range was analyzed in HLA-A*0201 transgenic mice. In the second approach, the antigenicity of approximately 100 different hepatitis B virus (HBV)-derived potential epitopes, all carrying A*0201 binding motifs, was assessed by using PBL from acute hepatitis patients. Pursuant to these approaches, it was determined that an affinity threshold value of approximately 500 nM (preferably 50 nM or less) determines the capacity of a peptide epitope to elicit a CTL response. These data are true for class I binding affinity measurements for naturally processed peptides and for synthesized T cell epitopes. These data also indicate the important role of determinant selection in the shaping of T cell responses (*see, e.g.*, Schaeffer *et al. Proc. Natl. Acad. Sci. USA* 86:4649-4653, 1989).

An affinity threshold associated with immunogenicity in the context of HLA class II DR molecules has also been delineated (*see, e.g.*, Southwood *et al. J. Immunology* 160:3363-3373, 1998, and co-pending U.S.S.N. 09/009,953 filed 1/21/98). In order to define a biologically significant threshold of DR binding affinity, a database of the binding affinities of 32 DR-restricted epitopes for their restricting element (*i.e.*, the HLA molecule that binds the motif) was compiled. In approximately half of the cases (15 of 32 epitopes), DR restriction was associated with high binding affinities, *i.e.* binding affinity values of 100 nM or less. In the other half of the cases (16 of 32), DR restriction was associated with intermediate affinity (binding affinity values in the 100-1000 nM range). In only one of 32 cases was DR restriction associated with an IC_{50} of 1000 nM or greater. Thus, 1000 nM can be defined as an affinity threshold associated with immunogenicity in the context of DR molecules.

The binding affinity of peptides for HLA molecules can be determined as described in Example 1, below.

IV.D. Peptide Epitope Binding Motifs and Supermotifs

Through the study of single amino acid substituted antigen analogs and the sequencing of endogenously bound, naturally processed peptides, critical residues required for allele-specific binding to HLA molecules have been identified. The presence of these residues correlates with binding affinity for HLA molecules. The identification of motifs and/or supermotifs that correlate with high and intermediate affinity binding is an important issue with respect to the identification of immunogenic peptide epitopes for

the inclusion in a vaccine. Kast *et al.* (*J. Immunol.* 152:3904-3912, 1994) have shown that motif-bearing peptides account for 90% of the epitopes that bind to allele-specific HLA class I molecules. In this study all possible peptides of 9 amino acids in length and overlapping by eight amino acids (240 peptides), which cover the entire sequence of the E6 and E7 proteins of human papillomavirus type 16, were evaluated for binding to five allele-specific HLA molecules that are expressed at high frequency among different ethnic groups. This unbiased set of peptides allowed an evaluation of the predictive value of HLA class I motifs. From the set of 240 peptides, 22 peptides were identified that bound to an allele-specific HLA molecule with high or intermediate affinity. Of these 22 peptides, 20 (*i.e.* 91%) were motif-bearing. Thus, this study demonstrates the value of motifs for the identification of peptide epitopes for inclusion in a vaccine: application of motif-based identification techniques will identify about 90% of the potential epitopes in a target antigen protein sequence.

Such peptide epitopes are identified in the Tables described below.

Peptides of the present invention may also comprise epitopes that bind to MHC class II DR molecules. A greater degree of heterogeneity in both size and binding frame position of the motif, relative to the N and C termini of the peptide, exists for class II peptide ligands. This increased heterogeneity of HLA class II peptide ligands is due to the structure of the binding groove of the HLA class II molecule which, unlike its class I counterpart, is open at both ends. Crystallographic analysis of HLA class II DRB*0101-peptide complexes showed that the major energy of binding is contributed by peptide residues complexed with complementary pockets on the DRB*0101 molecules. An important anchor residue engages the deepest hydrophobic pocket (*see, e.g.,* Madden, D.R. *Ann. Rev. Immunol.* 13:587, 1995) and is referred to as position 1 (P1). P1 may represent the N-terminal residue of a class II binding peptide epitope, but more typically is flanked towards the N-terminus by one or more residues. Other studies have also pointed to an important role for the peptide residue in the 6th position towards the C-terminus, relative to P1, for binding to various DR molecules.

In the past few years evidence has accumulated to demonstrate that a large fraction of HLA class I and class II molecules can be classified into a relatively few supertypes, each characterized by largely overlapping peptide binding repertoires, and consensus structures of the main peptide binding pockets. Thus, peptides of the present invention are identified by any one of several HLA-specific amino acid motifs (*see, e.g.,* Tables I-III), or if the presence of the motif corresponds to the ability to bind several

allele-specific HLA antigens, a supermotif. The HLA molecules that bind to peptides that possess a particular amino acid supermotif are collectively referred to as an HLA "supertype."

The peptide motifs and supermotifs described below, and summarized in Tables I-III, provide guidance for the identification and use of peptide epitopes in accordance with the invention.

Examples of peptide epitopes bearing a respective supermotif or motif are included in Tables as designated in the description of each motif or supermotif below. The Tables include a binding affinity ratio listing for some of the peptide epitopes. The ratio may be converted to IC_{50} by using the following formula: IC_{50} of the standard peptide/ratio = IC_{50} of the test peptide (*i.e.*, the peptide epitope). The IC_{50} values of standard peptides used to determine binding affinities for Class I peptides are shown in Table IV. The IC_{50} values of standard peptides used to determine binding affinities for Class II peptides are shown in Table V. The peptides used as standards for the binding assays described herein are examples of standards; alternative standard peptides can also be used when performing binding studies.

To obtain the peptide epitope sequences listed in each Table, protein sequence data for all of the HIV-1 isolates present in the 1999 Los Alamos database (<http://hiv-web.lanl.gov>) were evaluated for the presence of the designated supermotif or motif. A listing of the strains is provided in Table XXVI. Nine HIV-1 structural and regulatory proteins, gag, pol, env, nef, rev, tat, vif, vpr, and vpu, were included in the analysis. Peptide epitopes were additionally evaluated on the basis of their conservancy (*i.e.*, the amount of variance) among the available protein sequences for each HIV antigen. A criterion for conservancy used to generate the peptides set out in Tables VII-XX requires that the entire sequence of an HLA class I binding peptide be totally conserved in 15% of the sequences available for a specific HIV antigen. Similarly, a criterion for conservancy requires that the entire 9-mer core region of an HLA class II binding peptide be totally conserved in 15% of the sequences available for a specific protein. The percent conservancy of the selected peptide epitopes is indicated on the Tables. The frequency, *i.e.* the number of sequences of the HIV protein antigen in which the totally conserved peptide sequence was identified, is also shown. The "pos" (position) column in the Tables designates the amino acid position in the HIV protein that corresponds to the first amino acid residue of the epitope. The "number of amino acids" indicates the number of residues in the epitope sequence.

HLA Class I Motifs Indicative of CTL Inducing Peptide Epitopes:

The primary anchor residues of the HLA class I peptide epitope supermotifs and motifs delineated below are summarized in Table I. The HLA class I motifs set out in Table I(a) are those most particularly relevant to the invention claimed here. Primary and secondary anchor positions are summarized in Table II. Allele-specific HLA molecules that comprise HLA class I supertype families are listed in Table VI. In some cases, peptide epitopes may be listed in both a motif and a supermotif Table. The relationship of a particular motif and respective supermotif is indicated in the description of the individual motifs.

IV.D.1. HLA-A1 supermotif

The HLA-A1 supermotif is characterized by the presence in peptide ligands of a small (T or S) or hydrophobic (L, I, V, or M) primary anchor residue in position 2, and an aromatic (Y, F, or W) primary anchor residue at the C-terminal position of the epitope. The corresponding family of HLA molecules that bind to the A1 supermotif (*i.e.*, the HLA-A1 supertype) is comprised of at least A*0101, A*2601, A*2602, A*2501, and A*3201 (*see, e.g.*, DiBrino, M. *et al.*, *J. Immunol.* 151:5930, 1993; DiBrino, M. *et al.*, *J. Immunol.* 152:620, 1994; Kondo, A. *et al.*, *Immunogenetics* 45:249, 1997). Other allele-specific HLA molecules predicted to be members of the A1 superfamily are shown in Table VI. Peptides binding to each of the individual HLA proteins can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

Representative peptide epitopes that comprise the A1 supermotif are set forth on the attached Table VII.

IV.D.2. HLA-A2 supermotif

Primary anchor specificities for allele-specific HLA-A2.1 molecules (*see, e.g.*, Falk *et al.*, *Nature* 351:290-296, 1991; Hunt *et al.*, *Science* 255:1261-1263, 1992; Parker *et al.*, *J. Immunol.* 149:3580-3587, 1992; Ruppert *et al.*, *Cell* 74:929-937, 1993) and cross-reactive binding among HLA-A2 and -A28 molecules have been described. (*See, e.g.*, Fruci *et al.*, *Human Immunol.* 38:187-192, 1993; Tanigaki *et al.*, *Human Immunol.* 39:155-162, 1994; Del Guercio *et al.*, *J. Immunol.* 154:685-693, 1995; Kast *et al.*, *J. Immunol.* 152:3904-3912, 1994 for reviews of relevant data.) These primary anchor

residues define the HLA-A2 supermotif; which presence in peptide ligands corresponds to the ability to bind several different HLA-A2 and -A28 molecules. The HLA-A2 supermotif comprises peptide ligands with L, I, V, M, A, T, or Q as a primary anchor residue at position 2 and L, I, V, M, A, or T as a primary anchor residue at the C-terminal position of the epitope.

The corresponding family of HLA molecules (*i.e.*, the HLA-A2 supertype that binds these peptides) is comprised of at least: A*0201, A*0202, A*0203, A*0204, A*0205, A*0206, A*0207, A*0209, A*0214, A*6802, and A*6901. Other allele-specific HLA molecules predicted to be members of the A2 superfamily are shown in Table VI. As explained in detail below, binding to each of the individual allele-specific HLA molecules can be modulated by substitutions at the primary anchor and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

Representative peptide epitopes that comprise an A2 supermotif are set forth on the attached Table VIII. The motifs comprising the primary anchor residues V, A, T, or Q at position 2 and L, I, V, A, or T at the C-terminal position are those most particularly relevant to the invention claimed herein.

IV.D.3. HLA-A3 supermotif

The HLA-A3 supermotif is characterized by the presence in peptide ligands of A, L, I, V, M, S, or, T as a primary anchor at position 2, and a positively charged residue, R or K, at the C-terminal position of the epitope, *e.g.*, in position 9 of 9-mers (*see, e.g.*, Sidney *et al.*, *Hum. Immunol.* 45:79, 1996). Exemplary members of the corresponding family of HLA molecules (the HLA-A3 supertype) that bind the A3 supermotif include at least A*0301, A*1101, A*3101, A*3301, and A*6801. Other allele-specific HLA molecules predicted to be members of the A3 supertype are shown in Table VI. As explained in detail below, peptide binding to each of the individual allele-specific HLA proteins can be modulated by substitutions of amino acids at the primary and/or secondary anchor positions of the peptide, preferably choosing respective residues specified for the supermotif.

Representative peptide epitopes that comprise the A3 supermotif are set forth on the attached Table IX.

IV.D.4. HLA-A24 supermotif

The HLA-A24 supermotif is characterized by the presence in peptide ligands of an aromatic (F, W, or Y) or hydrophobic aliphatic (L, I, V, M, or T) residue as a primary anchor in position 2, and Y, F, W, L, I, or M as primary anchor at the C-terminal position of the epitope (*see, e.g.*, Sette and Sidney, *Immunogenetics*, in press, 1999). The corresponding family of HLA molecules that bind to the A24 supermotif (*i.e.*, the A24 supertype) includes at least A*2402, A*3001, and A*2301. Other allele-specific HLA molecules predicted to be members of the A24 supertype are shown in Table VI. Peptide binding to each of the allele-specific HLA molecules can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

Representative peptide epitopes that comprise the A24 supermotif are set forth on the attached Table X.

15 IV.D.5. HLA-B7 supermotif

The HLA-B7 supermotif is characterized by peptides bearing proline in position 2 as a primary anchor, and a hydrophobic or aliphatic amino acid (L, I, V, M, A, F, W, or Y) as the primary anchor at the C-terminal position of the epitope. The corresponding family of HLA molecules that bind the B7 supermotif (*i.e.*, the HLA-B7 supertype) is comprised of at least twenty six HLA-B proteins including: B*0702, B*0703, B*0704, B*0705, B*1508, B*3501, B*3502, B*3503, B*3504, B*3505, B*3506, B*3507, B*3508, B*5101, B*5102, B*5103, B*5104, B*5105, B*5301, B*5401, B*5501, B*5502, B*5601, B*5602, B*6701, and B*7801 (*see, e.g.*, Sidney, *et al.*, *J. Immunol.* 154:247, 1995; Barber, *et al.*, *Curr. Biol.* 5:179, 1995; Hill, *et al.*, *Nature* 360:434, 1992; Rammensee, *et al.*, *Immunogenetics* 41:178, 1995 for reviews of relevant data). Other allele-specific HLA molecules predicted to be members of the B7 supertype are shown in Table VI. As explained in detail below, peptide binding to each of the individual allele-specific HLA proteins can be modulated by substitutions at the primary and/or secondary anchor positions of the peptide, preferably choosing respective residues specified for the supermotif.

Representative peptide epitopes that comprise the B7 supermotif are set forth on the attached Table XI.

IV.D.6. HLA-B27 supermotif

The HLA-B27 supermotif is characterized by the presence in peptide ligands of a positively charged (R, H, or K) residue as a primary anchor at position 2, and a hydrophobic (F, Y, L, W, M, I, A, or V) residue as a primary anchor at the C-terminal position of the epitope (*see, e.g.,* Sidney and Sette, *Immunogenetics*, in press, 1999). Exemplary members of the corresponding family of HLA molecules that bind to the B27 supermotif (*i.e.,* the B27 supertype) include at least B*1401, B*1402, B*1509, B*2702, B*2703, B*2704, B*2705, B*2706, B*3801, B*3901, B*3902, and B*7301. Other allele-specific HLA molecules predicted to be members of the B27 supertype are shown in Table VI. Peptide binding to each of the allele-specific HLA molecules can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

Representative peptide epitopes that comprise the B27 supermotif are set forth on the attached Table XII.

IV.D.7. HLA-B44 supermotif

The HLA-B44 supermotif is characterized by the presence in peptide ligands of negatively charged (D or E) residues as a primary anchor in position 2, and hydrophobic residues (F, W, Y, L, I, M, V, or A) as a primary anchor at the C-terminal position of the epitope (*see, e.g.,* Sidney et al., *Immunol. Today* 17:261, 1996). Exemplary members of the corresponding family of HLA molecules that bind to the B44 supermotif (*i.e.,* the B44 supertype) include at least: B*1801, B*1802, B*3701, B*4001, B*4002, B*4006, B*4402, B*4403, and B*4006. Peptide binding to each of the allele-specific HLA molecules can be modulated by substitutions at primary and/or secondary anchor positions; preferably choosing respective residues specified for the supermotif.

IV.D.8. HLA-B58 supermotif

The HLA-B58 supermotif is characterized by the presence in peptide ligands of a small aliphatic residue (A, S, or T) as a primary anchor residue at position 2, and an aromatic or hydrophobic residue (F, W, Y, L, I, V, M, or A) as a primary anchor residue at the C-terminal position of the epitope (*see, e.g.,* Sidney and Sette, *Immunogenetics*, in press, 1999 for reviews of relevant data). Exemplary members of the corresponding family of HLA molecules that bind to the B58 supermotif (*i.e.,* the B58 supertype) include at least: B*1516, B*1517, B*5701, B*5702, and B*5801. Other allele-specific

HLA molecules predicted to be members of the B58 supertype are shown in Table VI. Peptide binding to each of the allele-specific HLA molecules can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

- 5 Representative peptide epitopes that comprise the B58 supermotif are set forth on the attached Table XIII.

IV.D.9. HLA-B62 supermotif

- 10 The HLA-B62 supermotif is characterized by the presence in peptide ligands of the polar aliphatic residue Q or a hydrophobic aliphatic residue (L, V, M, I, or P) as a primary anchor in position 2, and a hydrophobic residue (F, W, Y, M, I, V, L, or A) as a primary anchor at the C-terminal position of the epitope (*see, e.g.*, Sidney and Sette, *Immunogenetics*, in press, 1999). Exemplary members of the corresponding family of HLA molecules that bind to the B62 supermotif (*i.e.*, the B62 supertype) include at least:
- 15 B*1501, B*1502, B*1513, and B5201. Other allele-specific HLA molecules predicted to be members of the B62 supertype are shown in Table VI. Peptide binding to each of the allele-specific HLA molecules can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

- 20 Representative peptide epitopes that comprise the B62 supermotif are set forth on the attached Table XIV.

IV.D.10. HLA-A1 motif

- 25 The HLA-A1 motif is characterized by the presence in peptide ligands of T, S, or M as a primary anchor residue at position 2 and the presence of Y as a primary anchor residue at the C-terminal position of the epitope. An alternative allele-specific A1 motif is characterized by a primary anchor residue at position 3 rather than position 2. This motif is characterized by the presence of D, E, A, or S as a primary anchor residue in position 3, and a Y as a primary anchor residue at the C-terminal position of the epitope
- 30 (*see, e.g.*, DiBrino *et al.*, *J. Immunol.*, 152:620, 1994; Kondo *et al.*, *Immunogenetics* 45:249, 1997; and Kubo *et al.*, *J. Immunol.* 152:3913, 1994 for reviews of relevant data). Peptide binding to HLA A1 can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the motif.

Representative peptide epitopes that comprise either A1 motif are set forth on the attached Table XV. Those epitopes comprising T, S, or M at position 2 and Y at the C-terminal position are also included in the listing of HLA-A1 supermotif-bearing peptide epitopes listed in Table VII, as these residues are a subset of the A1 supermotif primary anchors.

IV.D.11. HLA-A*0201 motif

An HLA-A2*0201 motif was determined to be characterized by the presence in peptide ligands of L or M as a primary anchor residue in position 2, and L or V as a primary anchor residue at the C-terminal position of a 9-residue peptide (*see, e.g., Falk et al., Nature* 351:290-296, 1991) and was further found to comprise an I at position 2 and I or A at the C-terminal position of a nine amino acid peptide (*see, e.g., Hunt et al., Science* 255:1261-1263, March 6, 1992; Parker *et al., J. Immunol.* 149:3580-3587, 1992). The A*0201 allele-specific motif has also been defined by the present inventors to additionally comprise V, A, T, or Q as a primary anchor residue at position 2, and M or T as a primary anchor residue at the C-terminal position of the epitope (*see, e.g., Kast et al., J. Immunol.* 152:3904-3912, 1994). Thus, the HLA-A*0201 motif comprises peptide ligands with L, I, V, M, A, T, or Q as primary anchor residues at position 2 and L, I, V, M, A, or T as a primary anchor residue at the C-terminal position of the epitope. The preferred and tolerated residues that characterize the primary anchor positions of the HLA-A*0201 motif are identical to the residues describing the A2 supermotif. (For reviews of relevant data, *see, e.g., Del Guercio et al., J. Immunol.* 154:685-693, 1995; Ruppert *et al., Cell* 74:929-937, 1993; Sidney *et al., Immunol. Today* 17:261-266, 1996; Sette and Sidney, *Curr. Opin. in Immunol.* 10:478-482, 1998). Secondary anchor residues that characterize the A*0201 motif have additionally been defined (*see, e.g., Ruppert et al., Cell* 74:929-937, 1993). These are shown in Table II. Peptide binding to HLA-A*0201 molecules can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the motif.

Representative peptide epitopes that comprise an A*0201 motif are set forth on the attached Table VIII. The A*0201 motifs comprising the primary anchor residues V, A, T, or Q at position 2 and L, I, V, A, or T at the C-terminal position are those most particularly relevant to the invention claimed herein.

IV.D.12. HLA-A3 motif

The HLA-A3 motif is characterized by the presence in peptide ligands of L, M, V, I, S, A, T, F, C, G, or D as a primary anchor residue at position 2, and the presence of K, Y, R, H, F, or A as a primary anchor residue at the C-terminal position of the epitope (see, e.g., DiBrino *et al.*, *Proc. Natl. Acad. Sci USA* 90:1508, 1993; and Kubo *et al.*, *J. Immunol.* 152:3913-3924, 1994). Peptide binding to HLA-A3 can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the motif.

Representative peptide epitopes that comprise the A3 motif are set forth on the attached Table XVI. Those peptide epitopes that also comprise the A3 supermotif are also listed in Table IX. The A3 supermotif primary anchor residues comprise a subset of the A3- and A11-allele specific motif primary anchor residues.

IV.D.13. HLA-A11 motif

The HLA-A11 motif is characterized by the presence in peptide ligands of V, T, M, L, I, S, A, G, N, C, D, or F as a primary anchor residue in position 2, and K, R, Y, or H as a primary anchor residue at the C-terminal position of the epitope (see, e.g., Zhang *et al.*, *Proc. Natl. Acad. Sci USA* 90:2217-2221, 1993; and Kubo *et al.*, *J. Immunol.* 152:3913-3924, 1994). Peptide binding to HLA-A11 can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the motif.

Representative peptide epitopes that comprise the A11 motif are set forth on the attached Table XVII; peptide epitopes comprising the A3 allele-specific motif are also present in this Table because of the extensive overlap between the A3 and A11 motif primary anchor specificities. Further, those peptide epitopes that comprise the A3 supermotif are also listed in Table IX.

IV.D.14. HLA-A24 motif

The HLA-A24 motif is characterized by the presence in peptide ligands of Y, F, W, or M as a primary anchor residue in position 2, and F, L, I, or W as a primary anchor residue at the C-terminal position of the epitope (see, e.g., Kondo *et al.*, *J. Immunol.* 155:4307-4312, 1995; and Kubo *et al.*, *J. Immunol.* 152:3913-3924, 1994). Peptide binding to HLA-A24 molecules can be modulated by substitutions at primary and/or

secondary anchor positions; preferably choosing respective residues specified for the motif.

Representative peptide epitopes that comprise the A24 motif are set forth on the attached Table XVIII. These epitopes are also listed in Table X, which sets forth HLA-
 5 A24-supermotif-bearing peptide epitopes, as the primary anchor residues characterizing the A24 allele-specific motif comprise a subset of the A24 supermotif primary anchor residues.

Motifs Indicative of Class II HTL Inducing Peptide Epitopes

10 The primary and secondary anchor residues of the HLA class II peptide epitope supermotifs and motifs delineated below are summarized in Table III.

IV.D.15. HLA DR-1-4-7 supermotif

Motifs have also been identified for peptides that bind to three common HLA
 15 class II allele-specific HLA molecules: HLA DRB1*0401, DRB1*0101, and DRB1*0701 (see, e.g., the review by Southwood *et al. J. Immunology* 160:3363-3373,1998). Collectively, the common residues from these motifs delineate the HLA DR-1-4-7 supermotif. Peptides that bind to these DR molecules carry a supermotif characterized by a large aromatic or hydrophobic residue (Y, F, W, L, I, V, or M) as a primary anchor
 20 residue in position 1, and a small, non-charged residue (S, T, C, A, P, V, I, L, or M) as a primary anchor residue in position 6 of a 9-mer core region. Allele-specific secondary effects and secondary anchors for each of these HLA types have also been identified (Southwood *et al., supra*). These are set forth in Table III. Peptide binding to HLA-DRB1*0401, DRB1*0101, and/or DRB1*0701 can be modulated by substitutions at
 25 primary and/or secondary anchor positions, preferably choosing respective residues specified for the supermotif.

Conserved 9-mer core regions (*i.e.*, sequences that are 100% conserved in at least
 15% of the HIV antigen protein sequences used for the analysis), comprising the DR-1-4-7 supermotif, wherein position 1 of the supermotif is at position 1 of the nine-residue
 30 core, are set forth in Table XIXa. Respective exemplary peptide epitopes of 15 amino acid residues in length, each of which comprise a conserved nine residue core, are also shown in section "a" of the Table. Cross-reactive binding data for exemplary 15-residue supermotif-bearing peptides are shown in Table XIXb.

IV.D.16. HLA DR3 motifs

Two alternative motifs (*i.e.*, submotifs) characterize peptide epitopes that bind to HLA-DR3 molecules (*see, e.g.*, Geluk *et al.*, *J. Immunol.* 152:5742, 1994). In the first motif (submotif DR3A) a large, hydrophobic residue (L, I, V, M, F, or Y) is present in anchor position 1 of a 9-mer core, and D is present as an anchor at position 4, towards the carboxyl terminus of the epitope. As in other class II motifs, core position 1 may or may not occupy the peptide N-terminal position.

The alternative DR3 submotif provides for lack of the large, hydrophobic residue at anchor position 1, and/or lack of the negatively charged or amide-like anchor residue at position 4, by the presence of a positive charge at position 6 towards the carboxyl terminus of the epitope. Thus, for the alternative allele-specific DR3 motif (submotif DR3B): L, I, V, M, F, Y, A, or Y is present at anchor position 1; D, N, Q, E, S, or T is present at anchor position 4; and K, R, or H is present at anchor position 6. Peptide binding to HLA-DR3 can be modulated by substitutions at primary and/or secondary anchor positions, preferably choosing respective residues specified for the motif.

Conserved 9-mer core regions (*i.e.*, those sequences that are 100% conserved in at least 15% of the HIV antigen protein sequences used for the analysis) corresponding to a nine residue sequence comprising the DR3A submotif (wherein position 1 of the motif is at position 1 of the nine residue core) are set forth in Table XXa. Respective exemplary peptide epitopes of 15 amino acid residues in length, each of which comprise a conserved nine residue core, are also shown in Table XXa. Table XXb shows binding data of exemplary DR3 submotif A-bearing peptides.

Conserved 9-mer core regions (*i.e.*, those that are 100% conserved in at least 15% of the HIV antigen protein sequences used for the analysis) comprising the DR3B submotif and respective exemplary 15-mer peptides comprising the DR3 submotif-B epitope are set forth in Table XXc. Table XXd shows binding data of exemplary DR3 submotif B-bearing peptides.

Each of the HLA class I or class II peptide epitopes set out in the Tables herein are deemed singly to be an inventive aspect of this application. Further, it is also an inventive aspect of this application that each peptide epitope may be used in combination with any other peptide epitope.

IV.E. Enhancing Population Coverage of the Vaccine

Vaccines that have broad population coverage are preferred because they are more commercially viable and generally applicable to the most people. Broad population coverage can be obtained using the peptides of the invention (and nucleic acid compositions that encode such peptides) through selecting peptide epitopes that bind to HLA alleles which, when considered in total, are present in most of the population. Table XXI lists the overall frequencies of the HLA class I supertypes in various ethnicities (Table XXIa) and the combined population coverage achieved by the A2-, A3-, and B7-supertypes (Table XXIb). The A2-, A3-, and B7 supertypes are each present on the average of over 40% in each of these five major ethnic groups. Coverage in excess of 80% is achieved with a combination of these supermotifs. These results suggest that effective and non-ethnically biased population coverage is achieved upon use of a limited number of cross-reactive peptides. Although the population coverage reached with these three main peptide specificities is high, coverage can be expanded to reach 95% population coverage and above, and more easily achieve truly multispecific responses upon use of additional supermotif or allele-specific motif bearing peptides.

The B44-, A1-, and A24-supertypes are each present, on average, in a range from 25% to 40% in these major ethnic populations (Table XXIa). While less prevalent overall, the B27-, B58-, and B62 supertypes are each present with a frequency >25% in at least one major ethnic group (Table XXIa). Table XXIb summarizes the estimated prevalence of combinations of HLA supertypes that have been identified in five major ethnic groups. The incremental coverage obtained by the inclusion of A1-, A24-, and B44-supertypes to the A2, A3, and B7 coverage and coverage obtained with all of the supertypes described herein, is shown.

The data presented herein, together with the previous definition of the A2-, A3-, and B7-supertypes, indicates that all antigens, with the possible exception of A29, B8, and B46, can be classified into a total of nine HLA supertypes. By including epitopes from the six most frequent supertypes, an average population coverage of 99% is obtained for five major ethnic groups..

IV.F. Immune Response-Stimulating Peptide Analogs

In general, CTL and HTL responses are not directed against all possible epitopes. Rather, they are restricted to a few "immunodominant" determinants (Zinkernagel, *et al.*, *Adv. Immunol.* 27:5159, 1979; Bennink, *et al.*, *J. Exp. Med.* 168:19351939, 1988; Rawle,

et al., *J. Immunol.* 146:3977-3984, 1991). It has been recognized that immunodominance (Benacerraf, et al., *Science* 175:273-279, 1972) could be explained by either the ability of a given epitope to selectively bind a particular HLA protein (determinant selection theory) (Vitiello, et al., *J. Immunol.* 131:1635, 1983); Rosenthal, et al., *Nature* 267:156-158, 1977), or to be selectively recognized by the existing TCR (T cell receptor) specificities (repertoire theory) (Klein, J., *IMMUNOLOGY, THE SCIENCE OF SELF/NONSELF DISCRIMINATION*, John Wiley & Sons, New York, pp. 270-310, 1982). It has been demonstrated that additional factors, mostly linked to processing events, can also play a key role in dictating, beyond strict immunogenicity, which of the many potential determinants will be presented as immunodominant (Sercarz, et al., *Annu. Rev. Immunol.* 11:729-766, 1993).

The concept of dominance and subdominance is relevant to immunotherapy of both infectious diseases and cancer. For example, in the course of chronic viral disease, recruitment of subdominant epitopes can be important for successful clearance of the infection, especially if dominant CTL or HTL specificities have been inactivated by functional tolerance, suppression, mutation of viruses and other mechanisms (Franco, et al., *Curr. Opin. Immunol.* 7:524-531, 1995). In the case of cancer and tumor antigens, CTLs recognizing at least some of the highest binding affinity peptides might be functionally inactivated. Lower binding affinity peptides are preferentially recognized at these times, and may therefore be preferred in therapeutic or prophylactic anti-cancer vaccines.

In particular, it has been noted that a significant number of epitopes derived from known non-viral tumor associated antigens (TAA) bind HLA class I with intermediate affinity (IC_{50} in the 50-500 nM range). For example, it has been found that 8 of 15 known TAA peptides recognized by tumor infiltrating lymphocytes (TIL) or CTL bound in the 50-500 nM range. (These data are in contrast with estimates that 90% of known viral antigens were bound by HLA class I molecules with IC_{50} of 50 nM or less, while only approximately 10% bound in the 50-500 nM range (Sette, et al., *J. Immunol.*, 153:558-5592, 1994). In the cancer setting this phenomenon is probably due to elimination or functional inhibition of the CTL recognizing several of the highest binding peptides, presumably because of T cell tolerization events.

Without intending to be bound by theory, it is believed that because T cells to dominant epitopes may have been clonally deleted, selecting subdominant epitopes may allow existing T cells to be recruited, which will then lead to a therapeutic or prophylactic

response. However, the binding of HLA molecules to subdominant epitopes is often less vigorous than to dominant ones. Accordingly, there is a need to be able to modulate the binding affinity of particular immunogenic epitopes for one or more HLA molecules, and thereby to modulate the immune response elicited by the peptide, for example to prepare analog peptides which elicit a more vigorous response. This ability would greatly enhance the usefulness of peptide epitope-based vaccines and therapeutic agents.

Although peptides with suitable cross-reactivity among all alleles of a superfamily are identified by the screening procedures described above, cross-reactivity is not always as complete as possible, and in certain cases procedures to increase cross-reactivity of peptides can be useful; moreover, such procedures can also be used to modify other properties of the peptides such as binding affinity or peptide stability. Having established the general rules that govern cross-reactivity of peptides for HLA alleles within a given motif or supermotif, modification (*i.e.*, analoging) of the structure of peptides of particular interest in order to achieve broader (or otherwise modified) HLA binding capacity can be performed. More specifically, peptides which exhibit the broadest cross-reactivity patterns, can be produced in accordance with the teachings herein. The present concepts related to analog generation are set forth in greater detail in co-pending U.S.S.N. 09/226,775 filed 1/6/99.

In brief, the strategy employed utilizes the motifs or supermotifs which correlate with binding to certain HLA molecules. The motifs or supermotifs are defined by having primary anchors, and in many cases secondary anchors. Analog peptides can be created by substituting amino acid residues at primary anchor, secondary anchor, or at primary and secondary anchor positions. Generally, analogs are made for peptides that already bear a motif or supermotif. Preferred secondary anchor residues of supermotifs and motifs that have been defined for HLA class I and class II binding peptides are shown in Tables II and III, respectively.

For a number of the motifs or supermotifs in accordance with the invention, residues are defined which are deleterious to binding to allele-specific HLA molecules or members of HLA supertypes that bind the respective motif or supermotif (Tables II and III). Accordingly, removal of such residues that are detrimental to binding can be performed in accordance with the present invention. For example, in the case of the A3 supertype, when all peptides that have such deleterious residues are removed from the population of peptides used in the analysis, the incidence of cross-reactivity increased from 22% to 37% (*see, e.g.*, Sidney, J. *et al.*, *Hu. Immunol.* 45:79, 1996). Thus, one

strategy to improve the cross-reactivity of peptides within a given supermotif is simply to delete one or more of the deleterious residues present within a peptide and substitute a small "neutral" residue such as Ala (that may not influence T cell recognition of the peptide). An enhanced likelihood of cross-reactivity is expected if, together with
 5 elimination of detrimental residues within a peptide, "preferred" residues associated with high affinity binding to an allele-specific HLA molecule or to multiple HLA molecules within a superfamily are inserted.

To ensure that an analog peptide, when used as a vaccine, actually elicits a CTL response to the native epitope *in vivo* (or, in the case of class II epitopes, elicits helper T
 10 cells that cross-react with the wild type peptides), the analog peptide may be used to immunize T cells *in vitro* from individuals of the appropriate HLA allele. Thereafter, the immunized cells' capacity to induce lysis of wild type peptide sensitized target cells is evaluated. It will be desirable to use as antigen presenting cells, cells that have been
 15 either infected, or transfected with the appropriate genes, or, in the case of class II epitopes only, cells that have been pulsed with whole protein antigens, to establish whether endogenously produced antigen is also recognized by the relevant T cells.

Another embodiment of the invention is to create analogs of weak binding peptides, to thereby ensure adequate numbers of cross-reactive cellular binders. Class I
 20 binding peptides exhibiting binding affinities of 500-5000 nM, and carrying an acceptable but suboptimal primary anchor residue at one or both positions can be "fixed" by substituting preferred anchor residues in accordance with the respective supertype. The analog peptides can then be tested for crossbinding activity.

Another embodiment for generating effective peptide analogs involves the substitution of residues that have an adverse impact on peptide stability or solubility in,
 25 *e.g.*, a liquid environment. This substitution may occur at any position of the peptide epitope. For example, a cysteine (C) can be substituted out in favor of α -amino butyric acid. Due to its chemical nature, cysteine has the propensity to form disulfide bridges and sufficiently alter the peptide structurally so as to reduce binding capacity. Substituting α -amino butyric acid for C not only alleviates this problem, but actually improves binding
 30 and crossbinding capability in certain instances (*see, e.g.*, the review by Sette *et al.*, In: Persistent Viral Infections, Eds. R. Ahmed and I. Chen, John Wiley & Sons, England, 1999). Substitution of cysteine with α -amino butyric acid may occur at any residue of a peptide epitope, *i.e.* at either anchor or non-anchor positions.

IV.G. Computer Screening of Protein Sequences from Disease-Related Antigens for Supermotif- or Motif-Bearing Peptides

In order to identify supermotif- or motif-bearing epitopes in a target antigen, a native protein sequence, *e.g.*, a tumor-associated antigen, or sequences from an infectious organism, or a donor tissue for transplantation, is screened using a means for computing, such as an intellectual calculation or a computer, to determine the presence of a supermotif or motif within the sequence. The information obtained from the analysis of native peptide can be used directly to evaluate the status of the native peptide or may be utilized subsequently to generate the peptide epitope.

Computer programs that allow the rapid screening of protein sequences for the occurrence of the subject supermotifs or motifs are encompassed by the present invention; as are programs that permit the generation of analog peptides. These programs are implemented to analyze any identified amino acid sequence or operate on an unknown sequence and simultaneously determine the sequence and identify motif-bearing epitopes thereof; analogs can be simultaneously determined as well. Generally, the identified sequences will be from a pathogenic organism or a tumor-associated peptide. For example, the target molecules considered herein include, without limitation, the gag, pol, env, nef, rev, tat, vif, vpr, and vpu proteins of HIV.

In cases where the sequence of multiple variants of the same target protein are available, potential peptide epitopes can also be selected on the basis of their conservancy. For example, a criterion for conservancy may define that the entire sequence of an HLA class I binding peptide or the entire 9-mer core of a class II binding peptide, be conserved in a designated percentage, of the sequences evaluated for a specific protein antigen.

Because HIV rapidly mutates thereby resulting in the generation of virus strains that have divergent amino acid sequences, an alternative method of selecting epitopes for inclusion in a vaccine composition is employed herein. In order to target a broad population that may be infected with a number of different strains, it is preferable to include in vaccine compositions epitopes that are representative of HIV antigen sequences from different HIV strains. For example, by selecting 5 epitopes from the same region, each of which is 20% conserved among HIV strains, the combination of the epitopes achieves 100% coverage of that region. As appreciated by those in the art, lower or higher degrees of conservancy, such as the 15% conservancy used for identification of

the epitopes set out in Tables VII-XX, can be employed as appropriate for a given antigenic target.

It is important that the selection criteria utilized for prediction of peptide binding are as accurate as possible, to correlate most efficiently with actual binding. Prediction of peptides that bind, for example, to HLA-A*0201, on the basis of the presence of the appropriate primary anchors, is positive at about a 30% rate (*see, e.g.,* Ruppert, J. *et al. Cell* 74:929, 1993). However, by extensively analyzing peptide-HLA binding data disclosed herein, data in related patent applications, and data in the art, the present inventors have developed a number of allele-specific polynomial algorithms that dramatically increase the predictive value over identification on the basis of the presence of primary anchor residues alone. These algorithms take into account not only the presence or absence of primary anchors, but also consider the positive or deleterious presence of secondary anchor residues (to account for the impact of different amino acids at different positions). The algorithms are essentially based on the premise that the overall affinity (or ΔG) of peptide-HLA interactions can be approximated as a linear polynomial function of the type:

$$\Delta G = a_{1i} \times a_{2i} \times a_{3i} \dots \times a_{ni}$$

where a_{ji} is a coefficient that represents the effect of the presence of a given amino acid (j) at a given position (i) along the sequence of a peptide of n amino acids. An important assumption of this method is that the effects at each position are essentially independent of each other. This assumption is justified by studies that demonstrated that peptides are bound to HLA molecules and recognized by T cells in essentially an extended conformation. Derivation of specific algorithm coefficients has been described, for example, in Gulukota, K. *et al., J. Mol. Biol.* 267:1258, 1997.

Additional methods to identify preferred peptide sequences, which also make use of specific motifs, include the use of neural networks and molecular modeling programs (*see, e.g.,* Milik *et al., Nature Biotechnology* 16:753, 1998; Altuvia *et al., Hum. Immunol.* 58:1, 1997; Altuvia *et al., J. Mol. Biol.* 249:244, 1995; Buus, S. *Curr. Opin. Immunol.* 11:209-213, 1999; Brusic, V. *et al., Bioinformatics* 14:121-130, 1998; Parker *et al., J. Immunol.* 152:163, 1993; Meister *et al., Vaccine* 13:581, 1995; Hammer *et al., J. Exp. Med.* 180:2353, 1994; Sturniolo *et al., Nature Biotechnol.* 17:555 1999).

For example, it has been shown that in sets of A*0201 motif-bearing peptides containing at least one preferred secondary anchor residue while avoiding the presence of

any deleterious secondary anchor residues, 69% of the peptides will bind A*0201 with an IC_{50} less than 500 nM (Ruppert, J. *et al. Cell* 74:929, 1993). These algorithms are also flexible in that cut-off scores may be adjusted to select sets of peptides with greater or lower predicted binding properties, as desired.

5 In utilizing computer screening to identify peptide epitopes, a protein sequence or translated sequence may be analyzed using software developed to search for motifs, for example the "FINDPATTERNS" program (Devereux, *et al. Nucl. Acids Res.* 12:387-395, 1984) or MotifSearch 1.4 software program (D. Brown, San Diego, CA) to identify potential peptide sequences containing appropriate HLA binding motifs. The identified
10 peptides can be scored using customized polynomial algorithms to predict their capacity to bind specific HLA class I or class II alleles. As appreciated by one of ordinary skill in the art, a large array of computer programming software and hardware options are available in the relevant art which can be employed to implement the motifs of the invention in order to evaluate (*e.g.*, without limitation, to identify epitopes, identify
15 epitope concentration per peptide length, or to generate analogs) known or unknown peptide sequences.

In accordance with the procedures described above, HIV peptide epitopes and analogs thereof that are able to bind HLA supertype groups or allele-specific HLA molecules have been identified (Tables VII-XX).

20 IV.H. Preparation of Peptide Epitopes

Peptides in accordance with the invention can be prepared synthetically, by recombinant DNA technology or chemical synthesis, or from natural sources such as native tumors or pathogenic organisms. Peptide epitopes may be synthesized individually
25 or as polyepitopic peptides. Although the peptide will preferably be substantially free of other naturally occurring host cell proteins and fragments thereof, in some embodiments the peptides may be synthetically conjugated to native fragments or particles.

The peptides in accordance with the invention can be a variety of lengths, and either in their neutral (uncharged) forms or in forms which are salts. The peptides in
30 accordance with the invention are either free of modifications such as glycosylation, side chain oxidation, or phosphorylation; or they contain these modifications, subject to the condition that modifications do not destroy the biological activity of the peptides as described herein.

Desirably, the peptide epitope will be as small as possible while still maintaining substantially all of the immunologic activity of the native protein. When possible, it may be desirable to optimize HLA class I binding peptide epitopes of the invention to a length of about 8 to about 13 amino acid residues, preferably 9 to 10. HLA class II binding peptide epitopes may be optimized to a length of about 6 to about 30 amino acids in length, preferably to between about 13 and about 20 residues. Preferably, the peptide epitopes are commensurate in size with endogenously processed pathogen-derived peptides or tumor cell peptides that are bound to the relevant HLA molecules.

The identification and preparation of peptides of other lengths can also be carried out using the techniques described herein. Moreover, it is preferred to identify native peptide regions that contain a high concentration of class I and/or class II epitopes. Such a sequence is generally selected on the basis that it contains the greatest number of epitopes per amino acid length. It is to be appreciated that epitopes can be present in a frame-shifted manner, *e.g.* a 10 amino acid long peptide could contain two 9 amino acid long epitopes and one 10 amino acid long epitope; upon intracellular processing, each epitope can be exposed and bound by an HLA molecule upon administration of such a peptide. This larger, preferably multi-epitopic, peptide can be generated synthetically, recombinantly, or via cleavage from the native source.

The peptides of the invention can be prepared in a wide variety of ways. For the preferred relatively short size, the peptides can be synthesized in solution or on a solid support in accordance with conventional techniques. Various automatic synthesizers are commercially available and can be used in accordance with known protocols. (*See*, for example, Stewart & Young, SOLID PHASE PEPTIDE SYNTHESIS, 2D. ED., Pierce Chemical Co., 1984). Further, individual peptide epitopes can be joined using chemical ligation to produce larger peptides that are still within the bounds of the invention.

Alternatively, recombinant DNA technology can be employed wherein a nucleotide sequence which encodes an immunogenic peptide of interest is inserted into an expression vector, transformed or transfected into an appropriate host cell and cultivated under conditions suitable for expression. These procedures are generally known in the art, as described generally in Sambrook *et al.*, MOLECULAR CLONING, A LABORATORY MANUAL, Cold Spring Harbor Press, Cold Spring Harbor, New York (1989). Thus, recombinant polypeptides which comprise one or more peptide sequences of the invention can be used to present the appropriate T cell epitope.

The nucleotide coding sequence for peptide epitopes of the preferred lengths contemplated herein can be synthesized by chemical techniques, for example, the phosphotriester method of Matteucci, *et al.*, *J. Am. Chem. Soc.* 103:3185 (1981). Peptide analogs can be made simply by substituting the appropriate and desired nucleic acid base(s) for those that encode the native peptide sequence; exemplary nucleic acid substitutions are those that encode an amino acid defined by the motifs/super motifs herein. The coding sequence can then be provided with appropriate linkers and ligated into expression vectors commonly available in the art, and the vectors used to transform suitable hosts to produce the desired fusion protein. A number of such vectors and suitable host systems are now available. For expression of the fusion proteins, the coding sequence will be provided with operably linked start and stop codons, promoter and terminator regions and usually a replication system to provide an expression vector for expression in the desired cellular host. For example, promoter sequences compatible with bacterial hosts are provided in plasmids containing convenient restriction sites for insertion of the desired coding sequence. The resulting expression vectors are transformed into suitable bacterial hosts. Of course, yeast, insect or mammalian cell hosts may also be used, employing suitable vectors and control sequences.

IV.I. Assays to Detect T-Cell Responses

Once HLA binding peptides are identified, they can be tested for the ability to elicit a T-cell response. The preparation and evaluation of motif-bearing peptides are described in PCT publications WO 94/20127 and WO 94/03205. Briefly, peptides comprising epitopes from a particular antigen are synthesized and tested for their ability to bind to the appropriate HLA proteins. These assays may involve evaluating the binding of a peptide of the invention to purified HLA class I molecules in relation to the binding of a radioiodinated reference peptide. Alternatively, cells expressing empty class I molecules (*i.e.* lacking peptide therein) may be evaluated for peptide binding by immunofluorescent staining and flow microfluorimetry. Other assays that may be used to evaluate peptide binding include peptide-dependent class I assembly assays and/or the inhibition of CTL recognition by peptide competition. Those peptides that bind to the class I molecule, typically with an affinity of 500 nM or less, are further evaluated for their ability to serve as targets for CTLs derived from infected or immunized individuals, as well as for their capacity to induce primary *in vitro* or *in vivo* CTL responses that can

give rise to CTL populations capable of reacting with selected target cells associated with a disease. Corresponding assays are used for evaluation of HLA class II binding peptides. HLA class II motif-bearing peptides that are shown to bind, typically at an affinity of 1000 nM or less, are further evaluated for the ability to stimulate HTL responses.

5 Conventional assays utilized to detect T cell responses include proliferation assays, lymphokine secretion assays, direct cytotoxicity assays, and limiting dilution assays. For example, antigen-presenting cells that have been incubated with a peptide can be assayed for the ability to induce CTL responses in responder cell populations. Antigen-presenting cells can be normal cells such as peripheral blood mononuclear cells
10 or dendritic cells. Alternatively, mutant non-human mammalian cell lines that are deficient in their ability to load class I molecules with internally processed peptides and that have been transfected with the appropriate human class I gene, may be used to test for the capacity of the peptide to induce *in vitro* primary CTL responses.

Peripheral blood mononuclear cells (PBMCs) may be used as the responder cell
15 source of CTL precursors. The appropriate antigen-presenting cells are incubated with peptide, after which the peptide-loaded antigen-presenting cells are then incubated with the responder cell population under optimized culture conditions. Positive CTL activation can be determined by assaying the culture for the presence of CTLs that kill radio-labeled target cells, both specific peptide-pulsed targets as well as target cells
20 expressing endogenously processed forms of the antigen from which the peptide sequence was derived.

More recently, a method has been devised which allows direct quantification of antigen-specific T cells by staining with Fluorescein-labelled HLA tetrameric complexes (Altman, J. D. *et al.*, *Proc. Natl. Acad. Sci. USA* 90:10330, 1993; Altman, J. D. *et al.*,
25 *Science* 274:94, 1996). Other relatively recent technical developments include staining for intracellular lymphokines, and interferon release assays or ELISPOT assays. Tetramer staining, intracellular lymphokine staining and ELISPOT assays all appear to be at least 10-fold more sensitive than more conventional assays (Lalvani, A. *et al.*, *J. Exp. Med.* 186:859, 1997; Dunbar, P. R. *et al.*, *Curr. Biol.* 8:413, 1998; Murali-Krishna, K. *et al.*, *Immunity* 8:177, 1998).
30 *al.*, *Immunity* 8:177, 1998).

HTL activation may also be assessed using such techniques known to those in the art such as T cell proliferation and secretion of lymphokines, *e.g.* IL-2 (*see, e.g.* Alexander *et al.*, *Immunity* 1:751-761, 1994).

Alternatively, immunization of HLA transgenic mice can be used to determine immunogenicity of peptide epitopes. Several transgenic mouse models including mice with human A2.1, A11 (which can additionally be used to analyze HLA-A3 epitopes), and B7 alleles have been characterized and others (*e.g.*, transgenic mice for HLA-A1 and A24) are being developed. HLA-DR1 and HLA-DR3 mouse models have also been developed. Additional transgenic mouse models with other HLA alleles may be generated as necessary. Mice may be immunized with peptides emulsified in Incomplete Freund's Adjuvant and the resulting T cells tested for their capacity to recognize peptide-pulsed target cells and target cells transfected with appropriate genes. CTL responses may be analyzed using cytotoxicity assays described above. Similarly, HTL responses may be analyzed using such assays as T cell proliferation or secretion of lymphokines.

Exemplary immunogenic peptide epitopes are set out in Table XXIII.

IV.J. Use of Peptide Epitopes as Diagnostic Agents and for Evaluating Immune Responses

HLA class I and class II binding peptides as described herein can be used, in one embodiment of the invention, as reagents to evaluate an immune response. The immune response to be evaluated may be induced by using as an immunogen any agent that may result in the production of antigen-specific CTLs or HTLs that recognize and bind to the peptide epitope(s) to be employed as the reagent. The peptide reagent need not be used as the immunogen. Assay systems that may be used for such an analysis include relatively recent technical developments such as tetramers, staining for intracellular lymphokines and interferon release assays, or ELISPOT assays.

For example, a peptide of the invention may be used in a tetramer staining assay to assess peripheral blood mononuclear cells for the presence of antigen-specific CTLs following exposure to a pathogen or immunogen. The HLA-tetrameric complex is used to directly visualize antigen-specific CTLs (*see, e.g.*, Ogg *et al.*, *Science* 279:2103-2106, 1998; and Altman *et al.*, *Science* 174:94-96, 1996) and determine the frequency of the antigen-specific CTL population in a sample of peripheral blood mononuclear cells. A tetramer reagent using a peptide of the invention may be generated as follows: A peptide that binds to an HLA molecule is refolded in the presence of the corresponding HLA heavy chain and β_2 -microglobulin to generate a trimolecular complex. The complex is biotinylated at the carboxyl terminal end of the heavy chain at a site that was previously

engineered into the protein. Tetramer formation is then induced by the addition of streptavidin. By means of fluorescently labeled streptavidin, the tetramer can be used to stain antigen-specific cells. The cells may then be identified, for example, by flow cytometry. Such an analysis may be used for diagnostic or prognostic purposes.

5 Peptides of the invention may also be used as reagents to evaluate immune recall responses. (see, *e.g.*, Bertoni *et al.*, *J. Clin. Invest.* 100:503-513, 1997 and Penna *et al.*, *J. Exp. Med.* 174:1565-1570, 1991.) For example, patient PBMC samples from individuals infected with HIV may be analyzed for the presence of antigen-specific CTLs or HTLs using specific peptides. A blood sample containing mononuclear cells may be evaluated
10 by cultivating the PBMCs and stimulating the cells with a peptide of the invention. After an appropriate cultivation period, the expanded cell population may be analyzed, for example, for CTL or for HTL activity.

The peptides may also be used as reagents to evaluate the efficacy of a vaccine. PBMCs obtained from a patient vaccinated with an immunogen may be analyzed using,
15 for example, either of the methods described above. The patient is HLA typed, and peptide epitope reagents that recognize the allele-specific molecules present in that patient are selected for the analysis. The immunogenicity of the vaccine is indicated by the presence of HIV epitope-specific CTLs and/or HTLs in the PBMC sample.

The peptides of the invention may also be used to make antibodies, using
20 techniques well known in the art (see, *e.g.* *CURRENT PROTOCOLS IN IMMUNOLOGY*, Wiley/Greene, NY; and *Antibodies A Laboratory Manual* Harlow, Harlow and Lane, Cold Spring Harbor Laboratory Press, 1989), which may be useful as reagents to diagnose HIV infection. Such antibodies include those that recognize a peptide in the context of an HLA molecule, *i.e.*, antibodies that bind to a peptide-MHC complex.

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IV.K. Vaccine Compositions

Vaccines that contain an immunogenically effective amount of one or more peptides as described herein are a further embodiment of the invention. Once appropriately immunogenic epitopes have been defined, they can be delivered by various
30 means, herein referred to as "vaccine" compositions. Such vaccine compositions can include, for example, lipopeptides (*e.g.*, Vitiello, A. *et al.*, *J. Clin. Invest.* 95:341, 1995), peptide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres (see, *e.g.*, Eldridge, *et al.*, *Molec. Immunol.* 28:287-294, 1991; Alonso *et al.*, *Vaccine* 12:299-306, 1994; Jones *et al.*, *Vaccine* 13:675-681, 1995), peptide

compositions contained in immune stimulating complexes (ISCOMS) (*see, e.g.,* Takahashi *et al.*, *Nature* 344:873-875, 1990; Hu *et al.*, *Clin Exp Immunol.* 113:235-243, 1998), multiple antigen peptide systems (MAPs) (*see e.g.,* Tam, J. P., *Proc. Natl. Acad. Sci. U.S.A.* 85:5409-5413, 1988; Tam, J.P., *J. Immunol. Methods* 196:17-32, 1996), viral delivery vectors (Perkus, M. E. *et al.*, In: *Concepts in vaccine development*, Kaufmann, S. H. E., ed., p. 379, 1996; Chakrabarti, S. *et al.*, *Nature* 320:535, 1986; Hu, S. L. *et al.*, *Nature* 320:537, 1986; Kieny, M.-P. *et al.*, *AIDS Bio/Technology* 4:790, 1986; Top, F. H. *et al.*, *J. Infect. Dis.* 124:148, 1971; Chanda, P. K. *et al.*, *Virology* 175:535, 1990), particles of viral or synthetic origin (*e.g.,* Kofler, N. *et al.*, *J. Immunol. Methods.* 192:25, 1996; Eldridge, J. H. *et al.*, *Sem. Hematol.* 30:16, 1993; Falo, L. D., Jr. *et al.*, *Nature Med.* 7:649, 1995), adjuvants (Warren, H. S., Vogel, F. R., and Chedid, L. A. *Annu. Rev. Immunol.* 4:369, 1986; Gupta, R. K. *et al.*, *Vaccine* 11:293, 1993), liposomes (Reddy, R. *et al.*, *J. Immunol.* 148:1585, 1992; Rock, K. L., *Immunol. Today* 17:131, 1996), or, naked or particle absorbed cDNA (Ulmer, J. B. *et al.*, *Science* 259:1745, 1993; Robinson, H. L., Hunt, L. A., and Webster, R. G., *Vaccine* 11:957, 1993; Shiver, J. W. *et al.*, In: *Concepts in vaccine development*, Kaufmann, S. H. E., ed., p. 423, 1996; Cease, K. B., and Berzofsky, J. A., *Annu. Rev. Immunol.* 12:923, 1994 and Eldridge, J. H. *et al.*, *Sem. Hematol.* 30:16, 1993). Toxin-targeted delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

Furthermore, vaccines in accordance with the invention encompass compositions of one or more of the claimed peptide(s). The peptide(s) can be individually linked to its own carrier; alternatively, the peptide(s) can exist as a homopolymer or heteropolymer of active peptide units. Such a polymer has the advantage of increased immunological reaction and, where different peptide epitopes are used to make up the polymer, the additional ability to induce antibodies and/or CTLs that react with different antigenic determinants of the pathogenic organism or tumor-related peptide targeted for an immune response. The composition may be a naturally occurring region of an antigen or may be prepared, *e.g.,* recombinantly or by chemical synthesis.

Furthermore, useful carriers that can be used with vaccines of the invention are well known in the art, and include, *e.g.,* thyroglobulin, albumins such as human serum albumin, tetanus toxoid, polyamino acids such as poly L-lysine, poly L-glutamic acid, influenza, hepatitis B virus core protein, and the like. The vaccines can contain a physiologically tolerable (*i.e.,* acceptable) diluent such as water, or saline, preferably

phosphate buffered saline. The vaccines also typically include an adjuvant. Adjuvants such as incomplete Freund's adjuvant, aluminum phosphate, aluminum hydroxide, or alum are examples of materials well known in the art. Additionally, as disclosed herein, CTL responses can be primed by conjugating peptides of the invention to lipids, such as tripalmitoyl-S-glycerylcysteinylserine (P₃CSS).

As disclosed in greater detail herein, upon immunization with a peptide composition in accordance with the invention, via injection, aerosol, oral, transdermal, transmucosal, intrapleural, intrathecal, or other suitable routes, the immune system of the host responds to the vaccine by producing large amounts of CTLs and/or HTLs specific for the desired antigen. Consequently, the host becomes at least partially immune to later infection, or at least partially resistant to developing an ongoing chronic infection, or derives at least some therapeutic benefit when the antigen was tumor-associated.

In some instances it may be desirable to combine the class I peptide vaccines of the invention with vaccines which induce or facilitate neutralizing antibody responses to the target antigen of interest, particularly to viral envelope antigens. A preferred embodiment of such a composition comprises class I and class II epitopes in accordance with the invention. An alternative embodiment of such a composition comprises a class I and/or class II epitope in accordance with the invention, along with a PADRE™ (Epimmune, San Diego, CA) molecule (described, for example, in U.S. Patent Number 5,736,142). Furthermore, any of these embodiments can be administered as a nucleic acid mediated modality.

The vaccine compositions of the invention may also be used in combination with antiviral drugs such as interferon- α .

For therapeutic or prophylactic immunization purposes, the peptides of the invention can also be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus, for example, as a vector to express nucleotide sequences that encode the peptides of the invention. Upon introduction into an acutely or chronically infected host or into a non-infected host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits a host CTL and/or HTL response. Vaccinia vectors and methods useful in immunization protocols are described in, *e.g.*, U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover *et al.*, *Nature* 351:456-460 (1991). A wide variety of

other vectors useful for therapeutic administration or immunization of the peptides of the invention, *e.g.* adeno and adeno-associated virus vectors, retroviral vectors, *Salmonella typhi* vectors, detoxified anthrax toxin vectors, and the like, will be apparent to those skilled in the art from the description herein.

5 Antigenic peptides are used to elicit a CTL and/or HTL response *ex vivo*, as well. The resulting CTL or HTL cells, can be used to treat chronic infections, or tumors in patients that do not respond to other conventional forms of therapy, or will not respond to a therapeutic vaccine peptide or nucleic acid in accordance with the invention. *Ex vivo* CTL or HTL responses to a particular antigen (infectious or tumor-associated antigen) are
10 induced by incubating in tissue culture the patient's, or genetically compatible, CTL or HTL precursor cells together with a source of antigen-presenting cells (APC), such as dendritic cells, and the appropriate immunogenic peptide. After an appropriate incubation time (typically about 7-28 days), in which the precursor cells are activated and expanded into effector cells, the cells are infused back into the patient, where they will
15 destroy (CTL) or facilitate destruction (HTL) of their specific target cell (an infected cell or a tumor cell). Transfected dendritic cells may also be used as antigen presenting cells. Alternatively, dendritic cells are transfected, *e.g.*, with a minigene construct in accordance with the invention, in order to elicit immune responses. Minigenes will be discussed in greater detail in a following section.

20 Vaccine compositions may also be administered *in vivo* in combination with dendritic cell mobilization whereby loading of dendritic cells occurs *in vivo*.

DNA or RNA encoding one or more of the peptides of the invention can also be administered to a patient. This approach is described, for instance, in Wolff *et. al.*, *Science* 247:1465 (1990) as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566;
25 5,739,118; 5,736,524; 5,679,647; WO 98/04720; and in more detail below. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivacaine, polymers, peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (*see, e.g.*, U.S. Patent No. 5,922,687).

30 Preferably, the following principles are utilized when selecting an array of epitopes for inclusion in a polyepitopic composition for use in a vaccine, or for selecting discrete epitopes to be included in a vaccine and/or to be encoded by nucleic acids such as a minigene. Exemplary epitopes that may be utilized in a vaccine to treat or prevent HIV infection are set out in Tables XXXVII and XXXVIII. It is preferred that each of the following principles are balanced in order to make the selection. The multiple epitopes to

be incorporated in a given vaccine composition may be, but need not be, contiguous in sequence in the native antigen from which the epitopes are derived.

1.) Epitopes are selected which, upon administration, mimic immune responses that have been observed to be correlated with HIV clearance. For HLA Class I this includes 3-4 epitopes that come from at least one antigen of HIV. For HLA Class II a similar rationale is employed; again 3-4 epitopes are selected from at least one HIV antigen (*see e.g.*, Rosenberg *et al.*, *Science* 278:1447-1450).

2.) Epitopes are selected that have the requisite binding affinity established to be correlated with immunogenicity: for HLA Class I an IC_{50} of 500 nM or less, or for Class II an IC_{50} of 1000 nM or less.

3.) Sufficient supermotif bearing-peptides, or a sufficient array of allele-specific motif-bearing peptides, are selected to give broad population coverage. For example, it is preferable to have at least 80% population coverage. A Monte Carlo analysis, a statistical evaluation known in the art, can be employed to assess the breadth, or redundancy of, population coverage.

4.) When selecting epitopes from cancer-related antigens it is often preferred to select analogs because the patient may have developed tolerance to the native epitope. When selecting epitopes for infectious disease-related antigens it is preferable to select either native or analoged epitopes. Of particular relevance for infectious disease vaccines (but for cancer-related vaccines as well), are epitopes referred to as "nested epitopes." Nested epitopes occur where at least two epitopes overlap in a given peptide sequence. A peptide comprising "transcendent nested epitopes" is a peptide that has both HLA class I and HLA class II epitopes in it.

When providing nested epitopes, it is preferable to provide a sequence that has the greatest number of epitopes per provided sequence. Preferably, one avoids providing a peptide that is any longer than the amino terminus of the amino terminal epitope and the carboxyl terminus of the carboxyl terminal epitope in the peptide. When providing a longer peptide sequence, such as a sequence comprising nested epitopes, it is important to screen the sequence in order to insure that it does not have pathological or other deleterious biological properties.

5.) When creating a minigene, as disclosed in greater detail in the following section, an objective is to generate the smallest peptide possible that encompasses the epitopes of interest. The principles employed are similar, if not the same as those employed when selecting a peptide comprising nested epitopes. Furthermore, upon

determination of the nucleic acid sequence to be provided as a minigene, the peptide encoded thereby is analyzed to determine whether any "junctional epitopes" have been created. A junctional epitope is an actual binding epitope, as predicted, *e.g.*, by motif analysis, that only exists because two discrete peptide sequences are encoded directly next to each other. Junctional epitopes are generally to be avoided because the recipient may generate an immune response to that non-native epitope. Of particular concern is a junctional epitope that is a "dominant epitope." A dominant epitope may lead to such a zealous response that immune responses to other epitopes are diminished or suppressed.

10 IV.K.1. Minigene Vaccines

~~Due to~~ A growing body of experimental evidence demonstrates that a number of different approaches are available which allow simultaneous delivery of multiple epitopes. Nucleic acids encoding the peptides of the invention are a particularly useful embodiment of the invention. Epitopes for inclusion in a minigene are preferably selected according to the guidelines set forth in the previous section. A preferred means of administering nucleic acids encoding the peptides of the invention uses minigene constructs encoding a peptide comprising one or multiple epitopes of the invention. The use of multi-epitope minigenes is described below and in, *e.g.*, co-pending application U.S.S.N. 09/311,784; Ishioka *et al.*, *J. Immunol.* 162:3915-3925, 1999; An, L. and Whitton, J. L., *J. Virol.* 71:2292, 1997; Thomson, S. A. *et al.*, *J. Immunol.* 157:822, 1996; Whitton, J. L. *et al.*, *J. Virol.* 67:348, 1993; Hanke, R. *et al.*, *Vaccine* 16:426, 1998. For example, a multi-epitope DNA plasmid encoding nine dominant HLA-A*0201- and A11-restricted epitopes derived from the polymerase, envelope, and core proteins of HBV and human immunodeficiency virus (HIV), the PADRE™ universal helper T cell (HTL) epitope, and an endoplasmic reticulum-translocating signal sequence was engineered. Immunization of HLA transgenic mice with this plasmid construct resulted in strong CTL induction responses against the nine epitopes tested, similar to those observed with a lipopeptide of known immunogenicity in humans, and significantly greater than immunization in oil-based adjuvants. Moreover, the immunogenicity of DNA-encoded epitopes *in vivo* correlated with the *in vitro* responses of specific CTL lines against target cells transfected with the DNA plasmid. Thus, these data show that the minigene served to both: 1.) generate a CTL response and 2.) that the induced CTLs recognized cells expressing the

5 encoded epitopes. A similar approach may be used to develop minigenes encoding HIV epitopes.

For example, to create a DNA sequence encoding the selected epitopes (minigene) for expression in human cells, the amino acid sequences of the epitopes may be reverse translated. A human codon usage table can be used to guide the codon choice for each amino acid. These epitope-encoding DNA sequences may be directly adjoined, so that when translated, a continuous polypeptide sequence is created. To optimize expression and/or immunogenicity, additional elements can be incorporated into the minigene design. Examples of amino acid sequences that can be reverse translated and included in the minigene sequence include: HLA class I epitopes, HLA class II epitopes, a ubiquitination signal sequence, and/or an endoplasmic reticulum targeting signal. In addition, HLA presentation of CTL and HTL epitopes may be improved by including synthetic (*e.g.* poly-alanine) or naturally-occurring flanking sequences adjacent to the CTL or HTL epitopes; these larger peptides comprising the epitope(s) are within the scope of the invention.

The minigene sequence may be converted to DNA by assembling oligonucleotides that encode the plus and minus strands of the minigene. Overlapping oligonucleotides (30-100 bases long) may be synthesized, phosphorylated, purified and annealed under appropriate conditions using well known techniques. The ends of the oligonucleotides can be joined, for example, using T4 DNA ligase. This synthetic minigene, encoding the epitope polypeptide, can then be cloned into a desired expression vector.

Standard regulatory sequences well known to those of skill in the art are preferably included in the vector to ensure expression in the target cells. Several vector elements are desirable: a promoter with a down-stream cloning site for minigene insertion; a polyadenylation signal for efficient transcription termination; an *E. coli* origin of replication; and an *E. coli* selectable marker (*e.g.* ampicillin or kanamycin resistance). Numerous promoters can be used for this purpose, *e.g.*, the human cytomegalovirus (hCMV) promoter. See, *e.g.*, U.S. Patent Nos. 5,580,859 and 5,589,466 for other suitable promoter sequences.

Additional vector modifications may be desired to optimize minigene expression and immunogenicity. In some cases, introns are required for efficient gene expression, and one or more synthetic or naturally-occurring introns could be incorporated into the transcribed region of the minigene. The inclusion of mRNA stabilization sequences and

sequences for replication in mammalian cells may also be considered for increasing minigene expression.

Once an expression vector is selected, the minigene is cloned into the polylinker region downstream of the promoter. This plasmid is transformed into an appropriate *E. coli* strain, and DNA is prepared using standard techniques. The orientation and DNA sequence of the minigene, as well as all other elements included in the vector, are confirmed using restriction mapping and DNA sequence analysis. Bacterial cells harboring the correct plasmid can be stored as a master cell bank and a working cell bank.

In addition, immunostimulatory sequences (ISSs or CpGs) appear to play a role in the immunogenicity of DNA vaccines. These sequences may be included in the vector, outside the minigene coding sequence, if desired to enhance immunogenicity.

Article In some embodiments, a bi-cistronic expression vector which allows production of both the minigene-encoded epitopes and a second protein (included to enhance or decrease immunogenicity) can be used. Examples of proteins or polypeptides that could beneficially enhance the immune response if co-expressed include cytokines (e.g., IL-2, IL-12, GM-CSF), cytokine-inducing molecules (e.g., LeIF), costimulatory molecules, or for HTL responses, pan-DR binding proteins (PADRE™, Epimmune, San Diego, CA). Helper (HTL) epitopes can be joined to intracellular targeting signals and expressed separately from expressed CTL epitopes; this allows direction of the HTL epitopes to a cell compartment different than that of the CTL epitopes. If required, this could facilitate more efficient entry of HTL epitopes into the HLA class II pathway, thereby improving HTL induction. In contrast to HTL or CTL induction, specifically decreasing the immune response by co-expression of immunosuppressive molecules (e.g. TGF-β) may be beneficial in certain diseases.

Therapeutic quantities of plasmid DNA can be produced for example, by fermentation in *E. coli*, followed by purification. Aliquots from the working cell bank are used to inoculate growth medium, and grown to saturation in shaker flasks or a bioreactor according to well known techniques. Plasmid DNA can be purified using standard bioseparation technologies such as solid phase anion-exchange resins supplied by QIAGEN, Inc. (Valencia, California). If required, supercoiled DNA can be isolated from the open circular and linear forms using gel electrophoresis or other methods.

Purified plasmid DNA can be prepared for injection using a variety of formulations. The simplest of these is reconstitution of lyophilized DNA in sterile

phosphate-buffer saline (PBS). This approach, known as "naked DNA," is currently being used for intramuscular (IM) administration in clinical trials. To maximize the immunotherapeutic effects of minigene DNA vaccines, an alternative method for formulating purified plasmid DNA may be desirable. A variety of methods have been described, and new techniques may become available. Cationic lipids, glycolipids, and fusogenic liposomes can also be used in the formulation (see, *e.g.*, as described by WO 93/24640; Mannino & Gould-Fogerite, *BioTechniques* 6(7): 682 (1988); U.S. Pat No. 5,279,833; WO 91/06309; and Felgner, *et al.*, *Proc. Nat'l Acad. Sci. USA* 84:7413 (1987). In addition, peptides and compounds referred to collectively as protective, interactive, non-condensing compounds (PINC) could also be complexed to purified plasmid DNA to influence variables such as stability, intramuscular dispersion, or trafficking to specific organs or cell types.

Target cell sensitization can be used as a functional assay for expression and HLA class I presentation of minigene-encoded CTL epitopes. For example, the plasmid DNA is introduced into a mammalian cell line that is suitable as a target for standard CTL chromium release assays. The transfection method used will be dependent on the final formulation. Electroporation can be used for "naked" DNA, whereas cationic lipids allow direct *in vitro* transfection. A plasmid expressing green fluorescent protein (GFP) can be co-transfected to allow enrichment of transfected cells using fluorescence activated cell sorting (FACS). These cells are then chromium-51 (^{51}Cr) labeled and used as target cells for epitope-specific CTL lines; cytolysis, detected by ^{51}Cr release, indicates both production of, and HLA presentation of, minigene-encoded CTL epitopes. Expression of HTL epitopes may be evaluated in an analogous manner using assays to assess HTL activity.

In vivo immunogenicity is a second approach for functional testing of minigene DNA formulations. Transgenic mice expressing appropriate human HLA proteins are immunized with the DNA product. The dose and route of administration are formulation dependent (*e.g.*, IM for DNA in PBS, intraperitoneal (IP) for lipid-complexed DNA). Twenty-one days after immunization, splenocytes are harvested and restimulated for one week in the presence of peptides encoding each epitope being tested. Thereafter, for CTL effector cells, assays are conducted for cytolysis of peptide-loaded, ^{51}Cr -labeled target cells using standard techniques. Lysis of target cells that were sensitized by HLA loaded with peptide epitopes, corresponding to minigene-encoded epitopes, demonstrates DNA

vaccine function for *in vivo* induction of CTLs. Immunogenicity of HTL epitopes is evaluated in transgenic mice in an analogous manner.

Alternatively, the nucleic acids can be administered using ballistic delivery as described, for instance, in U.S. Patent No. 5,204,253. Using this technique, particles
5 comprised solely of DNA are administered. In a further alternative embodiment, DNA can be adhered to particles, such as gold particles.

IV.K.2. Combinations of CTL Peptides with Helper Peptides

Vaccine compositions comprising the peptides of the present invention, or analogs
10 thereof, which have immunostimulatory activity may be modified to provide desired attributes, such as improved serum half life, or to enhance immunogenicity.

For instance, the ability of a peptide to induce CTL activity can be enhanced by linking the peptide to a sequence which contains at least one epitope that is capable of inducing a T helper cell response. The use of T helper epitopes in conjunction with CTL
15 epitopes to enhance immunogenicity is illustrated, for example, in the co-pending applications U.S.S.N. 08/820,360, U.S.S.N. 08/197,484, and U.S.S.N. 08/464,234.

Particularly preferred CTL epitope/HTL epitope conjugates are linked by a spacer molecule. The spacer is typically comprised of relatively small, neutral molecules, such as amino acids or amino acid mimetics, which are substantially uncharged under
20 physiological conditions. The spacers are typically selected from, *e.g.*, Ala, Gly, or other neutral spacers of nonpolar amino acids or neutral polar amino acids. It will be understood that the optionally present spacer need not be comprised of the same residues and thus may be a hetero- or homo-oligomer. When present, the spacer will usually be at least one or two residues, more usually three to six residues. Alternatively, the CTL
25 peptide may be linked to the T helper peptide without a spacer.

The CTL peptide epitope may be linked to the T helper peptide epitope either directly or via a spacer either at the amino or carboxy terminus of the CTL peptide. The amino terminus of either the immunogenic peptide or the T helper peptide may be acylated. The HTL peptide epitopes used in the invention can be modified in the same
30 manner as CTL peptides. For instance, they may be modified to include D-amino acids or be conjugated to other molecules such as lipids, proteins, sugars and the like.

In certain embodiments, the T helper peptide is one that is recognized by T helper cells present in the majority of the population. This can be accomplished by selecting amino acid sequences that bind to many, most, or all of the HLA class II molecules.

These are known as "loosely HLA-restricted" or "promiscuous" T helper sequences.

Examples of amino acid sequences that are promiscuous include sequences from antigens such as tetanus toxoid at positions 830-843 (QYIKANSKFIGITE), *Plasmodium*

falciparum CS protein at positions 378-398 (DIEKKIAKMEKASSVFNVVNS), and

- 5 Streptococcus 18kD protein at positions 116 (GAVDSILGGVATYGAA). Other examples include peptides bearing a DR 1-4-7 supermotif, or either of the DR3 motifs.

Alternatively, it is possible to prepare synthetic peptides capable of stimulating T helper lymphocytes, in a loosely HLA-restricted fashion, using amino acid sequences not found in nature (see, e.g., PCT publication WO 95/07707). These synthetic compounds called Pan-DR-binding epitopes (e.g., PADRE™, Epimmune, Inc., San Diego, CA) are designed to most preferably bind most HLA-DR (human HLA class II) molecules. For instance, a pan-DR-binding epitope peptide having the formula: aKXVWANTLKAa, where "X" is either cyclohexylalanine, phenylalanine, or tyrosine, and a is either D-alanine or L-alanine, has been found to bind to most HLA-DR alleles, and to stimulate the response of T helper lymphocytes from most individuals, regardless of their HLA type. An alternative of a pan-DR binding epitope comprises all "L" natural amino acids and can be provided in the form of nucleic acids that encode the epitope.

HTL peptide epitopes can also be modified to alter their biological properties. For example, peptides comprising HTL epitopes can contain D-amino acids to increase their resistance to proteases and thus extend their serum half-life. Also, the epitope peptides of the invention can be conjugated to other molecules such as lipids, proteins or sugars, or any other synthetic compounds, to increase their biological activity. Specifically, the T helper peptide can be conjugated to one or more palmitic acid chains at either the amino or carboxyl termini.

In some embodiments it may be desirable to include in the pharmaceutical compositions of the invention at least one component which primes cytotoxic T lymphocytes. Lipids have been identified as agents capable of priming CTL *in vivo* against viral antigens. For example, palmitic acid residues can be attached to the ϵ - and α -amino groups of a lysine residue and then linked, e.g., via one or more linking residues such as Gly, Gly-Gly-, Ser, Ser-Ser, or the like, to an immunogenic peptide. The lipidated peptide can then be administered either directly in a micelle or particle, incorporated into a liposome, or emulsified in an adjuvant, e.g., incomplete Freund's adjuvant. In a preferred embodiment, a particularly effective immunogenic comprises

palmitic acid attached to ϵ - and α - amino groups of Lys, which is attached via linkage, *e.g.*, Ser-Ser, to the amino terminus of the immunogenic peptide.

As another example of lipid priming of CTL responses, *E. coli* lipoproteins, such as tripalmitoyl-S-glycerylcysteinylserine (P_3 CSS) can be used to prime virus specific CTL when covalently attached to an appropriate peptide. (*See, e.g.*, Deres, *et al.*, *Nature* 342:561, 1989). Peptides of the invention can be coupled to P_3 CSS, for example, and the lipopeptide administered to an individual to specifically prime a CTL response to the target antigen. Moreover, because the induction of neutralizing antibodies can also be primed with P_3 CSS-conjugated epitopes, two such compositions can be combined to more effectively elicit both humoral and cell-mediated responses to infection.

As noted herein, additional amino acids can be added to the termini of a peptide to provide for ease of linking peptides one to another, for coupling to a carrier support or larger peptide, for modifying the physical or chemical properties of the peptide or oligopeptide, or the like. Amino acids such as tyrosine, cysteine, lysine, glutamic or aspartic acid, or the like, can be introduced at the C- or N-terminus of the peptide or oligopeptide, particularly class I peptides. However, it is to be noted that modification at the carboxyl terminus of a CTL epitope may, in some cases, alter binding characteristics of the peptide. In addition, the peptide or oligopeptide sequences can differ from the natural sequence by being modified by terminal-NH₂ acylation, *e.g.*, by alkanoyl (C₁-C₂₀) or thioglycolyl acetylation, terminal-carboxyl amidation, *e.g.*, ammonia, methylamine, *etc.* In some instances these modifications may provide sites for linking to a support or other molecule.

IV.L. Administration of Vaccines for Therapeutic or Prophylactic Purposes

The peptides of the present invention and pharmaceutical and vaccine compositions of the invention are useful for administration to mammals, particularly humans, to treat and/or prevent HIV infection. Vaccine compositions containing the peptides of the invention are administered to a patient infected with HIV or to an individual susceptible to, or otherwise at risk for, HIV infection to elicit an immune response against HIV antigens and thus enhance the patient's own immune response capabilities. In therapeutic applications, peptide and/or nucleic acid compositions are administered to a patient in an amount sufficient to elicit an effective CTL and/or HTL response to the virus antigen and to cure or at least partially arrest or slow symptoms

and/or complications. An amount adequate to accomplish this is defined as "therapeutically effective dose." Amounts effective for this use will depend on, *e.g.*, the particular composition administered, the manner of administration, the stage and severity of the disease being treated, the weight and general state of health of the patient, and the judgment of the prescribing physician.

The vaccine compositions of the invention may also be used purely as prophylactic agents. Generally the dosage for an initial prophylactic immunization generally occurs in a unit dosage range where the lower value is about 1, 5, 50, 500, or 1000 μg and the higher value is about 10,000; 20,000; 30,000; or 50,000 μg . Dosage values for a human typically range from about 500 μg to about 50,000 μg per 70 kilogram patient. This is followed by boosting dosages of between about 1.0 μg to about 50,000 μg of peptide administered at defined intervals from about four weeks to six months after the initial administration of vaccine. The immunogenicity of the vaccine may be assessed by measuring the specific activity of CTL and HTL obtained from a sample of the patient's blood.

As noted above, peptides comprising CTL and/or HTL epitopes of the invention induce immune responses when presented by HLA molecules and contacted with a CTL or HTL specific for an epitope comprised by the peptide. The manner in which the peptide is contacted with the CTL or HTL is not critical to the invention. For instance, the peptide can be contacted with the CTL or HTL either *in vivo* or *in vitro*. If the contacting occurs *in vivo*, the peptide itself can be administered to the patient, or other vehicles, *e.g.*, DNA vectors encoding one or more peptides, viral vectors encoding the peptide(s), liposomes and the like, can be used, as described herein.

For pharmaceutical compositions, the immunogenic peptides of the invention, or DNA encoding them, are generally administered to an individual already infected with HIV. The peptides or DNA encoding them can be administered individually or as fusions of one or more peptide sequences. Those in the incubation phase or the acute phase of infection can be treated with the immunogenic peptides separately or in conjunction with other treatments, as appropriate.

For therapeutic use, administration should generally begin at the first diagnosis of HIV infection. This is followed by boosting doses until at least symptoms are substantially abated and for a period thereafter. In chronic infection, loading doses followed by boosting doses may be required.

Treatment of an infected individual with the compositions of the invention may hasten resolution of the infection in acutely infected individuals and prevent development of chronic infection. Where susceptible individuals are identified prior to or during infection, the composition can be targeted to them, thus minimizing the need for administration to a larger population.

The peptide or other compositions used for the treatment or prophylaxis of HIV infection can be used, *e.g.*, in persons who have not manifested symptoms of disease but who act as a disease vector. In this context, it is generally important to provide an amount of the peptide epitope delivered by a mode of administration sufficient to effectively stimulate a cytotoxic T cell response; compositions which stimulate helper T cell responses can also be given in accordance with this embodiment of the invention.

The dosage for an initial therapeutic immunization generally occurs in a unit dosage range where the lower value is about 1, 5, 50, 500, or 1,000 μg and the higher value is about 10,000; 20,000; 30,000; or 50,000 μg . Dosage values for a human typically range from about 500 μg to about 50,000 μg per 70 kilogram patient. Boosting dosages of between about 1.0 μg to about 50,000 μg of peptide pursuant to a boosting regimen over weeks to months may be administered depending upon the patient's response and condition as determined by measuring the specific activity of CTL and HTL obtained from the patient's blood. The peptides and compositions of the present invention may be employed in serious disease states, that is, life-threatening or potentially life threatening situations. In such cases, as a result of the minimal amounts of extraneous substances and the relative nontoxic nature of the peptides in preferred compositions of the invention, it is possible and may be felt desirable by the treating physician to administer substantial excesses of these peptide compositions relative to these stated dosage amounts.

Thus, for treatment of chronic infection, a representative dose is in the range disclosed above, namely where the lower value is about 1, 5, 50, 500, or 1,000 μg and the higher value is about 10,000; 20,000; 30,000; or 50,000 μg , preferably from about 500 μg to about 50,000 μg per 70 kilogram patient. Initial doses followed by boosting doses at established intervals, *e.g.*, from four weeks to six months, may be required, possibly for a prolonged period of time to effectively immunize an individual. In the case of chronic infection, administration should continue until at least clinical symptoms or laboratory tests indicate that the viral infection has been eliminated or substantially abated and for a

period thereafter. The dosages, routes of administration, and dose schedules are adjusted in accordance with methodologies known in the art.

The pharmaceutical compositions for therapeutic treatment are intended for parenteral, topical, oral, intrathecal, or local administration. Preferably, the pharmaceutical compositions are administered parentally, *e.g.*, intravenously, subcutaneously, intradermally, or intramuscularly. Thus, the invention provides compositions for parenteral administration which comprise a solution of the immunogenic peptides dissolved or suspended in an acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers may be used, *e.g.*, water, buffered water, 0.8% saline, 0.3% glycine, hyaluronic acid and the like. These compositions may be sterilized by conventional, well known sterilization techniques, or may be sterile filtered. The resulting aqueous solutions may be packaged for use as is, or lyophilized, the lyophilized preparation being combined with a sterile solution prior to administration. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions, such as pH-adjusting and buffering agents, tonicity adjusting agents, wetting agents, preservatives, and the like, for example, sodium acetate, sodium lactate, sodium chloride, potassium chloride, calcium chloride, sorbitan monolaurate, triethanolamine oleate, *etc.*

The concentration of peptides of the invention in the pharmaceutical formulations can vary widely, *i.e.*, from less than about 0.1%, usually at or at least about 2% to as much as 20% to 50% or more by weight, and will be selected primarily by fluid volumes, viscosities, *etc.*, in accordance with the particular mode of administration selected.

A human unit dose form of the peptide composition is typically included in a pharmaceutical composition that comprises a human unit dose of an acceptable carrier, preferably an aqueous carrier, and is administered in a volume of fluid that is known by those of skill in the art to be used for administration of such compositions to humans (*see, e.g., Remington's Pharmaceutical Sciences*, 17th Edition, A. Gennaro, Editor, Mack Publishing Co., Easton, Pennsylvania, 1985).

The peptides of the invention may also be administered via liposomes, which serve to target the peptides to a particular tissue, such as lymphoid tissue, or to target selectively to infected cells, as well as to increase the half-life of the peptide composition. Liposomes include emulsions, foams, micelles, insoluble monolayers, liquid crystals, phospholipid dispersions, lamellar layers and the like. In these preparations, the peptide to be delivered is incorporated as part of a liposome, alone or in conjunction with a

molecule which binds to a receptor prevalent among lymphoid cells, such as monoclonal antibodies which bind to the CD45 antigen, or with other therapeutic or immunogenic compositions. Thus, liposomes either filled or decorated with a desired peptide of the invention can be directed to the site of lymphoid cells, where the liposomes then deliver the peptide compositions. Liposomes for use in accordance with the invention are formed from standard vesicle-forming lipids, which generally include neutral and negatively charged phospholipids and a sterol, such as cholesterol. The selection of lipids is generally guided by consideration of, *e.g.*, liposome size, acid lability and stability of the liposomes in the blood stream. A variety of methods are available for preparing liposomes, as described in, *e.g.*, Szoka, *et al.*, *Ann. Rev. Biophys. Bioeng.* 9:467 (1980), and U.S. Patent Nos. 4,235,871, 4,501,728, 4,837,028, and 5,019,369.

For targeting cells of the immune system, a ligand to be incorporated into the liposome can include, *e.g.*, antibodies or fragments thereof specific for cell surface determinants of the desired immune system cells. A liposome suspension containing a peptide may be administered intravenously, locally, topically, *etc.* in a dose which varies according to, *inter alia*, the manner of administration, the peptide being delivered, and the stage of the disease being treated.

For solid compositions, conventional nontoxic solid carriers may be used which include, for example, pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharin, talcum, cellulose, glucose, sucrose, magnesium carbonate, and the like. For oral administration, a pharmaceutically acceptable nontoxic composition is formed by incorporating any of the normally employed excipients, such as those carriers previously listed, and generally 10-95% of active ingredient, that is, one or more peptides of the invention, and more preferably at a concentration of 25%-75%.

For aerosol administration, the immunogenic peptides are preferably supplied in finely divided form along with a surfactant and propellant. Typical percentages of peptides are 0.01%-20% by weight, preferably 1%-10%. The surfactant must, of course, be nontoxic, and preferably soluble in the propellant. Representative of such agents are the esters or partial esters of fatty acids containing from 6 to 22 carbon atoms, such as caproic, octanoic, lauric, palmitic, stearic, linoleic, linolenic, olesteric and oleic acids with an aliphatic polyhydric alcohol or its cyclic anhydride. Mixed esters, such as mixed or natural glycerides may be employed. The surfactant may constitute 0.1%-20% by weight of the composition, preferably 0.25-5%. The balance of the composition is ordinarily

propellant. A carrier can also be included, as desired, as with, *e.g.*, lecithin for intranasal delivery.

IV.M. Kits

5 The peptide and nucleic acid compositions of this invention can be provided in kit form together with instructions for vaccine administration. Typically the kit would include desired peptide compositions in a container, preferably in unit dosage form and instructions for administration. An alternative kit would include a minigene construct with desired nucleic acids of the invention in a container, preferably in unit dosage form
10 together with instructions for administration. Lymphokines such as IL-2 or IL-12 may also be included in the kit. Other kit components that may also be desirable include, for example, a sterile syringe, booster dosages, and other desired excipients.

 The invention will be described in greater detail by way of specific examples. The following examples are offered for illustrative purposes, and are not intended to limit
15 the invention in any manner. Those of skill in the art will readily recognize a variety of non-critical parameters that can be changed or modified to yield alternative embodiments in accordance with the invention.

V. EXAMPLES

20 The following examples illustrate identification, selection, and use of immunogenic Class I and Class II peptide epitopes for inclusion in vaccine compositions.

Example 1. HLA Class I and Class II Binding Assays

25 The following example of peptide binding to HLA molecules demonstrates quantification of binding affinities of HLA class I and class II peptides. Binding assays can be performed with peptides that are either motif-bearing or not motif-bearing.

 Epstein-Barr virus (EBV)-transformed homozygous cell lines, fibroblasts, CIR, or 721.22 transfectants were used as sources of HLA class I molecules. These cells were maintained *in vitro* by culture in RPMI 1640 medium supplemented with 2mM L-
30 glutamine (GIBCO, Grand Island, NY), 50μM 2-ME, 100μg/ml of streptomycin, 100U/ml of penicillin (Irvine Scientific) and 10% heat-inactivated FCS (Irvine Scientific, Santa Ana, CA). Cells were grown in 225-cm² tissue culture flasks or, for large-scale

cultures, in roller bottle apparatuses. The specific cell lines routinely used for purification of MHC class I and class II molecules are listed in Table XXIV.

Cell lysates were prepared and HLA molecules purified in accordance with disclosed protocols (Sidney *et al.*, *Current Protocols in Immunology* 18.3.1 (1998);

- 5 Sidney, *et al.*, *J. Immunol.* 154:247 (1995); Sette, *et al.*, *Mol. Immunol.* 31:813 (1994)). Briefly, cells were lysed at a concentration of 10^8 cells/ml in 50 mM Tris-HCl, pH 8.5, containing 1% Nonidet P-40 (Fluka Biochemika, Buchs, Switzerland), 150 mM NaCl, 5 mM EDTA, and 2 mM PMSF. Lysates were cleared of debris and nuclei by centrifugation at $15,000 \times g$ for 30min.

- 10 HLA molecules were purified from lysates by affinity chromatography. Lysates prepared as above were passed twice through two pre-columns of inactivated Sepharose CL4-B and protein A-Sepharose. Next, the lysate was passed over a column of Sepharose CL-4B beads coupled to an appropriate antibody. The antibodies used for the extraction of HLA from cell lysates are listed in Table XXV. The anti-HLA column was then
15 washed with 10-column volumes of 10mM Tris-HCL, pH 8.0, in 1% NP-40, PBS, 2-column volumes of PBS, and 2-column volumes of PBS containing 0.4% n-octylglucoside. Finally, MHC molecules were eluted with 50mM diethylamine in 0.15M NaCl containing 0.4% n-octylglucoside, pH 11.5. A 1/25 volume of 2.0M Tris, pH 6.8, was added to the eluate to reduce the pH to ~8.0. Eluates were then be concentrated by
20 centrifugation in Centriprep 30 concentrators at 2000 rpm (Amicon, Beverly, MA). Protein content was evaluated by a BCA protein assay (Pierce Chemical Co., Rockford, IL) and confirmed by SDS-PAGE.

- A detailed description of the protocol utilized to measure the binding of peptides to Class I and Class II MHC has been published (Sette *et al.*, *Mol. Immunol.* 31:813,
25 1994; Sidney *et al.*, in *Current Protocols in Immunology*, Margulies, Ed., John Wiley & Sons, New York, Section 18.3, 1998). Briefly, purified MHC molecules (5 to 500nM) were incubated with various unlabeled peptide inhibitors and 1-10nM ^{125}I -radiolabeled probe peptides for 48h in PBS containing 0.05% Nonidet P-40 (NP40) (or 20% w/v digitonin for H-2 IA assays) in the presence of a protease inhibitor cocktail. The final
30 concentrations of protease inhibitors (each from CalBioChem, La Jolla, CA) were 1 mM PMSF, 1.3 nM 1.10 phenanthroline, 73 μM pepstatin A, 8mM EDTA, 6mM N-ethylmaleimide (for Class II assays), and 200 μM N alpha-p-tosyl-L-lysine chloromethyl ketone (TLCK). All assays were performed at pH 7.0 with the exception of DRB1*0301,

which was performed at pH 4.5, and DRB1*1601 (DR2w21 β_1) and DRB4*0101 (DRw53), which were performed at pH 5.0. pH was adjusted as described elsewhere (see Sidney *et al.*, in *Current Protocols in Immunology*, Margulies, Ed., John Wiley & Sons, New York, Section 18.3, 1998).

5 Following incubation, MHC-peptide complexes were separated from free peptide by gel filtration on 7.8 mm x 15 cm TSK200 columns (TosoHaas 16215, Montgomeryville, PA), eluted at 1.2 mls/min with PBS pH 6.5 containing 0.5% NP40 and 0.1% NaN₃. Because the large size of the radiolabeled peptide used for the DRB1*1501 (DR2w2 β_1) assay makes separation of bound from unbound peaks more difficult under
10 these conditions, all DRB1*1501 (DR2w2 β_1) assays were performed using a 7.8mm x 30cm TSK2000 column eluted at 0.6 mls/min. The eluate from the TSK columns was passed through a Beckman 170 radioisotope detector, and radioactivity was plotted and integrated using a Hewlett-Packard 3396A integrator, and the fraction of peptide bound was determined.

15 Radiolabeled peptides were iodinated using the chloramine-T method. Representative radiolabeled probe peptides utilized in each assay, and its assay specific IC₅₀ nM, are summarized in Tables IV and V. Typically, in preliminary experiments, each MHC preparation was titrated in the presence of fixed amounts of radiolabeled peptides to determine the concentration of HLA molecules necessary to bind 10-20% of
20 the total radioactivity. All subsequent inhibition and direct binding assays were performed using these HLA concentrations.

Since under these conditions [label]<[HLA] and IC₅₀≥[HLA], the measured IC₅₀ values are reasonable approximations of the true K_D values. Peptide inhibitors are typically tested at concentrations ranging from 120 μ g/ml to 1.2 ng/ml, and are tested in
25 two to four completely independent experiments. To allow comparison of the data obtained in different experiments, a relative binding figure is calculated for each peptide by dividing the IC₅₀ of a positive control for inhibition by the IC₅₀ for each tested peptide (typically unlabeled versions of the radiolabeled probe peptide). For database purposes, and inter-experiment comparisons, relative binding values are compiled. These values
30 can subsequently be converted back into IC₅₀ nM values by dividing the IC₅₀ nM of the positive controls for inhibition by the relative binding of the peptide of interest. This method of data compilation has proven to be the most accurate and consistent for

comparing peptides that have been tested on different days, or with different lots of purified MHC.

Because the antibody used for HLA-DR purification (LB3.1) is α -chain specific, β_1 molecules are not separated from β_3 (and/or β_4 and β_5) molecules. The β_1 specificity of the binding assay is obvious in the cases of DRB1*0101 (DR1), DRB1*0802 (DR8w2), and DRB1*0803 (DR8w3), where no β_3 is expressed. It has also been demonstrated for DRB1*0301 (DR3) and DRB3*0101 (DR52a), DRB1*0401 (DR4w4), DRB1*0404 (DR4w14), DRB1*0405 (DR4w15), DRB1*1101 (DR5), DRB1*1201 (DR5w12), DRB1*1302 (DR6w19) and DRB1*0701 (DR7). The problem of β chain specificity for DRB1*1501 (DR2w2 β_1), DRB5*0101 (DR2w2 β_2), DRB1*1601 (DR2w21 β_1), DRB5*0201 (DR51Dw21), and DRB4*0101 (DRw53) assays is circumvented by the use of fibroblasts. Development and validation of assays with regard to DR β molecule specificity have been described previously (*see, e.g., Southwood et al., J. Immunol.* 160:3363-3373, 1998).

Binding assays as outlined above may be used to analyze supermotif and/or motif-bearing epitopes as, for example, described in Example 2.

Example 2. Identification of HLA Supermotif- and Motif-Bearing CTL Candidate Epitopes

Vaccine compositions of the invention may include multiple epitopes that comprise multiple HLA supermotifs or motifs to achieve broad population coverage. This example illustrates the identification of supermotif- and motif-bearing epitopes for the inclusion in such a vaccine composition. Calculation of population coverage was performed using the strategy described below.

Computer searches and algorithms for identification of supermotif and/or motif-bearing epitopes

The searches performed to identify the motif-bearing peptide sequences in Examples 2 and 5 employed the protein sequence data from HIV-1 clade B virus strains that were available in the 1994 Los Alamos database.

Computer searches for epitopes bearing HLA Class I or Class II supermotifs or motifs were performed as follows. All translated HIV protein sequences were analyzed using a text string search software program, *e.g., MotifSearch 1.4* (D. Brown, San Diego)

to identify potential peptide sequences containing appropriate HLA binding motifs; alternative programs are readily produced in accordance with information in the art in view of the motif/supermotif disclosure herein. Furthermore, such calculations can be made mentally. Identified A2-, A3-, and DR-supermotif sequences were scored using polynomial algorithms to predict their capacity to bind to specific HLA-Class I or Class II molecules. These polynomial algorithms take into account both extended and refined motifs (that is, to account for the impact of different amino acids at different positions), and are essentially based on the premise that the overall affinity (or ΔG) of peptide-HLA molecule interactions can be approximated as a linear polynomial function of the type:

$$\Delta G = a_{1i} \times a_{2i} \times a_{3i} \dots \times a_{ni}$$

where a_{ji} is a coefficient which represents the effect of the presence of a given amino acid (j) at a given position (i) along the sequence of a peptide of n amino acids. The crucial assumption of this method is that the effects at each position are essentially independent of each other (i.e., independent binding of individual side-chains). When residue j occurs at position i in the peptide, it is assumed to contribute a constant amount j_i to the free energy of binding of the peptide irrespective of the sequence of the rest of the peptide. This assumption is justified by studies from our laboratories that demonstrated that peptides are bound to MHC and recognized by T cells in essentially an extended conformation (data omitted herein).

The method of derivation of specific algorithm coefficients has been described in Gulukota *et al.*, *J. Mol. Biol.* 267:1258-126, 1997; (see also Sidney *et al.*, *Human Immunol.* 45:79-93, 1996; and Southwood *et al.*, *J. Immunol.* 160:3363-3373, 1998). Briefly, for all i positions, anchor and non-anchor alike, the geometric mean of the average relative binding (ARB) of all peptides carrying j is calculated relative to the remainder of the group, and used as the estimate of j_i . For Class II peptides, if multiple alignments are possible, only the highest scoring alignment is utilized, following an iterative procedure. To calculate an algorithm score of a given peptide in a test set, the ARB values corresponding to the sequence of the peptide are multiplied. If this product exceeds a chosen threshold, the peptide is predicted to bind. Appropriate thresholds are chosen as a function of the degree of stringency of prediction desired.

Selection of HLA-A2 supertype cross-reactive peptides

Complete protein sequences from nine HIV structural and regulatory proteins were aligned, then scanned, utilizing motif identification software, to identify conserved 9- and 10-mer sequences containing the HLA-A2-supermotif main anchor specificity.

- 5 The analysis included all isolates in the 1994 Los Alamos database. The conservation criteria varied according to antigen: greater than 80% of clade B isolates for gag, pol, env; greater than 70% for nef, rev, tat, vif, vpr; great than 60% for vpu.)

- A total of 233 conserved, HLA-A2 supermotif-positive sequences were identified. The peptides corresponding to the sequences were then synthesized and tested for their
10 capacity to bind purified HLA-A*0201 molecules *in vitro* (HLA-A*0201 is considered a prototype A2 supertype molecule). Thirty peptides bound A*0201 with IC_{50} values ≤ 500 nM; of these 30, 5 bound with high binding affinities (IC_{50} values ≤ 50 nM) and 25 bound with intermediate binding affinities, in the 50-500 nM range (Table XXVII).

- The thirty A*0201-binding peptides were subsequently tested for the capacity to
15 bind to additional A2-supertype molecules (A*0202, A*0203, A*0206, and A*6802). As shown in Table XXVII, 20 of the 30 peptides were found to be A2-supertype cross-reactive binders, binding at least 3 of the 5 A2-supertype alleles tested.

Selection of HLA-A3 supermotif-bearing epitopes

- 20 The HIV protein sequences scanned above were also examined for the presence of peptides with the HLA-A3-supermotif primary anchors. A total of 353 conserved 9- or 10-mer motif-containing sequences were identified. The corresponding peptides were synthesized and tested for binding to HLA-A*0301 and HLA-A*1101 molecules, the two most prevalent A3-supertype alleles. Sixty-six of the peptides were found to bind one of
25 the two alleles with binding affinities of ≤ 500 nM (Table XXVIII). These peptides were then tested for binding cross-reactivity to the other common A3-supertype alleles (A*3101, A*3301, and A*6801). Twenty one of the peptides bound at least three of the five HLA-A3-supertype molecules tested (Table XXVIII). Table XXVIII also includes two 11-mer peptides that were not selected using the search criteria outlined above, but
30 have been shown to be A3-supertype cross-reactive binders.

Selection of HLA-B7 supermotif bearing epitopes

When the same HIV target antigen protein sequences were also analyzed for the presence of conserved 9- or 10-mer peptides with the HLA-B7-supermotif, 54 sequences were identified. The corresponding peptides were synthesized and tested for binding to HLA-B*0702, the most common B7-supertype allele (*i.e.*, the prototype B7 supertype allele). Sixteen peptides bound B*0702 with IC₅₀ of ≤500 nM (Table XXIX). These peptides were then tested for binding to other common B7-supertype molecules (B*3501, B*5101, B*5301, and B*5401). As shown in Table XXIX, eight of the sixteen peptides were capable of binding to three or more of the five B7-supertype alleles tested.

Selection of A1 and A24 motif-bearing epitopes

To further increase population coverage, HLA-A1 and -A24 epitopes can also be incorporated into potential vaccine constructs. An analysis of the protein sequence data from the HIV target antigens utilized above can also be performed to identify HLA-A1- and A24-motif-containing conserved sequences.

Other similar, but less extensive, studies performed by the present inventors have identified five conserved HIV-derived peptides that bind to A*0101 with an IC₅₀ of 500 nM or less. (Table XXX). In a similar context, 11 conserved HLA-A*2402-binding HIV-derived peptides have also been identified, 5 of which bind with an IC₅₀ of 100 nM or less (Table XXXI).

Example 3. Confirmation of Immunogenicity

*Evaluation of A*0201 immunogenicity*

It has been shown that CTL induced in A*0201/K^b transgenic mice exhibit specificity similar to CTL induced in the human system (*see, e.g.*, Vitiello *et al.*, *J. Exp. Med.* 173:1007-1015, 1991; Wentworth *et al.*, *Eur. J. Immunol.* 26:97-101, 1996). Accordingly, these mice were used to evaluate the immunogenicity of 19 of the 20 A2-supertype cross-reactive peptides identified in Example 2 above.

CTL induction in transgenic mice following peptide immunization has been described (Vitiello *et al.*, *J. Exp. Med.* 173:1007-1015, 1991; Alexander *et al.*; *J. Immunol.* 159:4753-4761, 1997). In these studies, mice were injected subcutaneously at the base of the tail with each peptide (50 µg/mouse) emulsified in IFA in the presence of an excess of an IA^b-restricted helper peptide (140 µg/mouse) (HBV core 128-140, Sette *et*

al., *J. Immunol.* 153:5586-5592, 1994). Eleven days after injection, splenocytes were incubated in the presence of peptide-loaded syngenic LPS blasts. After six days, cultures were assayed for cytotoxic activity using peptide-pulsed targets. The data, summarized in Table XXXII, indicate that eight peptides were capable of inducing primary CTL responses in A*0201/K^b transgenic mice. (For these studies, a peptide was considered positive if it induced CTL (L.U. 30/10⁶ cells \geq 2 in at least two transgenic animals (Wentworth *et al.*, *Eur. J. Immunol.* 26:97-101, 1996).

The cross-reactive candidate CTL epitopes were also tested for the ability to stimulate recall CTL responses HIV-infected patients. Briefly, PBMC from patients infected with HIV were cultured in the presence of 10 μ g/ml of synthetic peptide. After 7 and 14 days, the cultures were restimulated with peptide. The cultures were assayed for cytolytic activity on day 21 using target cells pulsed with the specific peptide in a ⁵¹Cr release assay. These data are also summarized in Table XXXII. As shown, 15 of the 19 peptides analyzed were recognized in recall CTL responses using PBMC from HIV-infected patients.

The set of peptides screened for immunogenicity contained two redundant peptides, 1261.14 and 1261.04, which differ in length by a single amino acid. While both peptides exhibit supertype degenerate binding, only the short of the two peptides exhibited immunogenicity. One supertype peptide not tested, 1211.09, has been reported to be recognized by CTL lines isolated from HIV-infected patients. In summary, 16 A2-supertype cross-reactive peptides have been identified that are immunogenic in humans; 53% of these peptides are also recognized in HLA-A2 transgenic mice. The sixteen peptides represent epitopes from five HIV antigens: env, gag, pol, vpr, and nef.

*Evaluation of A*03/A11 immunogenicity*

Twenty one of the A3-supertype cross-reactive peptides identified in Example 2 above were evaluated for immunogenicity (Table XXXIII). Peptides were screened using HLA-A11/K^b transgenic mice, using the protocol described above for HLA-A2 transgenic mice (Alexander *et al.*, *J. Immunol.* 159:4753-4761, 1997) and using PBMC obtained from HIV-infected patients to test for the ability to stimulate CTL recall responses. Ten peptides that were capable of inducing CTL in HLA-A11 transgenic mice were identified.

Three peptides, 966.01, 940.03, and 1069.47, have been shown by collaborators to be immunogenic in HIV-infected patients. Peptides 966.01 and 1069.47 also induced CTL responses in transgenic mice, peptide 940.03 exhibited immunogenicity in patients only.

5 In summary, 11 of 23 A3-supertype cross-reactive binding peptides were found to be immunogenic in either HLA-A11 transgenic mice or HIV-infected patients. These peptides represent epitopes from three HIV antigens: pol, env, and nef.

Evaluation of B7 immunogenicity

10 Immunogenicity screening of the B7-supertype cross-reactive binding peptides identified in Example 2 can be evaluated using HLA-B7 transgenic mice and PBMC from in HIV-infected patients in a manner analagous to the evaluation of A2-and A3-supermotif-bearing peptides. Three of these peptides have been previously reported as being immunogenic in HIV-infected patients.

15

Example 4. Implementation of the Extended Supermotif to Improve the Binding Capacity of Native Epitopes by Creating Analogs

HLA motifs and supermotifs (comprising primary and/or secondary residues) are useful in the identification and preparation of highly cross-reactive native peptides, as demonstrated herein. Moreover, the definition of HLA motifs and supermotifs also allows one to engineer highly cross-reactive epitopes by identifying residues within a native peptide sequence which can be analogued, or "fixed" to confer upon the peptide certain characteristics, e.g. greater cross-reactivity within the group of HLA molecules that comprise a supertype, and/or greater binding affinity for some or all of those HLA molecules. Examples of analog peptides that exhibit modulated binding affinity are set forth in this example.

20

25

Analoging at Primary Anchor Residues

As shown in Example 2, twenty HIV-derived, A2-supertype-restricted epitopes were identified. Peptide engineering strategies are implemented to further increase the cross-reactivity of the candidate epitopes identified above which bind 3/5 of the A2 supertype alleles tested. On the basis of the data disclosed, e.g., in related and co-pending U.S.S.N 09/226,775, the main anchors of A2-supermotif-bearing peptides are altered, for example, to introduce a preferred L, I, V, or M at position 2, and I or V at the C-terminus.

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To analyze the cross-reactivity of the analog peptides, each engineered analog is initially tested for binding to the prototype A2 supertype allele A*0201, then, if A*0201 binding capacity is maintained, for A2-supertype cross-reactivity.

Alternatively, a peptide may be tested for binding to one or all supertype members and then analogued to modulate binding affinity to any one (or more) of the supertype members to add population coverage.

Similarly, analogs of HLA-A3 supermotif-bearing epitopes may also be generated. For example, peptides binding to 3/5 of the A3-supertype molecules may be engineered at primary anchor residues to possess a preferred residue (V, S, M, or A) at position 2.

The analog peptides are then tested for the ability to bind A*03 and A*11 (prototype A3 supertype alleles). Those peptides that demonstrate ≤ 500 nM binding capacity are then tested for A3-supertype cross-reactivity.

Similarly to the A2- and A3- motif bearing peptides, peptides binding 3 or more B7-supertype alleles may be improved, where possible, to achieve increased cross-reactive binding. B7 supermotif-bearing peptides may, for example, be engineered to possess a preferred residue (V, I, L, or F) at the C-terminal primary anchor position, as demonstrated by Sidney *et al.* (*J. Immunol.* 157:3480-3490, 1996).

20 *Analoging at Secondary Anchor Residues*

Moreover, HLA supermotifs are of value in engineering highly cross-reactive peptides and/or peptides that bind HLA molecules with increased affinity by identifying particular residues at secondary anchor positions that are associated with such properties. For example, the binding capacity of a B7 supermotif-bearing peptide representing a discreet single amino acid substitution at position 1 can be analyzed. A peptide such as t Peptide 1261.01 (Table XXIX), can, for example, be analogued to substitute L for F at position 1 and subsequently be evaluated for increased binding affinity/ and or increased cross-reactivity. This procedure will identify analogued peptides with modulated binding affinity.

30 Engineered analogs with sufficiently improved binding capacity or cross-reactivity are tested for immunogenicity in HLA-B7-transgenic mice, following for example, IFA immunization or lipopeptide immunization. The analogued peptides may be additionally tested for the ability to stimulate a recall response using PBMC from HIV-infected patients. In conclusion, these data demonstrate that by the use of even single

amino acid substitutions, it is possible to increase the binding affinity and/or cross-reactivity of peptide ligands for HLA supertype molecules.

Example 5. Identification of HIV-derived sequences with HLA-DR binding motifs

- 5 Peptide epitopes bearing an HLA class II supermotif or motif may also be identified as outlined below using methodology similar to that described in Examples 1-3.

Selection of HLA-DR-supermotif-bearing epitopes.

- 10 To identify HIV-derived, HLA class II HTL epitopes, the protein sequences from the same HIV antigens used for the identification of HLA Class I supermotif/motif sequences were analyzed for the presence of sequences bearing an HLA-DR-motif or supermotif. Specifically, 15-mer sequences were selected comprising a DR-supermotif, further comprising a 9-mer core, and three-residue N- and C-terminal flanking regions (15 amino acids total).

- 15 Protocols for predicting peptide binding to DR molecules have been developed (Southwood *et al.*, *J. Immunol.* 160:3363-3373, 1998). These protocols, specific for individual DR molecules, allow the scoring, and ranking, of 9-mer core regions. Each protocol not only scores peptide sequences for the presence of DR-supermotif primary anchors (i.e., at position 1 and position 6) within a 9-mer core, but additionally evaluates
20 sequences for the presence of secondary anchors Δ Using allele specific selection tables (see, *e.g.*, Southwood *et al.*, *ibid.*), it has been found that these protocols efficiently select peptide sequences with a high probability of binding a particular DR molecule. Additionally, it has been found that performing these protocols in tandem, specifically those for DR1, DR4w4, and DR7, can efficiently select DR cross-reactive peptides.

- 25 The HIV-derived peptides identified above were tested for their binding capacity for various common HLA-DR molecules. All peptides were initially tested for binding to the DR molecules in the primary panel: DR1, DR4w4, and DR7. Peptides binding at least 2 of these 3 DR molecules were then tested for binding to DR2w2 β 1, DR2w2 β 2, DR6w19, and DR9 molecules in secondary assays. Finally, peptides binding at least 2 of
30 the 4 secondary panel DR molecules, and thus cumulatively at least 4 of 7 different DR molecules, were screened for binding to DR4w15, DR5w11, and DR8w2 molecules in tertiary assays. Peptides binding at least 7 of the 10 DR molecules comprising the primary, secondary, and tertiary screening assays were considered cross-reactive DR

binders. The composition of these screening panels, and the phenotypic frequency of associated antigens, are shown in Table XXXIV.

Thirteen HIV-derived peptides were found to bind at least 7 of 10 common HLA-DR alleles. The sequence of these 13 peptides, and their binding capacity for each assay in the primary through tertiary panels, are shown in Table XXXV. This set of peptide epitopes is predominantly derived from pol, but also includes epitopes from gag and env.

Selection of DR3 motif peptides

Because HLA-DR3 is an allele that is prevalent in Caucasian, Black, and Hispanic populations, DR3 binding capacity is an important criterion in the selection of HTL epitopes. However, data generated previously indicated that DR3 only rarely cross-reacts with other DR alleles (Sidney *et al.*, *J. Immunol.* 149:2634-2640, 1992; Geluk *et al.*, *J. Immunol.* 152:5742-5748, 1994; Southwood *et al.*, *J. Immunol.* 160:3363-3373, 1998). This is not entirely surprising in that the DR3 peptide-binding motif appears to be distinct from the specificity of most other DR alleles. For maximum efficiency in developing vaccine candidates it would be desirable for DR3 motifs to be clustered in proximity with DR supermotif regions. Thus, peptides shown to be candidates may also be assayed for their DR3 binding capacity. However, in view of the distinct binding specificity of the DR3 motif, peptides binding only to DR3 can also be considered as candidates for inclusion in a vaccine formulation.

To efficiently identify peptides that bind DR3, the nine target HIV antigens were analyzed for conserved sequences carrying one of the two DR3 specific binding motifs reported by Geluk *et al.* (*J. Immunol.* 152:5742-5748, 1994). The corresponding peptides were then synthesized and tested for the ability to bind DR3 with an affinity of 1 μ M or better, i.e., less than 1 μ M. Five peptides were found that met this binding criterion (Table XXXVI), and thereby qualify as HLA class II high affinity binders. Of these five, four represent epitopes from pol, and one is from vpu.

DR3 binding epitopes identified in this manner may then be included in vaccine compositions with DR supermotif-bearing peptide epitopes.

30

Example 6. Immunogenicity of HIV-derived HTL epitopes

Immunogenicity of HTL epitopes can be evaluated in a manner analogous to the determination of immunogenicity of CTL epitopes using appropriate transgenic mice

models and/or assessing the ability to stimulate recall responses using PBMC isolated from HIV-infected individuals.

The immunogenicity of 11 of the 13 HLA class II DR-supermotif binding epitopes identified in Example 5 was evaluated in a study testing PBMC isolated from HIV-
 5 infected individuals for recall proliferative responses. All eleven of these peptides were found to stimulate DR-restricted proliferative responses (Table XXXVII).

The DR3-motif bearing peptides can also be evaluated in a similar manner. Such studies demonstrate the immunogenicity of class II epitopes derived from HIV proteins.

10 Example 7. Calculation of phenotypic frequencies of HLA-supertypes in various ethnic backgrounds to determine breadth of population coverage

This example illustrates the assessment of the breadth of population coverage of a vaccine composition comprised of multiple epitopes comprising multiple supermotifs and/or motifs.

15 In order to analyze population coverage, gene frequencies of HLA alleles were determined. Gene frequencies for each HLA allele were calculated from antigen or allele frequencies utilizing the binomial distribution formulae $gf=1-(SQRT(1-af))$ (see, e.g., Sidney *et al.*, *Human Immunol.* 45:79-93, 1996). To obtain overall phenotypic
 20 frequencies, cumulative gene frequencies were calculated, and the cumulative antigen frequencies derived by the use of the inverse formula $[af=1-(1-Cgf)^2]$.

Where frequency data was not available at the level of DNA typing, correspondence to the serologically defined antigen frequencies was assumed. To obtain total potential supertype population coverage no linkage disequilibrium was assumed, and only alleles confirmed to belong to each of the supertypes were included (minimal
 25 estimates). Estimates of total potential coverage achieved by inter-loci combinations were made by adding to the A coverage the proportion of the non-A covered population that could be expected to be covered by the B alleles considered (e.g., $total=A+B*(1-A)$). Confirmed members of the A3-like supertype are A3, A11, A31, A*3301, and A*6801. Although the A3-like supertype may also include A34, A66, and A*7401, these alleles
 30 were not included in overall frequency calculations. Likewise, confirmed members of the A2-like supertype family are A*0201, A*0202, A*0203, A*0204, A*0205, A*0206, A*0207, A*6802, and A*6901. Finally, the B7-like supertype-confirmed alleles are: B7, B*3501-03, B51, B*5301, B*5401, B*5501-2, B*5601, B*6701, and B*7801 (potentially also B*1401, B*3504-06, B*4201, and B*5602).

Population coverage achieved by combining the A2-, A3- and B7-supertypes is approximately 86% in five major ethnic groups (see Table XXI). Coverage may be extended by including peptides bearing the A1 and A24 motifs. On average, A1 is present in 12% and A24 in 29% of the population across five different major ethnic groups (Caucasian, North American Black, Chinese, Japanese, and Hispanic). Together, these alleles are represented with an average frequency of 39% in these same ethnic populations. The total coverage across the major ethnicities when A1 and A24 are combined with the coverage of the A2-, A3- and B7-supertype alleles is >95%. An analogous approach can be used to estimate population coverage achieved with combinations of class II motif-bearing epitopes.

Summary of candidate HLA class I epitopes

In summary, on the basis of the data presented in the above examples, 47 candidate CTL peptide epitopes derived from HIV have been identified (see, Table XXXVIII). Of these 47 epitopes, 6 are derived from gag, 22 from pol, 10 from env, 3 from nef, and one epitope each from rev, vif, and vpr. This set of epitopes includes 16 HLA-A2 supermotif-bearing epitopes (two from gag, eight from pol, three from env, two from vpr, and one from nef), all of which are recognized in HIV-infected patients. The 10 HLA-A3 supermotif-bearing candidate epitopes include 6 pol-derived epitopes, two env-derived epitopes and one epitope each from gag, vif, and nef. With the exception of peptides 1273.08 and 1273.03, all of the epitopes are immunogenic in HLA transgenic mice. The two additional peptides are included to enhance antigen diversity.

The CTL candidate epitope set also includes 8 B7-restricted peptides. Of these eight, 3 epitopes have been reported as immunogenic in patients. Five B7-supermotif-bearing peptides were included as candidates based on supertype binding. Immunogenicity studies in humans (e.g., Bertoni *et al.*, *J. Clin. Invest.* 100:503, 1997; Doolan *et al.*, *Immunity* 7:97, 1997; and Threlkeld *et al.*, *J. Immunol.* 159:1648, 1997) have shown that highly cross-reactive binding peptides are almost always recognized as epitopes. Given these results, and in view of the limited immunogenicity data available for B7 supermotif-bearing peptides, the use of B7-supertype binding affinity is an important selection criterion in identifying candidate epitopes for inclusion in a vaccine that is immunogenic in a diverse population.

Similarly, A1- and A24-restricted peptides were included on the basis of both demonstrated immunogenicity of the candidate epitopes and on the basis of binding

affinity. Five of the candidate epitopes have been reported to be recognized in recall CTL responses from HIV-infected patients. Because a high percentage of the peptides with binding affinities ≤ 100 nM are found to be immunogenic, four A24-restricted peptides were included as vaccine candidates. An additional five A24-restricted epitopes and four A1-restricted epitopes that bound their respective alleles with an IC_{50} of ≤ 500 nM were also included to provide a greater degree of population coverage.

With these 47 CTL epitopes (as disclosed herein and from the art), an average population coverage is predicted to be greater than 95% in each of five major ethnic populations. Using the game theory Monte Carlo simulation analysis, which is known in the art (see *e.g.*, Osborne, M.J. and Rubinstein, A. "A course in game theory" MIT Press, 1994), it is estimated that 90% of the individuals in a population comprised of the Caucasian, North American Black, Japanese, Chinese, and Hispanic ethnic groups would recognize 7 or more of the vaccine epitopes described herein (Figure 1)

15 *Summary of candidate HLA class II epitopes*

A list of HIV-derived HTL epitopes that would be preferred for use in the design of minigene constructs or other vaccine formulations is summarized in Table XXXIX. The set of HTL epitopes includes 13 DR supermotif-bearing peptides and 5 DR3 motif-bearing peptides. The majority of the epitopes are derived from pol, 3 are from gag, 2 are from env and one is derived from vpu. The total estimated population coverage represented by this panel of HTL epitopes is estimated to be greater than 91% in each of five major ethnic groups (Table XL).

25 Example 8. CTL Recognition Of Endogenous Processed Antigens After Priming

This example determines that CTL induced by native or analogued peptide epitopes identified and selected as described in Examples 1-6 recognize endogenously synthesized, *i.e.*, native antigens.

Effector cells isolated from transgenic mice that are immunized with peptide epitopes as in Example 3, for example HLA-A2 supermotif-bearing epitopes, are re-stimulated *in vitro* using peptide-coated stimulator cells. Six days later, effector cells are assayed for cytotoxicity and the cell lines that contain peptide-specific cytotoxic activity are further re-stimulated. An additional six days later, these cell lines are tested for cytotoxic activity on ^{51}Cr labeled Jurkat-A2.1/K^b target cells in the absence or presence of

peptide, and also tested on ^{51}Cr labeled target cells bearing the endogenously synthesized antigen, *i.e.* cells that are stably transfected with HIV expression vectors.

The result will demonstrate that CTL lines obtained from animals primed with peptide epitope recognize endogenously synthesized HIV antigen. The choice of transgenic mouse model to be used for such an analysis depends upon the epitope(s) that is being evaluated. In addition to HLA-A*0201/K^b transgenic mice, several other transgenic mouse models including mice with human A11, which may also be used to evaluate A3 epitopes, and B7 alleles have been characterized and others (*e.g.*, transgenic mice for HLA-A1 and A24) are being developed. HLA-DR1 and HLA-DR3 mouse models have also been developed, which may be used to evaluate HTL epitopes.

Example 9. Activity Of CTL-HTL Conjugated Epitopes In Transgenic Mice

This example illustrates the induction of CTLs and HTLs in transgenic mice by use of a HIV CTL/HTL peptide conjugate whereby the vaccine composition comprises peptides administered to an HIV-infected patient or an individual at risk for HIV. The peptide composition can comprise multiple CTL and/or HTL epitopes. This analysis demonstrates enhanced immunogenicity that can be achieved by inclusion of one or more HTL epitopes in a vaccine composition. Such a peptide composition can comprise a lipidated HTL epitope conjugated to a preferred CTL epitope containing, for example, at least one CTL epitope selected from Table XXVI-XXIX, or an analog of that epitope. The HTL epitope is, for example, selected from Table XXXII.

Lipopeptide preparation: Lipopeptides are prepared by coupling the appropriate fatty acid to the amino terminus of the resin bound peptide. A typical procedure is as follows: A dichloromethane solution of a four-fold excess of a pre-formed symmetrical anhydride of the appropriate fatty acid is added to the resin and the mixture is allowed to react for two hours. The resin is washed with dichloromethane and dried. The resin is then treated with trifluoroacetic acid in the presence of appropriate scavengers [*e.g.* 5% (v/v) water] for 60 minutes at 20°C. After evaporation of excess trifluoroacetic acid, the crude peptide is washed with diethyl ether, dissolved in methanol and precipitated by the addition of water. The peptide is collected by filtration and dried.

Immunization procedures: Immunization of transgenic mice is performed as described (Alexander *et al.*, *J. Immunol.* 159:4753-4761, 1997). For example, A2/K^b mice, which are transgenic for the human HLA A2.1 allele and are useful for the assessment of the immunogenicity of HLA-A*0201 motif- or HLA-A2 supermotif-

bearing epitopes, are primed subcutaneously (base of the tail) with 0.1 ml of peptide conjugate formulated in saline, or DMSO/saline. Seven days after priming, splenocytes obtained from these animals are restimulated with syngenic irradiated LPS-activated lymphoblasts coated with peptide.

- 5 Cell lines: Target cells for peptide-specific cytotoxicity assays are Jurkat cells transfected with the HLA-A2.1/K^b chimeric gene (*e.g.*, Vitiello *et al.*, *J. Exp. Med.* 173:1007, 1991)

- 10 *In vitro* CTL activation: One week after priming, spleen cells (30×10^6 cells/flask) are co-cultured at 37°C with syngeneic, irradiated (3000 rads), peptide coated lymphoblasts (10×10^6 cells/flask) in 10 ml of culture medium/T25 flask. After six days, effector cells are harvested and assayed for cytotoxic activity.

- 15 Assay for cytotoxic activity: Target cells (1.0 to 1.5×10^6) are incubated at 37°C in the presence of 200 μ l of ^{51}Cr . After 60 minutes, cells are washed three times and resuspended in R10 medium. Peptide is added where required at a concentration of 1 μ g/ml. For the assay, 10^4 ^{51}Cr -labeled target cells are added to different concentrations of effector cells (final volume of 200 μ l) in U-bottom 96-well plates. After a 6 hour incubation period at 37°C, a 0.1 ml aliquot of supernatant is removed from each well and radioactivity is determined in a Micromedic automatic gamma counter. The percent specific lysis is determined by the formula: percent specific release = $100 \times$
- 20 $(\text{experimental release} - \text{spontaneous release}) / (\text{maximum release} - \text{spontaneous release})$. To facilitate comparison between separate CTL assays run under the same conditions, % ^{51}Cr release data is expressed as lytic units/ 10^6 cells. One lytic unit is arbitrarily defined as the number of effector cells required to achieve 30% lysis of 10,000 target cells in a 6 hour ^{51}Cr release assay. To obtain specific lytic units/ 10^6 , the lytic units/ 10^6 obtained in
- 25 the absence of peptide is subtracted from the lytic units/ 10^6 obtained in the presence of peptide. For example, if 30% ^{51}Cr release is obtained at the effector (E): target (T) ratio of 50:1 (*i.e.*, 5×10^5 effector cells for 10,000 targets) in the absence of peptide and 5:1 (*i.e.*, 5×10^4 effector cells for 10,000 targets) in the presence of peptide, the specific lytic units would be: $[(1/50,000) - (1/500,000)] \times 10^6 = 18 \text{ LU}$.

- 30 The results are analyzed to assess the magnitude of the CTL responses of animals injected with the immunogenic CTL/HTL conjugate vaccine preparation and are compared to the magnitude of the CTL response achieved using the CTL epitope as outlined in Example 3. Analyses similar to this may be performed to evaluate the

immunogenicity of peptide conjugates containing multiple CTL epitopes and/or multiple HTL epitopes. In accordance with these procedures it is found that a CTL response is induced, and concomitantly that an HTL response is induced upon administration of such compositions.

5

Example 10. Selection of CTL and HTL epitopes for inclusion in an HIV-specific vaccine.

This example illustrates the procedure for the selection of peptide epitopes for vaccine compositions of the invention. The peptides in the composition may be in the
10 form of a nucleic acid sequence, either single or one or more sequences (*i.e.*, minigene) that encodes peptide(s), or may be single and/or polyepitopic peptides.

The following principles are utilized when selecting an array of epitopes for inclusion in a vaccine composition. Each of the following principles are balanced in order to make the selection.

15 1.) Epitopes are selected which, upon administration, mimic immune responses that have been observed to be correlated with HIV clearance. For HLA Class I this includes 3-4 epitopes that come from at least one antigen of HIV. In other words, it has been observed that patients who spontaneously clear HIV generate an immune response to at least 3 epitopes on at least one HIV antigen. For HLA Class II a similar rationale is
20 employed; again 3-4 epitopes are selected from at least one HIV antigen.

2.) Epitopes are selected that have the requisite binding affinity established to be correlated with immunogenicity: for HLA Class I an IC_{50} of 500 nM or less, or for Class II an IC_{50} of 1000 nM or less.

25 3.) Sufficient supermotif bearing peptides, or a sufficient array of allele-specific motif bearing peptides, are selected to give broad population coverage. For example, epitopes are selected to provide at least 80% population coverage. A Monte Carlo analysis, a statistical evaluation known in the art and discussed herein, can be employed to assess breadth, or redundancy, of population coverage.

30 4.) When selecting epitopes for HIV antigens it may be preferable to select native epitopes. Therefore, of particular relevance for infectious disease vaccines, are epitopes referred to as "nested epitopes." Nested epitopes occur where at least two epitopes overlap in a given peptide sequence. A peptide comprising "transcendent nested epitopes" is a peptide that has both HLA class I and HLA class II epitopes in it.

When providing nested epitopes, a sequence that has the greatest number of epitopes per provided sequence is provided. A limitation on this principle is to avoid providing a peptide that is any longer than the amino terminus of the amino terminal epitope and the carboxyl terminus of the carboxyl terminal epitope in the peptide. When providing a longer peptide sequence, such as a sequence comprising nested epitopes, the sequence is screened in order to insure that it does not have pathological or other deleterious biological properties.

5.) When creating a minigene, as disclosed in greater detail in Example 11, an objective is to generate the smallest peptide possible that encompasses the epitopes of interest. The principles employed are similar, if not the same as those employed when selecting a peptide comprising nested epitopes. Additionally, however, upon determination of the nucleic acid sequence to be provided as a minigene, the peptide encoded thereby is analyzed to determine whether any "junctional epitopes" have been created. A junctional epitope is an actual binding epitope, as predicted, *e.g.*, by motif analysis. Junctional epitopes are generally to be avoided because the recipient may generate an immune response to that epitope, which is not present in a native HIV protein sequence. Of particular concern is a junctional epitope that is a "dominant epitope." A dominant epitope may lead to such a zealous response that immune responses to other epitopes are diminished or suppressed.

Peptide epitopes for inclusion in vaccine compositions are, for example, selected from those listed in Tables XXVI-XXIX and Table XXXII. A vaccine composition comprised of selected peptides, when administered, is safe, efficacious, and elicits an immune response similar in magnitude of an immune response that clears an acute HIV infection.

Example 11. Construction of Minigene Multi-Epitope DNA Plasmids

This example provides general guidance for the construction of a minigene expression plasmid. Minigene plasmids may, of course, contain various configurations of CTL and/or HTL epitopes or epitope analogs as described herein. Expression plasmids have been constructed and evaluated as described, for example, in co-pending U.S.S.N. 09/311,784 filed 5/13/99 and in Ishioka *et al.*, *J. Immunol.* 162:3915-3925, 1999. An example of such a plasmid for the expression of HIV epitopes is shown in Figure 2, which illustrates the orientation of HIV peptide epitopes in a minigene construct.

A minigene expression plasmid may include multiple CTL and HTL peptide epitopes. In the present example, HLA-A2, -A3, -B7 supermotif-bearing peptide epitopes and HLA-A1 and -A24 motif-bearing peptide epitopes are used in conjunction with DR supermotif-bearing epitopes and/or DR3 epitopes (Figure 2). Preferred epitopes are identified, for example, in Tables XXVI-XXIX and XXXII. HLA class I supermotif or motif-bearing peptide epitopes derived from multiple HIV antigens, are selected such that multiple supermotifs/motifs are represented to ensure broad population coverage. Similarly, HLA class II epitopes are selected from multiple HIV antigens to provide broad population coverage, *i.e.* both HLA DR-1-4-7 supermotif-bearing epitopes and HLA DR-3 motif-bearing epitopes are selected for inclusion in the minigene construct. The selected CTL and HTL epitopes are then incorporated into a minigene for expression in an expression vector.

Such a construct may additionally include sequences that direct the HTL epitopes to the endoplasmic reticulum. For example, the Ii protein may be fused to one or more HTL epitopes as described in co-pending application U.S.S.N. 09/311,784 filed 5/13/99, wherein the CLIP sequence of the Ii protein is removed and replaced with an HLA class II epitope sequence so that HLA class II epitope is directed to the endoplasmic reticulum, where the epitope binds to an HLA class II molecules.

This example illustrates the methods to be used for construction of a minigene-bearing expression plasmid. Other expression vectors that may be used for minigene compositions are available and known to those of skill in the art.

The minigene DNA plasmid contains a consensus Kozak sequence and a consensus murine kappa Ig-light chain signal sequence followed by CTL and/or HTL epitopes selected in accordance with principles disclosed herein. The construct can also include, for example, The sequence encodes an open reading frame fused to the Myc and His antibody epitope tag coded for by the pcDNA 3.1 Myc-His vector.

Overlapping oligonucleotides, for example eight oligonucleotides, averaging approximately 70 nucleotides in length with 15 nucleotide overlaps, are synthesized and HPLC-purified. The oligonucleotides encode the selected peptide epitopes as well as appropriate linker nucleotides, Kozak sequence, and signal sequence. The final multiepitope minigene is assembled by extending the overlapping oligonucleotides in three sets of reactions using PCR. A Perkin/Elmer 9600 PCR machine is used and a total of 30 cycles are performed using the following conditions: 95°C for 15 sec, annealing

temperature (5° below the lowest calculated T_m of each primer pair) for 30 sec, and 72°C for 1 min.

For the first PCR reaction, 5 µg of each of two oligonucleotides are annealed and extended: Oligonucleotides 1+2, 3+4, 5+6, and 7+8 are combined in 100 µl reactions containing *Pfu* polymerase buffer (1x= 10 mM KCL, 10 mM (NH₄)₂SO₄, 20 mM Tris-chloride, pH 8.75, 2 mM MgSO₄, 0.1% Triton X-100, 100 µg/ml BSA), 0.25 mM each dNTP, and 2.5 U of *Pfu* polymerase. The full-length dimer products are gel-purified, and two reactions containing the product of 1+2 and 3+4, and the product of 5+6 and 7+8 are mixed, annealed, and extended for 10 cycles. Half of the two reactions are then mixed, and 5 cycles of annealing and extension carried out before flanking primers are added to amplify the full length product for 25 additional cycles. The full-length product is gel-purified and cloned into pCR-blunt (Invitrogen) and individual clones are screened by sequencing.

Example 12. The plasmid construct and the degree to which it induces immunogenicity.

The degree to which the plasmid construct prepared using the methodology outlined in Example 11 is able to induce immunogenicity is evaluated through *in vivo* injections into mice and subsequent *in vitro* assessment of CTL and HTL activity, which are analysed using cytotoxicity and proliferation assays, respectively, as detailed *e.g.*, in U.S.S.N. 09/311,784 filed 5/13/99 and Alexander *et al.*, *Immunity* 1:751-761, 1994. To assess the capacity of the pMin minigene construct to induce CTLs *in vivo*, HLA-A11/K^b transgenic mice, for example, are immunized intramuscularly with 100 µg of naked cDNA. As a means of comparing the level of CTLs induced by cDNA immunization, a control group of animals is also immunized with an actual peptide composition that comprises multiple epitopes synthesized as a single polypeptide as they would be encoded by the minigene.

Splenocytes from immunized animals are stimulated twice with each of the respective compositions (peptide epitopes encoded in the minigene or the polyepitopic peptide), then assayed for peptide-specific cytotoxic activity in a ⁵¹Cr release assay. The results indicate the magnitude of the CTL response directed against the A3-restricted epitope, thus indicating the *in vivo* immunogenicity of the minigene vaccine and polyepitopic vaccine. It is, therefore, found that the minigene elicits immune responses directed toward the HLA-A3 supermotif peptide epitopes as does the polyepitopic peptide vaccine. A similar analysis is also performed using other HLA-A2 and HLA-B7

transgenic mouse models to assess CTL induction by HLA-A2 and HLA-B7 motif or supermotif epitopes.

To assess the capacity of a class II epitope encoding minigene to induce HTLs *in vivo*, I-A^b restricted mice, for example, are immunized intramuscularly with 100 µg of plasmid DNA. As a means of comparing the level of HTLs induced by DNA immunization, a group of control animals is also immunized with an actual peptide composition emulsified in complete Freund's adjuvant.

CD4⁺ T cells, *i.e.* HTLs, are purified from splenocytes of immunized animals and stimulated with each of the respective compositions (peptides encoded in the minigene). The HTL response is measured using a ³H-thymidine incorporation proliferation assay, (see, *e.g.*, Alexander et al. *Immunity* 1:751-761, 1994). the results indicate the magnitude of the HTL response, thus demonstrating the *in vivo* immunogenicity of the minigene.

DNA minigenes, constructed as described in Example 11, may also be evaluated as a vaccine in combination with a boosting agent using a prime boost protocol. The boosting agent may consist of recombinant protein (*e.g.*, Barnett *et al.*, *Aids Res. and Human Reotroviruses* 14, Supplement 3:S299-S309, 1998) or recombinant vaccinia, for example, expressing a minigene or DNA encoding the complete protein of interest (see, *e.g.*, Hanke et al., *Vaccine* 16:439-445, 1998; Sedegah *et al.*, *Proc. Natl. Acad. Sci USA* 95:7648-53, 1998; Hanke and McMichael, *Immunol. Letters* 66:177-181, 1999; and Robinson *et al.*, *Nature Med.* 5:526-34, 1999).

For example, the efficacy of the DNA minigene may be evaluated in transgenic mice. In this example, A2.1/K^b transgenic mice are immunized IM with 100 µg of the DNA minigene encoding the immunogenic peptides. After an incubation period (ranging from 3-9 weeks), the mice are boosted IP with 10⁷ pfu/mouse of a recombinant vaccinia virus expressing the same sequence encoded by the DNA minigene. Control mice are immunized with 100 µg of DNA or recombinant vaccinia without the minigene sequence, or with DNA encoding the minigene, but without the vaccinia boost. After an additional incubation period of two weeks, splenocytes from the mice are immediately assayed for peptide-specific activity in an ELISPOT assay. Additionally, splenocytes are stimulated *in vitro* with the A2-restricted peptide epitopes encoded in the minigene and recombinant vaccinia, then assayed for peptide-specific activity in an IFN-γ ELISA. It is found that the minigene utilized in a prime-boost mode elicits greater immune responses toward the HLA-A2 supermotif peptides than with DNA alone. Such an analysis is also performed

using other HLA-A11 and HLA-B7 transgenic mouse models to assess CTL induction by HLA-A3 and HLA-B7 motif or supermotif epitopes.

Example 13. Peptide Composition for Prophylactic Uses

5 Vaccine compositions of the present invention are used to prevent HIV infection in persons who are at risk for such infection. For example, a polyepitopic peptide epitope composition (or a nucleic acid comprising the same) containing multiple CTL and HTL epitopes such as those selected in Examples 9 and/or 10, which are also selected to target greater than 80% of the population, is administered to individuals at risk for HIV
10 infection. The composition is provided as a single lipidated polypeptide that encompasses multiple epitopes. The vaccine is administered in an aqueous carrier comprised of Freund's Incomplete Adjuvant. The dose of peptide for the initial immunization is from about 1 to about 50,000 µg, generally 100-5,000 µg, for a 70 kg patient. The initial administration of vaccine is followed by booster dosages at 4 weeks
15 followed by evaluation of the magnitude of the immune response in the patient, by techniques that determine the presence of epitope-specific CTL populations in a PBMC sample. Additional booster doses are administered as required. The composition is found to be both safe and efficacious as a prophylaxis against HIV infection.

Alternatively, the polyepitopic peptide composition can be administered as a
20 nucleic acid in accordance with methodologies known in the art and disclosed herein.

Example 14. Polyepitopic Vaccine Compositions Derived from Native HIV Sequences

A native HIV polyprotein sequence is screened, preferably using computer algorithms defined for each class I and/or class II supermotif or motif, to identify
25 "relatively short" regions of the polyprotein that comprise multiple epitopes and is preferably less in length than an entire native antigen. This relatively short sequence that contains multiple distinct, even overlapping, epitopes is selected and used to generate a minigene construct. The construct is engineered to express the peptide, which corresponds to the native protein sequence. The "relatively short" peptide is generally
30 less than 250 amino acids in length, often less than 100 amino acids in length, preferably less than 75 amino acids in length, and more preferably less than 50 amino acids in length. The protein sequence of the vaccine composition is selected because it has maximal number of epitopes contained within the sequence, *i.e.*, it has a high concentration of epitopes. As noted herein, epitope motifs may be nested or overlapping

(i.e., frame shifted relative to one another). For example, with frame shifted overlapping epitopes, two 9-mer epitopes and one 10-mer epitope can be present in a 10 amino acid peptide. Such a vaccine composition is administered for therapeutic or prophylactic purposes.

5 The vaccine composition will preferably include, for example, three CTL epitopes and at least one HTL epitope from HIV. This polyepitopic native sequence is administered either as a peptide or as a nucleic acid sequence which encodes the peptide. Alternatively, an analog can be made of this native sequence, whereby one or more of the epitopes comprise substitutions that alter the cross-reactivity and/or binding affinity
10 properties of the polyepitopic peptide.

 The embodiment of this example provides for the possibility that an as yet undiscovered aspect of immune system processing will apply to the native nested sequence and thereby facilitate the production of therapeutic or prophylactic immune response-inducing vaccine compositions. Additionally such an embodiment provides for
15 the possibility of motif-bearing epitopes for an HLA makeup that is presently unknown. Furthermore, this embodiment (absent analogs) directs the immune response to multiple peptide sequences that are actually present in native HIV antigens thus avoiding the need to evaluate any junctional epitopes. Lastly, the embodiment provides an economy of scale when producing nucleic acid vaccine compositions.

20 Related to this embodiment, computer programs can be derived in accordance with principles in the art, which identify in a target sequence, the greatest number of epitopes per sequence length.

Example 15. Polyepitopic Vaccine Compositions Directed To Multiple Diseases

25 The HIV peptide epitopes of the present invention are used in conjunction with peptide epitopes from target antigens related to one or more other diseases, to create a vaccine composition that is useful for the prevention or treatment of HIV as well as the one or more other disease(s). Examples of the other diseases include, but are not limited to, HCV and HBV.

30 For example, a polyepitopic peptide composition comprising multiple CTL and HTL epitopes that target greater than 98% of the population may be created for administration to individuals at risk for both HBV and HIV infection. The composition can be provided as a single polypeptide that incorporates the multiple epitopes from the

various disease-associated sources, or can be administered as a composition comprising one or more discrete epitopes.

Example 16. Use of peptides to evaluate an immune response

5 Peptides of the invention may be used to analyze an immune response for the presence of specific CTL or HTL populations directed to HIV. Such an analysis may be performed in a manner as that described by Ogg *et al.*, *Science* 279:2103-2106, 1998. In the following example, peptides in accordance with the invention are used as a reagent for diagnostic or prognostic purposes, not as an immunogen.

10 In this example highly sensitive human leukocyte antigen tetrameric complexes ("tetramers") are used for a cross-sectional analysis of, for example, HIV HLA-A*0201-specific CTL frequencies from HLA A*0201-positive individuals at different stages of infection or following immunization using an HIV peptide containing an A*0201 motif. Tetrameric complexes are synthesized as described (Musey *et al.*, *N. Engl. J. Med.*
15 337:1267, 1997). Briefly, purified HLA heavy chain (A*0201 in this example) and β 2-microglobulin are synthesized by means of a prokaryotic expression system. The heavy chain is modified by deletion of the transmembrane-cytosolic tail and COOH-terminal addition of a sequence containing a BirA enzymatic biotinylation site. The heavy chain, β 2-microglobulin, and peptide are refolded by dilution. The 45-kD refolded product is
20 isolated by fast protein liquid chromatography and then biotinylated by BirA in the presence of biotin (Sigma, St. Louis, Missouri), adenosine 5'triphosphate and magnesium. Streptavidin-phycoerythrin conjugate is added in a 1:4 molar ratio, and the tetrameric product is concentrated to 1 mg/ml. The resulting product is referred to as tetramer-phycoerythrin.

25 For the analysis of patient blood samples, approximately one million PBMCs are centrifuged at 300g for 5 minutes and resuspended in 50 μ l of cold phosphate-buffered saline. Tri-color analysis is performed with the tetramer-phycoerythrin, along with anti-CD8-Tricolor, and anti-CD38. The PBMCs are incubated with tetramer and antibodies on ice for 30 to 60 min and then washed twice before formaldehyde fixation. Gates are
30 applied to contain >99.98% of control samples. Controls for the tetramers include both A*0201-negative individuals and A*0201-positive uninfected donors. The percentage of cells stained with the tetramer is then determined by flow cytometry. The results indicate the number of cells in the PBMC sample that contain epitope-restricted CTLs, thereby

readily indicating the extent of immune response to the HIV epitope, and thus the stage of infection with HIV, the status of exposure to HIV, or exposure to a vaccine that elicits a protective or therapeutic response.

5 Example 17. Use of Peptide Epitopes to Evaluate Recall Responses

The peptide epitopes of the invention are used as reagents to evaluate T cell responses, such as acute or recall responses, in patients. Such an analysis may be performed on patients who have recovered from infection, who are chronically infected with HIV, or who have been vaccinated with an HIV vaccine.

10 For example, the class I restricted CTL response of persons who have been vaccinated may be analyzed. The vaccine may be any HIV vaccine. PBMC are collected from vaccinated individuals and HLA typed. Appropriate peptide epitopes of the invention that, optimally, bear supermotifs to provide cross-reactivity with multiple HLA supertype family members, are then used for analysis of samples derived from individuals
15 who bear that HLA type.

PBMC from vaccinated individuals are separated on Ficoll-Histopaque density gradients (Sigma Chemical Co., St. Louis, MO), washed three times in HBSS (GIBCO Laboratories), resuspended in RPMI-1640 (GIBCO Laboratories) supplemented with L-glutamine (2mM), penicillin (50U/ml), streptomycin (50 µg/ml), and Hepes (10mM)
20 containing 10% heat-inactivated human AB serum (complete RPMI) and plated using microculture formats. A synthetic peptide comprising an epitope of the invention is added at 10 µg/ml to each well and HBV core 128-140 epitope is added at 1 µg/ml to each well as a source of T cell help during the first week of stimulation.

In the microculture format, 4×10^5 PBMC are stimulated with peptide in 8
25 replicate cultures in 96-well round bottom plate in 100 µl/well of complete RPMI. On days 3 and 10, 100 ml of complete RPMI and 20 U/ml final concentration of rIL-2 are added to each well. On day 7 the cultures are transferred into a 96-well flat-bottom plate and restimulated with peptide, rIL-2 and 10^5 irradiated (3,000 rad) autologous feeder cells. The cultures are tested for cytotoxic activity on day 14. A positive CTL response
30 requires two or more of the eight replicate cultures to display greater than 10% specific ^{51}Cr release, based on comparison with uninfected control subjects as previously described (Rehermann, *et al.*, *Nature Med.* 2:1104,1108, 1996; Rehermann *et al.*, *J. Clin. Invest.* 97:1655-1665, 1996; and Rehermann *et al.* *J. Clin. Invest.* 98:1432-1440, 1996).

Target cell lines are autologous and allogeneic EBV-transformed B-LCL that are either purchased from the American Society for Histocompatibility and Immunogenetics (ASHI, Boston, MA) or established from the pool of patients as described (Guilhot, *et al. J. Virol.* 66:2670-2678, 1992).

5 Cytotoxicity assays are performed in the following manner. Target cells consist of either allogeneic HLA-matched or autologous EBV-transformed B lymphoblastoid cell line that are incubated overnight with the synthetic peptide epitope of the invention at 10 μ M, and labeled with 100 μ Ci of 51 Cr (Amersham Corp., Arlington Heights, IL) for 1 hour after which they are washed four times with HBSS.

10 Cytolytic activity is determined in a standard 4-h, split well 51 Cr release assay using U-bottomed 96 well plates containing 3,000 targets/well. Stimulated PBMC are tested at effector/target (E/T) ratios of 20-50:1 on day 14. Percent cytotoxicity is determined from the formula: $100 \times [(\text{experimental release} - \text{spontaneous release}) / (\text{maximum release} - \text{spontaneous release})]$. Maximum release is determined by
 15 lysis of targets by detergent (2% Triton X-100; Sigma Chemical Co., St. Louis, MO). Spontaneous release is <25% of maximum release for all experiments.

The results of such an analysis indicate the extent to which HLA-restricted CTL populations have been stimulated by previous exposure to HIV or an HIV vaccine.

The class II restricted HTL responses may also be analyzed. Purified PBMC are
 20 cultured in a 96-well flat bottom plate at a density of 1.5×10^5 cells/well and are stimulated with 10 μ g/ml synthetic peptide, whole antigen, or PHA. Cells are routinely plated in replicates of 4-6 wells for each condition. After seven days of culture, the medium is removed and replaced with fresh medium containing 10U/ml IL-2. Two days later, 1 μ Ci 3 H-thymidine is added to each well and incubation is continued for an additional 18
 25 hours. Cellular DNA is then harvested on glass fiber mats and analyzed for 3 H-thymidine incorporation. Antigen-specific T cell proliferation is calculated as the ratio of 3 H-thymidine incorporation in the presence of antigen divided by the 3 H-thymidine incorporation in the absence of antigen.

30 Example 18. Induction Of Specific CTL Response In Humans

A human clinical trial for an immunogenic composition comprising CTL and HTL epitopes of the invention is set up as an IND Phase I, dose escalation study and carried

out as a randomized, double-blind, placebo-controlled trial. Such a trial is designed, for example, as follows:

A total of about 27 subjects are enrolled and divided into 3 groups:

Group I: 3 subjects are injected with placebo and 6 subjects are injected with 5 μ g of peptide composition;

Group II: 3 subjects are injected with placebo and 6 subjects are injected with 50 μ g peptide composition;

Group III: 3 subjects are injected with placebo and 6 subjects are injected with 500 μ g of peptide composition.

After 4 weeks following the first injection, all subjects receive a booster inoculation at the same dosage.

The endpoints measured in this study relate to the safety and tolerability of the peptide composition as well as its immunogenicity. Cellular immune responses to the peptide composition are an index of the intrinsic activity of this the peptide composition, and can therefore be viewed as a measure of biological efficacy. The following summarize the clinical and laboratory data that relate to safety and efficacy endpoints.

Safety: The incidence of adverse events is monitored in the placebo and drug treatment group and assessed in terms of degree and reversibility.

Evaluation of Vaccine Efficacy: For evaluation of vaccine efficacy, subjects are bled before and after injection. Peripheral blood mononuclear cells are isolated from fresh heparinized blood by Ficoll-Hypaque density gradient centrifugation, aliquoted in freezing media and stored frozen. Samples are assayed for CTL and HTL activity.

The vaccine is found to be both safe and efficacious.

25 Example 19. Phase II Trials In Patients Infected With HIV

Phase II trials are performed to study the effect of administering the CTL-HTL peptide compositions to patients having chronic HIV infection. The main objectives of the trials are to determine an effective dose and regimen for inducing CTLs in chronically infected HIV patients, to establish the safety of inducing a CTL and HTL response in these patients, and to see to what extent activation of CTLs improves the clinical picture of chronically infected HIV patients, as manifested by a reduction in viral load and an increase in CD4⁺ cells counts. Such a study is designed, for example, as follows:

The studies are performed in multiple centers. The trial design is an open-label, uncontrolled, dose escalation protocol wherein the peptide composition is administered as

a single dose followed six weeks later by a single booster shot of the same dose. The dosages are 50, 500 and 5,000 micrograms per injection. Drug-associated adverse effects (severity and reversibility) are recorded.

There are three patient groupings. The first group is injected with 50 micrograms of the peptide composition and the second and third groups with 500 and 5,000 micrograms of peptide composition, respectively. The patients within each group range in age from 21-65, include both males and females, and represent diverse ethnic backgrounds. All of them are infected with HIV for over five years and are HCV, HBV and delta hepatitis virus (HDV) negative, but have positive levels of HIV antigen.

The viral load and CD4⁺ levels are monitored to assess the effects of administering the peptide compositions. The vaccine composition is found to be both safe and efficacious in the treatment of HIV infection.

Example 20. Induction of CTL Responses Using a Prime Boost Protocol

A prime boost protocol similar in its underlying principle to that used to evaluate the efficacy of a DNA vaccine in transgenic mice, which was described in Example 12, may also be used for the administration of the vaccine to humans. Such a vaccine regimen may include an initial administration of, for example, naked DNA followed by a boost using recombinant virus encoding the vaccine, or recombinant protein/polypeptide or a peptide mixture administered in an adjuvant.

For example, the initial immunization may be performed using an expression vector, such as that constructed in Example 11, in the form of naked nucleic acid administered IM (or SC or ID) in the amounts of 0.5-5 mg at multiple sites. The nucleic acid (0.1 to 1000 µg) can also be administered using a gene gun. Following an incubation period of 3-4 weeks, a booster dose is then administered. The booster can be recombinant fowlpox virus administered at a dose of $5 \cdot 10^7$ to $5 \cdot 10^9$ pfu. An alternative recombinant virus, such as an MVA, canarypox, adenovirus, or adeno-associated virus, can also be used for the booster, or the polyepitopic protein or a mixture of the peptides can be administered. For evaluation of vaccine efficacy, patient blood samples will be obtained before immunization as well as at intervals following administration of the initial vaccine and booster doses of the vaccine. Peripheral blood mononuclear cells are isolated from fresh heparinized blood by Ficoll-Hypaque density gradient centrifugation, aliquoted in freezing media and stored frozen. Samples are assayed for CTL and HTL activity.

Example 21. Administration of Vaccine Compositions Using Dendritic Cells

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Another way of identifying motif-bearing peptides is to elute them from cells bearing defined MHC molecules. For example, EBV transformed B cell lines used for tissue typing, have been extensively characterized to determine which HLA molecules they express. In certain cases these cells express only a single type of HLA molecule. These cells can then be infected with a pathogenic organism or transfected with nucleic acids that express the antigen of interest, e.g. HIV regulatory or structural proteins. Thereafter, peptides produced by endogenous antigen processing of peptides produced consequent to infection (or as a result of transfection) will bind to HLA molecules within the cell and be transported and displayed on the cell surface.

30

Alternatively, cell lines that do not express any endogenous HLA molecules can be transfected with an expression construct encoding a single HLA allele. These cells

may then be used as described, *i.e.*, they may be infected with a pathogenic organism or transfected with nucleic acid encoding an antigen of interest to isolate peptides corresponding to the pathogen or antigen of interest that have been presented on the cell surface. Peptides obtained from such an analysis will bear motif(s) that correspond to binding to the single HLA allele that is expressed in the cell.

As appreciated by one in the art, one can perform a similar analysis on a cell bearing more than one HLA allele and subsequently determine peptides specific for each HLA allele expressed. Moreover, one of skill would also recognize that means other than infection or transfection, such as loading with a protein antigen, can be used to provide a source of antigen to the cell.

The above examples are provided to illustrate the invention but not to limit its scope. For example, the human terminology for the Major Histocompatibility Complex, namely HLA, is used throughout this document. It is to be appreciated that these principles can be extended to other species as well. Thus, other variants of the invention will be readily apparent to one of ordinary skill in the art and are encompassed by the appended claims. All publications, patents, and patent application cited herein are hereby incorporated by reference for all purposes.

TABLE I

SUPERMOTIFS	POSITION 2 (Primary Anchor)	POSITION 3 (Primary Anchor)	POSITION C Terminus (Primary Anchor)
A1	T <i>L</i> V <i>M</i> S		F <i>W</i> Y
A2	L <i>I</i> V <i>M</i> A <i>T</i> Q		I <i>V</i> M <i>AT<i>L</i></i>
A3	V <i>S</i> M <i>A</i> T <i>L</i> I		R K
A24	Y <i>F</i> W <i>I</i> V <i>L</i> M <i>T</i>		F <i>I</i> Y <i>W</i> L <i>M</i>
B7	P		V <i>I</i> L <i>F</i> M <i>W</i> Y <i>A</i>
B27	R H K		F <i>Y</i> L <i>W</i> M <i>I</i> V <i>A</i>
B44	E D		F <i>W</i> Y <i>L</i> I M <i>VA</i>
B58	A T S		F <i>W</i> Y <i>L</i> I V <i>MA</i>
B62	Q <i>L</i> I <i>VMP</i>		F <i>W</i> Y <i>M</i> I <i>VLA</i>
MOTIFS			
A1	T S M		Y
A1		D E A S	Y
A2.1	L <i>M</i> V <i>Q</i> I A <i>T</i>		V <i>L</i> I M <i>AT</i>
A3	L <i>M</i> V <i>IS<i>A</i>T<i>F</i>C<i>GD</i></i>		K <i>Y</i> R <i>H</i> F <i>A</i>
A11	V <i>T</i> M <i>L</i> I S <i>A</i> G <i>NC<i>D</i>F</i>		K <i>R</i> Y H
A24	Y F W M		F L I W
A*3101	M <i>V</i> T <i>A</i> L I S		R K
A*3301	M <i>V</i> A <i>L</i> F <i>IST</i>		R K
A*6801	A <i>V</i> T <i>MS<i>L</i>I</i>		R K
B*0702	P		L <i>M</i> F <i>W</i> Y <i>A</i> I V
B*3501	P		L <i>M</i> F <i>W</i> Y <i>IVA</i>
B51	P		L <i>I</i> V <i>F</i> W <i>YAM</i>
B*5301	P		I <i>M</i> F <i>W</i> Y <i>A</i> L V
B*5401	P		A <i>T</i> I <i>V</i> L <i>M</i> F <i>W</i> Y

Bolded residues are preferred, italicized residues are less preferred: A peptide is considered motif-bearing if it has primary anchors at each primary anchor position for a motif or supermotif as specified in the above table.

TABLE Ia

SUPERMOTIFS	POSITION	POSITION	POSITION
	2 (Primary Anchor)	3 (Primary Anchor)	C Terminus (Primary Anchor)
A1	T <i>ILVMS</i>		FWY
A2	<i>VQAT</i>		VLIMAT
A3	V <i>SMATLI</i>		RK
A24	Y <i>FWIVLMT</i>		FIYWLM
B7	P		VILFMWYA
B27	RHK		FYLWMIVA
B58	ATS		FWYLVMA
B62	Q <i>LIVMP</i>		FWYMIVLA
MOTIFS			
A1	TSM		Y
A1		DEAS	Y
A2.1	<i>VQAT</i> *		VLIMAT
A3.2	LMVISATFCGD		KYRHFA
A11	VTMLISAGNCDF		KRHY
A24	YFW		FLIW

*If 2 is V, or Q, the C-term is not L

Bolded residues are preferred, italicized residues are less preferred: A peptide is considered motif-bearing if it has primary anchors at each primary anchor position for a motif or supermotif as specified in the above table.

TABLE II

		POSITION								
		1	2	3	4	5	6	7	8	C-terminus
<u>SUPERMOTIFS</u>										
A1			1° Anchor TLVMS							1° Anchor FWY
A2			1° Anchor LIVMATQ							1° Anchor LIVMAT
A3	preferred		1° Anchor VSMATLI	YFW (4/5)		YFW (3/5)	YFW (4/5)	P (4/5)		1° Anchor RK
	deleterious	DE (3/5); P (5/5)		DE (4/5)						
A24			1° Anchor YFWIVLM T							1° Anchor FIYWLM
B7	preferred	FWY (5/5) LIVM (3/5)	1° Anchor P	FWY (4/5)					FWY (3/5)	1° Anchor VILFMWYA
	deleterious	DE (3/5); P(5/5); G(4/5); A(3/5); QN (3/5)				DE (3/5)	G (4/5)	QN (4/5)	DE (4/5)	
B27			1° Anchor RHK							1° Anchor FYLWMIVA
B44			1° Anchor ED							1° Anchor FWYLIMVA
B58			1° Anchor ATS							1° Anchor FWYLVMA
B62			1° Anchor QLIVMP							1° Anchor FWYMIVLA

POSITION

1	2	3	4	5	6	7	8	C-terminus
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POSITION

1	2	3	4	5	6	7	8	C-terminus
---	---	---	---	---	---	---	---	------------

MOTIFS

A1 preferred 9-mer	GFYW	$\frac{1^{\circ}\text{Anchor}}{\text{STM}}$	DEA	YFW	P	DEQN	YFW	$\frac{1^{\circ}\text{Anchor}}{\text{Y}}$
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deleterious DE

A1 preferred 9-mer	GRHK	ASTCLIV M	$\frac{1^{\circ}\text{Anchor}}{\text{DE/AS}}$	GSTC	ASTC	LIVM	DE	$\frac{1^{\circ}\text{Anchor}}{\text{Y}}$
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deleterious A

RHKDEPY FW	DE	PQN	RHK	PG	GP
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POSITION

	1	2	3	4	5	6	7	8	9 or C-terminus	C-terminus
A1 preferred 10-mer	YFW	<u>1°Anchor</u> STM	DEAQN	A	YFWQN		PASTC	GDE	P	<u>1°Anchor</u> Y
deleterious	GP		RHKGLIV M	DE	RHK	QNA	RHKYFW	RHK	A	
A1 preferred 10-mer	YFW	STCLIVM	<u>1°Anchor</u> DE4S	A	YFW		PG	G	YFW	<u>1°Anchor</u> Y
deleterious	RHK	RHKDEPY FW			P	G		PRHK	QN	
A2.1 preferred 9-mer	YFW	<u>1°Anchor</u> LMIVQAT	YFW	STC	YFW		A	P	<u>1°Anchor</u> VLIMAT	
deleterious	DEP		DERKH			RKH	DERKH			
A2.1 preferred 10-mer	AYFW	<u>1°Anchor</u> LMIVQAT	LVIM	G		G		FYWL VIM		<u>1°Anchor</u> VLIMAT
deleterious	DEP		DE	RKHA	P		RKH	DERK H	RKH	

POSITION

	1	2	3	4	5	6	7	8	9 or C-terminus
A3101 preferred	RHK	<u>1°Anchor</u> MVTALIS	YFW	P		YFW	YFW	AP	<u>1°Anchor</u> RK
deleterious	DEP		DE		ADE	DE	DE	DE	
A3301 preferred		<u>1°Anchor</u> MVALF/S T	YFW				AYFW		<u>1°Anchor</u> RK
deleterious	GP		DE						
A6801 preferred	YFWSTC	<u>1°Anchor</u> AVTMSLI			YFWLIV M		YFW	P	<u>1°Anchor</u> RK
deleterious	GP		DEG		RHK			A	
B0702 preferred	RHKFWY	<u>1°Anchor</u> P	RHK		RHK	RHK	RHK	PA	<u>1°Anchor</u> LMFWYIV
deleterious	DEQNP		DEP	DE	DE	GDE	QN	DE	
B3501 preferred	FWYLIVM	<u>1°Anchor</u> P	FWY				FWY		<u>1°Anchor</u> LMFWYIV
deleterious	AGP				G	G			

		POSITION								
		1	2	3	4	5	6	7	8	9 or C-terminus
B51	preferred	LIVMFVY	<u>1°Anchor</u> P	FWY	STC	FWY		G	FWY	<u>1°Anchor</u> LIVFWYAM
	deleterious	AGPDERHKSTC				DE	G	DEQN	GDE	
B5301	preferred	LIVMFVY	<u>1°Anchor</u> P	FWY	STC	FWY		LIVMFVY	FWY	<u>1°Anchor</u> IMFWYALV
	deleterious	AGPQN					G	RHKQN	DE	
B5401	preferred	FWY	<u>1°Anchor</u> P	FWYLIVM		LIVM		ALIVM	FWYAP	<u>1°Anchor</u> ATIVLMFW Y
	deleterious	GPQNDE		GDESTC		RHKDE	DE	QNDGE	DE	

Italicized residues indicate less preferred or "tolerated" residues.
The information in Table II is specific for 9-mers unless otherwise specified.

TABLE III

MOTIFS	POSITION					
	1° anchor 1	2	3	4	5	1° anchor 6
DR4 preferred deleterious	FMYLIVW	M	T	W	I	VSTCPALIM
DR1 preferred deleterious	MFLIVWY	C	CH	PAMQ FD	CWD	VMATSPLIC
DR7 preferred deleterious	MFLIVWY	M	W	A		IVMSACTPL
DR Supermotif	MFLIVWY	C		G		GRD
DR3 MOTIFS	1° anchor 1	2	3	1° anchor 4	5	1° anchor 6
motif a preferred	LIVMFY			D		
motif b preferred	LIVMFAY			DNQUEST		KRH
						VMSTACPLI
						IV
						G
						AVM
						MH
						WDE

Italicized residues indicate less preferred or "tolerated" residues.

Table IV. HLA Class I Standard Peptide Binding Affinity.

ALLELE	STANDARD PEPTIDE	SEQUENCE	STANDARD BINDING AFFINITY (nM)
A*0101	944.02	YLEPAIAKY	25
A*0201	941.01	FLPSDYFPSV	5.0
A*0202	941.01	FLPSDYFPSV	4.3
A*0203	941.01	FLPSDYFPSV	10
A*0205	941.01	FLPSDYFPSV	4.3
A*0206	941.01	FLPSDYFPSV	3.7
A*0207	941.01	FLPSDYFPSV	23
A*6802	1141.02	ETQAGYPAL	40
A*0301	941.12	KVFPYALINK	11
A*1101	940.06	AVDLYHFLK	6.0
A*3101	941.12	KVFPYALINK	18
A*3301	1083.02	STLPETYVRR	29
A*6801	941.12	KVFPYALINK	8.0
A*2402	979.02	AYIDNYNKF	12
B*0702	1075.23	APRTLVL	5.5
B*3501	1021.05	FPFKYAAAF	7.2
B51	1021.05	FPFKYAAAF	5.5
B*5301	1021.05	FPFKYAAAF	9.3
B*5401	1021.05	FPFKYAAAF	10

Table V. HLA Class II Standard Peptide Binding Affinity.

Allele	Nomenclature	Standard Peptide	Sequence	Binding Affinity (nM)
DRB1*0101	DR1	515.01	PKYVKQNTLKLAT	5.0
DRB1*0301	DR3	829.02	YKTIAFDEEARR	300
DRB1*0401	DR4w4	515.01	PKYVKQNTLKLAT	45
DRB1*0404	DR4w14	717.01	YARFQSQTTLKQKT	50
DRB1*0405	DR4w15	717.01	YARFQSQTTLKQKT	38
DRB1*0701	DR7	553.01	QYIKANSKFIGITE	25
DRB1*0802	DR8w2	553.01	QYIKANSKFIGITE	49
DRB1*0803	DR8w3	553.01	QYIKANSKFIGITE	1600
DRB1*0901	DR9	553.01	QYIKANSKFIGITE	75
DRB1*1101	DR5w11	553.01	QYIKANSKFIGITE	20
DRB1*1201	DR5w12	1200.05	EALIHQLKINPYVLS	298
DRB1*1302	DR6w19	650.22	QYIKANAKFIGITE	3.5
DRB1*1501	DR2w2 β 1	507.02	GRTQDENPVVHFFKNIV TPRTPPP	9.1
DRB3*0101	DR52a	511	NGQIGNDPNRDIL	470
DRB4*0101	DRw53	717.01	YARFQSQTTLKQKT	58
DRB5*0101	DR2w2 β 2	553.01	QYIKANSKFIGITE	20

The "Nomenclature" column lists the allelic designations used in Tables XIX and XX.

Table VI

HLA-supertype	Allele-specific HLA-supertype members	
	Verified ^a	Predicted ^b
A1	A*0101, A*2501, A*2601, A*2602, A*3201	A*0102, A*2604, A*3601, A*4301, A*8001
A2	A*0201, A*0202, A*0203, A*0204, A*0205, A*0206, A*0207, A*0209, A*0214, A*6802, A*6901	A*0208, A*0210, A*0211, A*0212, A*0213
A3	A*0301, A*1101, A*3101, A*3301, A*6601	A*0302, A*1102, A*2603, A*3302, A*3303, A*3401, A*3402, A*6601, A*6602, A*7401
A24	A*2301, A*2402, A*3001	A*2403, A*2404, A*3002, A*3003
B7	B*0702, B*0703, B*0704, B*0705, B*1508, B*3501, B*3502, B*3503, B*3504, B*3505, B*3506, B*3507, B*3508, B*5101, B*5102, B*5103, B*5104, B*5105, B*5301, B*5401, B*5501, B*5502, B*5601, B*5602, B*6701, B*7801	B*1511, B*4201, B*5901
B27	B*1401, B*1402, B*1509, B*2702, B*2703, B*2704, B*2705, B*2706, B*3801, B*3901, B*3902, B*7301	B*2701, B*2707, B*2708, B*3802, B*3903, B*3904, B*3905, B*4801, B*4802, B*1510, B*1518, B*1503
B44	B*1801, B*1802, B*3701, B*4402, B*4403, B*4404, B*4001, B*4002, B*4006	B*4101, B*4501, B*4701, B*4901, B*5001
B58	B*5701, B*5702, B*5801, B*5802, B*1516, B*1517	B*1301, B*1302, B*1504, B*1505, B*1506, B*1507, B*1515, B*1520, B*1521, B*1512, B*1514, B*1519
B62	B*1501, B*1502, B*1513, B*5201	

a. Verified alleles includes alleles whose specificity has been determined by pool sequencing analysis, peptide binding assays, or by analysis of the sequences of CTL epitopes.

b. Predicted alleles are alleles whose specificity is predicted on the basis of B and F pocket structure to overlap with the supertype specifically.

Table VII
HIV A01 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101	SEQ ID NO
ENV	KLWVTYY	44	8	11	17		1
ENV	NLWVTYY	44	8	35	56		2
ENV	DTEVINW	75	8	19	53		3
ENV	VTEFNW	102	8	34	53		4
ENV	RIGPQTF	357	8	11	17		5
ENV	GIGPQTF	360	8	01	33		6
ENV	SIGSQAF	360	8	01	33		7
ENV	KLREIKQF	405	8	01	25		8
ENV	STNGTET	537	8	01	17		9
ENV	AVGIGAF	595	8	11	17		10
ENV	HLLKLTW	650	8	13	20		11
ENV	HLLQLTVW	650	8	34	53		12
ENV	HMLQLTVW	650	8	10	16		13
ENV	RVLAVRY	665	8	33	52		14
ENV	NVPWSSW	693	8	13	20		15
ENV	EIWDNMTW	716	8	13	20		16
ENV	DLALDKW	754	8	21	33		17
ENV	ELLELDKW	754	8	20	31		18
ENV	DITNWLWY	769	8	10	16		19
ENV	WLWYIKIF	773	8	50	78		20
ENV	LIGLRIF	787	8	16	25		21
ENV	LIGLRIF	787	8	29	45		22
ENV	SIRLVNGF	842	8	13	20		23
ENV	SIRLVSGF	842	8	13	20		24
ENV	DLRLCLF	856	8	17	27		25
ENV	DLRLCLF	856	8	38	59		26
ENV	RSICLESY	858	8	35	55		27
ENV	ELLGRRGW	881	8	31	37		28
ENV	TVYGVVW	48	9	55	86		29
ENV	NVTENFMW	101	9	34	53		30
ENV	DSSNSTGY	218	9	01	20		31
ENV	ILKCDKKF	271	9	12	19		32
ENV	RIGPQTFY	357	9	11	17		33
ENV	GIGPQTFY	360	9	01	33		34
ENV	SIGSQAFY	360	9	01	33		35
ENV	DLEITHSF	428	9	21	33		36
ENV	HSFNCGEF	434	9	36	56		37
ENV	HSFNCGEF	434	9	16	25		38
ENV	RIKQINMW	488	9	30	47		39
ENV	RIKQINMW	488	9	12	19		40
ENV	GSENGTET	538	9	02	18		41
ENV	GIGAVFLG	598	9	11	18		42
ENV	MLGAMFLG	599	9	04	36		43
ENV	TIGAMFLG	599	9	03	27		44
ENV	LICTAVPW	688	9	19	30		45
ENV	LICTNVPW	688	9	17	27		46
ENV	LICTTVPW	688	9	12	19		47
ENV	ALDKWASLW	757	9	11	17		48
ENV	ELDKWASLW	757	9	18	28		49
ENV	GLIGLRIF	786	9	15	23		50

Table VII
HIV A01 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101	SEQ ID NO
ENV	GLIGLRIVF	786	9	29	45		51
ENV	IVNRVRQGY	799	9	38	59		52
ENV	RSIRLVNGF	841	9	12	19		53
ENV	RSIRLVSGF	841	9	13	20		54
ENV	VSGFLALAW	846	9	16	25		55
ENV	FSYIHLRDF	863	9	18	28		56
ENV	SLKGLRLGW	889	9	11	39		57
ENV	SLRGLQKRW	889	9	05	18		58
ENV	RLGWGLKY	894	9	09	29		59
ENV	VTVYGVVPW	47	10	55	86		60
ENV	QMIHDIISLW	116	10	29	45		61
ENV	ITQACPVSF	245	10	29	45		62
ENV	VSEPIPIHY	253	10	28	44		63
ENV	PIIYCAPAGF	260	10	27	42		64
ENV	PIIYCTPAGF	260	10	10	16		65
ENV	AILKCNDKKF	270	10	12	19		66
ENV	NTSPSRVAY	376	10	01	33		67
ENV	HSFNCGGEFF	434	10	35	55		68
ENV	HSFNCRGEFF	434	10	16	25		69
ENV	NTENKTEIF	537	10	01	17		70
ENV	NTTGNITET	537	10	01	17		71
ENV	KLICITAVPW	687	10	19	30		72
ENV	KLICITTPWP	687	10	17	27		73
ENV	TTNVPWNSS	691	10	11	19		74
ENV	SIVNRVRQGY	798	10	36	56		75
ENV	LVSGLALAW	845	10	16	25		76
ENV	DLRNLCLFSY	856	10	16	25		77
ENV	DLRSLCLFSY	856	10	35	55		78
ENV	IVELLGRGW	879	10	22	34		79
ENV	SSLKGLRLGW	886	10	10	16		80
ENV	WVTVYGVVPV	46	11	55	86		81
ENV	PWKEATITL	54	11	22	34		82
ENV	TLFCASDAKA	64	11	40	63		83
ENV	VITQACPVSF	244	11	14	22		84
ENV	KVSEFPIPIHY	252	11	28	44		85
ENV	GTAGNSSRAA	375	11	01	33		86
ENV	TTHSFNCGGE	432	11	16	25		87
ENV	TTHSFNCRGE	432	11	12	19		88
ENV	VMIISFNCGGE	432	11	13	20		89
ENV	HSFNCGGEFFY	434	11	35	55		90
ENV	HSFNCRGEFFY	434	11	16	25		91
ENV	NMWQEVGKA	494	11	15	23		92
ENV	DMRDNRWSEL	552	11	37	58		93
ENV	AVGIGAVFLGF	595	11	11	17		94
ENV	YLRDQQLLGI	672	11	27	42		95
ENV	YLRDQQLLGI	672	11	18	28		96
ENV	CTTNVPWNSS	690	11	11	17		97
ENV	WMEWEREIDN	723	11	10	16		98
ENV	LLALDKWASL	755	11	11	17		99
ENV							100

Table VII
HIV A01 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101	SEQ ID NO
ENV	LLELDKWASL	755	11	18	28		101
ENV	ALDKWASLW	757	11	10	16		102
ENV	ELDKWASLWN	757	11	16	25		103
ENV	ISNWLWYIKIF	770	11	11	17		104
ENV	ITKWLWYIKIF	770	11	12	19		105
ENV	ITNWLWYIKIF	770	11	14	22		106
ENV	LSIVNRVROGY	797	11	34	53		107
ENV	RVRQGYSPLSF	802	11	47	73		108
ENV	RLVSGFLALA	844	11	16	25		109
ENV	CLFSYIHLRDF	861	11	18	28		110
ENV	RIVELLGRRG	878	11	22	34		111
ENV	GLRLGWGLK	892	11	09	29		112
ENV	RLGWGLKYL	894	11	07	23		113
ENV	ASRELERF	38	8	46	72		114
GAG	SSQVSONY	145	8	15	31		115
GAG	KVIEEKAF	178	8	24	38		116
GAG	KVIEEKAF	178	8	28	44		117
GAG	TLQEQIAW	263	8	12	19		118
GAG	TLQEQIGW	263	8	27	42		119
GAG	PIPVGDIY	279	8	11	17		120
GAG	PIPVGEIY	279	8	35	55		121
GAG	ASQEVKNW	333	8	11	17		122
GAG	ATQDVKNW	333	8	15	23		123
GAG	ATQEVKNW	333	8	18	28		124
GAG	IMMQKSNF	408	8	11	17		125
GAG	IMMQKSNF	408	8	27	42		126
GAG	IMMQKSNF	408	8	55	87		127
GAG	CTERQANF	459	8	01	25		128
GAG	ETIDKDLV	537	8	13	20		129
GAG	LTSLKSLF	549	8	12	19		130
GAG	LTSLKSLF	549	8	16	25		131
GAG	LSGGKLDLAW	8	9	12	19		132
GAG	GSEELKSLY	73	9	14	31		133
GAG	NSSQVSONY	144	9	36	56		134
GAG	ISPTLNLA	168	9	17	27		135
GAG	LSPTLNLA	168	9	54	84		136
GAG	FSPEVIMF	185	9	53	83		137
GAG	TINEAAEW	225	9	12	19		138
GAG	STLQEQIAW	262	9	27	42		139
GAG	STLQEQIGW	262	9	18	28		140
GAG	PVGDIYKRW	281	9	40	63		141
GAG	PVGDIYKRW	281	9	60	94		142
GAG	GLNKIVRMY	293	9	10	17		143
GAG	NIMMQRGNF	407	9	13	22		144
GAG	TIMMQRGNF	407	9	11	18		145
GAG	SSKGRPGNF	476	9	20	31		146
GAG	PTAPPAESF	495	9	15	23		147
GAG	PTAPPAESF	495	9	02	67		148
GAG	PTAPPAESF	507	9	01	33		149
GAG	PTAPPAESF	507	9	15	23		150
GAG	PLASLKSFL	548	9			0.0017	

Table VII
HIV A01 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101	SEQ ID NO
GAG	PLTSLKSLF	548	9	12	19		151
GAG	PLTSLRSLF	548	9	12	19		152
GAG	VLSGGKLDAA	7	10	15	23		153
GAG	RLRPGKKKY	20	10	34	53		154
GAG	SLFNIVATLY	79	10	15	23		155
GAG	SLYNIVATLY	79	10	22	34		156
GAG	ALSPRTLNAA	167	10	29	45		157
GAG	WVKVIEKAF	176	10	10	16		158
GAG	WVKVVEKAF	176	10	24	38		159
GAG	DTINEAAEW	224	10	28	44		160
GAG	ETINEAAEW	224	10	31	48		161
GAG	TSTLQEQIAW	261	10	22	34		162
GAG	TSTLQEQIGW	261	10	12	19		163
GAG	DIQGPKEPF	308	10	27	42		164
GAG	DIRQGPKEPF	308	10	19	30		165
GAG	ATIMMRGNF	406	10	41	64		166
GAG	PSHKGRPGNF	475	10	11	28		167
GAG	PSNKGKPGNF	475	10	23	36		168
GAG	PSSKGRPGNF	475	10	14	22		169
GAG	SVLSGGKLLDA	6	11	15	23		170
GAG	IVWASRELERF	35	11	19	30		171
GAG	LVWASRELER	35	11	25	39		172
GAG	RSLYNTVATL	78	11	15	24		173
GAG	TSTLQEQIA	260	11	11	17		174
GAG	TSTLQEQIG	260	11	27	43		175
GAG	PIPVGEYKRW	279	11	34	53		176
GAG	ILGLNKIVRMV	291	11	57	89		177
GAG	ASAQDLKGG	392	11	01	50		178
GAG	ATAQDLKGG	392	11	01	50		179
GAG	PTAPPESFGF	495	11	10	16		180
GAG	PTAPPESFRF	495	11	14	22		181
GAG	PTAPPESFRF	507	11	02	67		182
GAG	PTAPPESFRF	507	11	01	33		183
GAG	PTAPPESFRF	507	11	12	22		184
NEF	ATNADCAW	71	8	12	19		185
NEF	PMYKGAFF	105	8	12	31		186
NEF	DLDLWVY	185	8	20	31		187
NEF	EILDWVY	185	8	33	52		188
NEF	WVYHTQGF	191	8	13	20		189
NEF	WVYHTQGY	191	8	21	33		190
NEF	GIRYPLTF	213	8	13	20		191
NEF	GTRFPLTF	213	8	13	20		192
NEF	PLTFGWCF	219	8	43	67		193
NEF	WSKSSIVGW	5	9	20	31		194
NEF	QVPLRPMTF	100	9	10	16		195
NEF	QVPLRPMTY	100	9	46	72	0.0008	196
NEF	WVYHTQGF	191	9	13	20		197
NEF	WVYHTQGYF	191	9	21	33		198
NEF	HTQGFDPDW	194	9	14	22		199
NEF	HTQGYFPDW	194	9	25	39		200

Table VII
HIV A01 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101	SEQ ID NO
NEF	NTQGYFPDW	194	9	12	19		201
NEF	YTPGIRY	207	9	17	27		202
NEF	YTPGPTRF	207	9	13	20		203
NEF	DLWVYHTQGF	188	10	13	20		204
NEF	DLWVYHTQGY	213	10	21	33		205
NEF	GIRYPLTFGW	213	10	13	20		206
NEF	GTRPLTFGW	213	10	12	19		207
NEF	HMARLHPEY	320	10	10	16		208
NEF	NTAATNADCA	68	11	12	19		209
NEF	PLRPMYKGA	102	11	12	19		210
NEF	DLWVYHTQGF	188	11	13	20		211
NEF	DLWVYHTQGY	188	11	21	33		212
NEF	HMARLHPEY	320	11	10	16		213
NEF	DINLPKW	122	8	13	20		214
POL	EINLPKW	122	8	12	19		215
POL	MIGGIGF	133	8	62	97		216
POL	QIGCTLNF	179	8	41	64		217
POL	QLGCTLNF	179	8	16	25		218
POL	KIGPENPY	238	8	51	80		219
POL	RIGPENPY	238	8	11	17		220
POL	VLDVGDAY	297	8	60	94		221
POL	SVPLDKDF	306	8	18	28		222
POL	MTKILEPF	353	8	44	69		223
POL	QLPEKDSW	434	8	13	20		224
POL	VLPEKDSW	434	8	13	20		225
POL	KLVGKLNW	448	8	62	97		226
POL	ATESIVW	568	8	19	30		227
POL	ETWWTYY	591	8	10	16		228
POL	PIVGAETF	625	8	28	44		229
POL	IVGAETFY	626	8	28	44		230
POL	KTELQAIY	668	8	12	19		231
POL	NIVTDSQY	686	8	62	97		232
POL	LIKKEKYY	717	8	35	55		233
POL	AVIVASGY	828	8	59	92		234
POL	ETGQETAY	844	8	59	92		235
POL	ILKLAGRW	853	8	34	53		236
POL	LLKLAGRW	853	8	25	39		237
POL	IITDNGSNF	866	8	51	80		238
POL	TTVKAACW	876	8	15	23		239
POL	AVKAACW	877	8	32	50		240
POL	TVKAACW	877	8	24	38		241
POL	QIIKIQNF	968	8	12	19		242
POL	QITKIQNF	968	8	35	55		243
POL	KIQNERVY	971	8	52	81		244
POL	PIRRELQVW	30	9	13	20		245
POL	FSFQITLW	85	9	14	22		246
POL	KMIGGIGF	132	9	62	97		247
POL	ELNKRQDF	268	9	57	89		248
POL	TVLDVGDAY	296	9	57	89	0.0180	249
POL	VLDVGDAYF	297	9	60	94		250

Table VII
HIV A01 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101	SEQ ID NO
POL	FSVPLDKDF	305	9	18	28		251
POL	PLDKDRKY	308	9	19	30		252
POL	ETPGIRYQY	327	9	52	81	0.0052	253
POL	SMTKILEPF	352	9	43	67		254
POL	ELREHLLKW	393	9	17	27		255
POL	ELRQHLLRW	393	9	15	23		256
POL	IVLPEKDSW	433	9	13	20		257
POL	KLNWASQIY	452	9	60	94	0.0070	258
POL	VIWGTKPKF	573	9	47	73		259
POL	KLPIKETW	582	9	20	31		260
POL	RLPIKETW	582	9	26	41		261
POL	WTDYWQATW	594	9	14	22		262
POL	WTEYWOATW	594	9	24	38		263
POL	ATWIPEWEF	600	9	52	81		264
POL	NTPLVYKLV	610	9	57	89		265
POL	PIVGAETFY	625	9	28	44	0.0007	266
POL	ETKLGKAGY	641	9	35	55	0.0010	267
POL	OLIKKEKVV	716	9	28	44	0.0007	268
POL	SSGIRKVLV	745	9	26	41		269
POL	QVDCSPGIW	805	9	57	89		270
POL	ETGQETAYF	844	9	57	89		271
POL	FLKLAGRW	852	9	32	50		272
POL	FLKLAGRW	852	9	25	39		273
POL	STTVKAACW	875	9	15	23		274
POL	TTVKAACWW	876	9	15	23		275
POL	KTAVQMAVF	925	9	57	89		276
POL	QMAVFIHNF	929	9	60	94	0.0056	277
POL	KIQNFRVYV	971	9	52	81		278
POL	LTQIGCTLNF	177	10	41	64		279
POL	LTQIGCTLNF	177	10	15	23		280
POL	GMDGPKVKQ	201	10	51	80	0.0130	281
POL	ISKIGPENPY	236	10	42	66		282
POL	ISRIGPENPY	236	10	11	17		283
POL	AIKKKDKTKW	251	10	57	89		284
POL	STKWRKLVDF	257	10	58	91		285
POL	ELNKRRTQDFW	268	10	57	89	0.2800	286
POL	VTVDVGDAY	295	10	56	88		287
POL	TVLDVGDAYF	296	10	57	89		288
POL	SSMTKILEPF	351	10	33	52	0.2500	289
POL	VYQYMDLLY	368	10	51	80		290
POL	PIQLPEKDSW	432	10	13	20		291
POL	PIVLPEKDSW	432	10	13	20		292
POL	ILKEPVHGVY	498	10	40	63	0.0017	293
POL	ELQKQGGQW	520	10	13	20		294
POL	ELQKQGGQW	520	10	15	23		295
POL	WTYQIYQEPF	529	10	42	66		296
POL	KIATESIVW	566	10	14	22		297
POL	IVIWGTKPKF	572	10	47	73		298
POL	PIQKETWEAW	584	10	15	23		299
POL	PIQKETWETW	584	10	27	42		300

Table VII
HIV A01 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101	SEQ ID NO
POL	ETWETWWTID	588	10	10	16		301
POL	ETWETWWTTE	588	10	10	16		302
POL	NTPLVKLWY	610	10	57	89	0.0041	303
POL	EVNIVTDSQY	684	10	59	92	0.0510	304
POL	VSAGIRKVLV	744	10	15	23		305
POL	VSSGIRKVLV	744	10	26	41		306
POL	LVAVHVASGY	826	10	53	83	0.0390	307
POL	TIHIDNGSNF	864	10	14	22		308
POL	VIHIDNGSNF	864	10	24	38		309
POL	TSAAVKAACW	874	10	27	42		310
POL	TSTTVKAACW	874	10	14	22		311
POL	STTVKAACW	875	10	15	23		312
POL	GIKQEGIPY	886	10	22	34	0.0010	313
POL	GIKQEGIPY	886	10	11	17		314
POL	IIKIQNFRVY	969	10	12	19		315
POL	ITKIQNFRVY	969	10	36	57	0.0010	316
POL	NSPTRELQV	28	11	12	19		317
POL	VSFSPQITLW	78	11	07	15		318
POL	GITLNFQITF	79	11	01	17		319
POL	PSLSFPQITLW	79	11	02	33		320
POL	GTLNCPQITL	80	11	01	33		321
POL	PTFNFPQITLW	80	11	03	33		322
POL	SSFSFPQITLW	82	11	13	30		323
POL	VLEDINLPKW	119	11	12	20		324
POL	VLEINLPKW	119	11	53	19		325
POL	GIGGFIKVRQY	136	11	21	83		326
POL	LLTQIGCTLNF	176	11	17	33		327
POL	MLTQIGCTLNF	176	11	10	27		328
POL	MLTQIGCTLN	176	11	41	16		330
POL	KISKIGPENPY	235	11	11	64		331
POL	KISKIGPENPY	235	11	58	91		332
POL	DSTKWRKLVD	256	11	56	88		333
POL	SVTVLDVGDGDA	294	11	56	88		334
POL	VTVLDVGDGDA	295	11	18	28		335
POL	SVPLDKDFRK	306	11	32	50		336
POL	SINNETPGIRY	323	11	11	17		337
POL	STNNETPGIRY	323	11	33	52		338
POL	QSSMTKILEPF	350	11	42	66		339
POL	IVIVQYMDL	367	11	14	22		340
POL	ELREHLKKG	393	11	12	19		341
POL	ELROHLRWG	393	11	60	94		342
POL	WMGYELHPDK	418	11	62	97		343
POL	DIQKLVGKLN	445	11	40	63		344
POL	ELKEPVHGVY	497	11	38	59		345
POL	ILKEPVHGVY	498	11	41	64		346
POL	SIVIWGKTPKF	571	11	15	23		347
POL	PIKETWEAW	584	11	27	42		348
POL	PIKETWETW	584	11	10	16		349
POL	ETWETWWTID	588	11	54	86		350
POL	FVNTPLVLKL	608	11				

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HIV A01 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101	SEQ ID NO
POL	LIKKEKVVYLA	717	11	20	31		351
POL	LIKKEKVVLSW	717	11	13	20		352
POL	LVSSGIRKVLV	743	11	15	23		353
POL	LVSSGIRKVLV	743	11	26	41		354
POL	ISNWRAMAS	768	11	32	50		355
POL	ILVAVIIVASGY	825	11	53	83		356
POL	KVIHTDNGSNF	863	11	21	33		357
POL	FTSAAYKAAC	873	11	27	42		358
POL	FTSTTVKAAC	873	11	14	22		359
POL	TSAAVKAACW	874	11	27	42		360
POL	TSTTVKAACW	874	11	14	22		361
POL	HLKTAQMAV	923	11	57	89		362
POL	AVQMAVHHN	927	11	60	94		363
POL	QIKIQNFRVY	968	11	12	19		364
POL	QITKIQNFRVY	968	11	35	55		365
POL	IKIQNFRVY	969	11	12	19		366
POL	ITKIQNFRVY	969	11	36	57		367
POL	PIWKGPAKLL	985	11	35	55	0.0110	368
POL	PLWKGPAKLL	985	11	18	28		369
POL	ILYQSNPY	23	8	27	42		370
REV	AVRIKILY	17	9	13	20		371
REV	KILYQSNPY	22	9	26	41		372
REV	IKILYQSNPY	20	11	18	28		373
TAT	PVDPLNLPW	3	9	20	31		374
TAT	PVDPLNLPW	3	9	14	22		375
TAT	FLNKGGLGISY	41	10	14	22		376
VIF	SLVKHHIMY	23	8	44	69		377
VIF	RLVITTYW	65	8	12	19		378
VIF	QLIHLVYF	110	8	14	22		379
VIF	QLIHLMIYF	110	8	14	22		380
VIF	ILYYFDCF	113	8	16	25		381
VIF	IIMHYDCF	113	8	15	23		382
VIF	IVSPRCEY	133	8	14	22		383
VIF	KSLVKHHIMY	22	9	18	28		384
VIF	NSLVKHHIMY	22	9	24	38		385
VIF	GLITGERDW	73	9	22	34		386
VIF	GLITGERDW	73	9	12	19		387
VIF	SIEWRLRRY	89	9	11	17		388
VIF	QVDRMKIRTW	12	10	12	19		389
VIF	QVDRMRINTW	12	10	10	16		390
VIF	QVDRMRINTW	12	10	31	48		391
VIF	HLGHGVSEW	83	10	25	39		392
VIF	HLGGGVSEW	83	10	26	41		393
VIF	VSEWRLLRY	88	10	11	17		394
VIF	LIHLVYFDCF	111	10	16	25		395
VIF	LIIMHYFDCF	111	10	15	23		396
VIF	SVKKLTEDRW	174	10	13	20		397
VIF	GVSIEWRLRR	87	11	10	16		398
VIF	GLADQLIHHH	106	11	11	17		399
VIF	QLIHLVYFDCF	110	11	13	20		400

Table VII
HIV A01 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101	SEQ ID NO
VIF	QLIIMHYDCF	110	11	14	22		401
VIF	PSVKLTEDR	173	11	13	20		402
VPR	KSEAVRHF	27	8	15	23		403
VPR	WLHGLGQY	38	8	11	17		404
VPR	RLQQLLF	62	8	45	70		405
VPR	AVRHFRPW	30	9	14	22		406
VPR	AVRHFRPW	30	9	34	53		407
VPR	ELKNEAVRHF	25	10	17	27		408
VPR	ELKSEAVRHF	25	10	15	23		409
VPR	WLHGLGQHY	38	10	20	31		410
VPR	HIYETYGDTW	45	10	17	27		411
VPR	HIYNTYGDW	45	10	14	22		412
VPR	YIYETYGDTW	45	10	14	22		413
VPR	IIRLQQLF	60	10	41	64		414
VPR	ILQQLFHF	63	10	35	55		415
VPR	AIIRLQQLF	59	11	38	59		416
VPR	RIQQLLFHF	62	11	34	53		417
VPU	LHAIVVW	26	8	10	16		418
VPU	IVVWTVF	30	8	15	23		419
VPU	WTIVFIEY	34	8	12	19		420
VPU	EMGHHPW	89	8	11	17		421
VPU	AIVVWTVF	29	9	14	22		422
VPU	VVWTVFIEY	31	10	12	19		423
VPU	GVEMGHHP	91	10	01	50		424
VPU	KVDYRIVAF	7	11	01	33		425
VPU	IVVWTVFIEY	30	11	12	19		426
VPU	RIKEIRDDSDY	64	11	01	50		427
VPU	RIKEIRDDSDY	64	11	01	50		428

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
ENV	LILGLVII	21	8	09	15						429
ENV	GLVIICSA	28	8	10	16						430
ENV	GMLMCSA	28	8	12	19						431
ENV	QLYATVYA	34	8	01	50						432
ENV	WVTVYGV	46	8	58	91						433
ENV	TVYGVVP	48	8	55	86						434
ENV	GVFVWKEA	52	8	34	53						435
ENV	PWKEATT	54	8	22	34						436
ENV	ATTLFCA	59	8	24	38						437
ENV	TLFCASDA	64	8	54	84						438
ENV	EVHNVWAT	77	8	36	56						439
ENV	ATHACVPT	83	8	56	88						440
ENV	NVTENFNM	101	8	34	53						441
ENV	NMWKNDMV	107	8	12	19						442
ENV	NMWKNMNV	107	8	34	53						443
ENV	EQMHEDII	115	8	24	38						444
ENV	DQSLKPCV	126	8	50	78						445
ENV	SLKPCVKL	128	8	55	86						446
ENV	KLTPLCVT	134	8	53	83						447
ENV	LTPLCVTL	135	8	54	84						448
ENV	VTSTGNSA	161	8	01	20						449
ENV	ALFYKLDV	202	8	10	16						450
ENV	ALFYRLDV	202	8	12	19						451
ENV	NISPKNNT	217	8	01	33						452
ENV	LINCNTSA	237	8	17	27						453
ENV	NTSAITQA	241	8	14	22						454
ENV	NTSVITQA	241	8	13	20						455
ENV	ITQACPKV	245	8	37	58						456
ENV	PIPIHYCA	258	8	40	63						457
ENV	PIPIHYCT	258	8	18	28						458
ENV	PIHYCAPA	260	8	37	58						459
ENV	PIHYCTPA	260	8	18	28						460
ENV	CAPAGFAI	264	8	29	45						461
ENV	CTPAGFAI	264	8	10	16						462
ENV	GTGPKKNV	281	8	17	27						463
ENV	NVSTVQCT	287	8	51	80						464
ENV	TVQCTHGI	290	8	51	80						465
ENV	CTHGKIPV	294	8	33	52						466
ENV	CTHGIRPV	294	8	26	41						467
ENV	GIRPVVST	297	8	33	52						468
ENV	GIRPVVST	297	8	26	41						469
ENV	PVSTQLL	300	8	60	94						470
ENV	VVSTQLLL	301	8	60	94						471
ENV	QLLNGSL	305	8	57	89						472
ENV	LLNGSLA	306	8	55	86						473
ENV	SLAEEVV	311	8	14	22						474
ENV	LAEEVVI	312	8	13	20						475
ENV	IRSENLT	319	8	10	16						476
ENV	CTRPNNNT	345	8	29	45						477
ENV	NTRKSIRI	351	8	10	16						478

Table VIII
HIV A02 Super Motif: Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
ENV	NTSPRSRV	376	8	01	33						479
ENV	TAGNSSRA	376	8	01	33						480
ENV	IIGDIRQA	377	8	30	49						481
ENV	MQNGTNIT	458	8	01	17						482
ENV	IITEGNITL	478	8	01	50						483
ENV	NITLPCRI	482	8	11	17						484
ENV	TITLPCRI	482	8	14	22						485
ENV	RIKQIINM	488	8	30	47						486
ENV	RIKQIVNM	488	8	12	19						487
ENV	INNMVQEV	492	8	17	27						488
ENV	WQEVGKAM	496	8	18	28						489
ENV	WQVVGQAM	496	8	11	17						490
ENV	EVGKAMYA	498	8	18	28						491
ENV	RVGQAMYA	498	8	10	16						492
ENV	KAMYAPPI	502	8	23	36						493
ENV	QAMYAPPI	502	8	14	22						494
ENV	RAMYAPPI	502	8	12	19						495
ENV	QIRCSSNI	512	8	11	17						496
ENV	NITGLILT	519	8	11	17						497
ENV	NITGLLLT	519	8	35	55						498
ENV	ELYKYKVV	560	8	56	89						499
ENV	KVKVIEPL	565	8	25	39						500
ENV	KIEPLGVA	568	8	23	37						501
ENV	PTKAKRRV	576	8	22	34						502
ENV	VVEREKRA	588	8	32	50						503
ENV	VQREKRA	588	8	17	27						504
ENV	VQREKRAV	589	8	17	27						505
ENV	RAVGIGAV	594	8	12	19						506
ENV	GALFLGFL	601	8	12	19						507
ENV	GAVFLGFL	601	8	13	20						508
ENV	FLGFLGAA	604	8	22	34						509
ENV	FLGAGST	608	8	48	75						510
ENV	AAGSTMGA	611	8	55	86						511
ENV	STMGAASI	614	8	58	91						512
ENV	TMGAASIT	615	8	39	61						513
ENV	GAASITLT	617	8	39	61						514
ENV	AASITLT	618	8	39	61						515
ENV	SITLTVQA	620	8	36	56						516
ENV	LTVQARQL	623	8	32	50						517
ENV	TVQARQLL	624	8	38	59						518
ENV	ROLLSGIV	628	8	36	56						519
ENV	IVQQQNNL	634	8	49	77						520
ENV	IVQQQSNL	634	8	26	41						521
ENV	VQQQNNLL	635	8	32	50						522
ENV	VQQQNNLL	635	8	26	41						523
ENV	QONNLLRA	635	8	32	50						524
ENV	QONNLLRA	637	8	26	41						525
ENV	QONNLLRA	637	8	26	41						526
ENV	NLLRAIEA	640	8	26	41						527
ENV	AIEAQIHL	644	8	51	80						528
ENV			8	49	77						

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
ENV	AQHIILKL	647	8	13	20						529
ENV	AQHILLQL	647	8	35	55						530
ENV	AQHIMLQL	647	8	10	16						531
ENV	QHIILKLT	648	8	13	20						532
ENV	QHIILQLT	648	8	34	53						533
ENV	QHIILQLT	648	8	10	16						534
ENV	QHIILQLT	648	8	10	16						535
ENV	LQITVWGI	652	8	44	69						536
ENV	TVWGIKQL	655	8	59	92						537
ENV	QIQARVVL	660	8	41	64						538
ENV	QIQARVLA	661	8	41	64						539
ENV	LQARVLAV	662	8	33	52						540
ENV	VLAVERYL	666	8	34	53						541
ENV	YLKDDQLL	672	8	31	48						542
ENV	YLRDQQLL	672	8	18	28						543
ENV	KLICITAV	687	8	19	30						544
ENV	KLICITNV	687	8	17	27						545
ENV	KLICITTV	687	8	12	19						546
ENV	WMEVEREI	723	8	12	19						547
ENV	LLALDKWA	755	8	19	30						548
ENV	LLELDKWA	755	8	21	33						549
ENV	ALDKWASL	757	8	11	17						550
ENV	ELDKWASL	757	8	18	28						551
ENV	SLWNWFDI	763	8	17	27						552
ENV	ITKWLWYI	770	8	16	25						553
ENV	ITNWLWYI	770	8	19	30						554
ENV	YKIFIMI	776	8	43	67						555
ENV	FIMIVGGL	780	8	44	69						556
ENV	IMIVGGI	781	8	35	56						557
ENV	IVGGLIGL	783	8	42	66						558
ENV	IVGGLVGL	783	8	10	16						559
ENV	GLIGLRII	786	8	15	23						560
ENV	GLIGLRIV	786	8	32	50						561
ENV	GLRIIFAV	789	8	18	28						562
ENV	GLRIIFAV	789	8	29	45						563
ENV	GLRIIFAV	789	8	15	23						564
ENV	IIFAVLSI	792	8	20	31						565
ENV	IIFAVLSI	792	8	38	59						566
ENV	VLSIVNRV	796	8	10	16						567
ENV	PLSFQTLI	809	8	20	31						568
ENV	PLSFQTLI	809	8	13	20						569
ENV	PLSFQTLI	809	8	01	33						570
ENV	GLDRPGGT	823	8	20	31						571
ENV	RLVNGFLA	844	8	13	20						572
ENV	RLVSGFLA	844	8	20	31						573
ENV	LVNGFLAL	845	8	14	22						574
ENV	LVSGLFAL	845	8	19	30						575
ENV	LALA WDDL	850	8	25	39						576
ENV	CLFSYHRL	861	8	42	66						577
ENV	RLRDLILI	867	8	13	20						578
ENV	IAARTVEL	874	8	12	19						579
ENV	AAATVELL	876	8	11	17						580
ENV	ELLGHISL	881	8	09	15						581

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
ENV	LQYWSQEL	907	8	16	25						579
ENV	GQELKNSA	911	8	12	19						580
ENV	SOELKNSA	911	8	12	19						581
ENV	SAVSLNNA	917	8	11	17						582
ENV	AVSLNNAI	918	8	11	17						583
ENV	SLLNATAI	920	8	14	22						584
ENV	LLNATAIA	921	8	15	23						585
ENV	DTIAIAVA	923	8	10	16						586
ENV	NATAIAVA	923	8	14	22						587
ENV	AIAVAEGT	926	8	32	50						588
ENV	VAEGTDRI	929	8	19	30						589
ENV	VAEGTDRV	929	8	16	25						591
ENV	GTDRVIEV	932	8	11	17						592
ENV	ILIIIPRI	947	8	13	20						593
ENV	PTIRIQGL	951	8	12	19						594
ENV	ROGLERAI	955	8	35	55						595
ENV	VTYYGVVP	47	9	55	86	0.0003					596
ENV	GVPVWKEAT	52	9	22	34	0.0002					597
ENV	PVWKEATTT	54	9	22	34	0.0002					598
ENV	EATTLFCA	58	9	24	38	0.0002					599
ENV	TTLFCASDA	61	9	52	81	0.0002					600
ENV	DAKAYDTEV	70	9	17	27	0.0001					601
ENV	DTEVIINVA	75	9	18	28	0.0002					602
ENV	NVWATHACV	80	9	49	77	0.0002					603
ENV	WATHACVPT	82	9	56	88	0.0002					604
ENV	PTDNPQEI	89	9	25	39	0.0002					605
ENV	PTDNPQEV	89	9	21	33	0.0002					606
ENV	MVEQMIEDI	113	9	23	36	0.0023					607
ENV	QMIEDISL	116	9	29	45	0.0180					608
ENV	IISLWDQSL	121	9	38	59						609
ENV	VISLWDQSL	121	9	10	16	0.0001					610
ENV	SLKPCVKLT	128	9	55	86	0.0002					611
ENV	CVKLTPLCV	132	9	55	86	0.0002					612
ENV	KLTPLCVTL	134	9	52	81	0.1600					613
ENV	PLCVILNCT	137	9	22	34	0.0005					614
ENV	EIKNCSFNI	181	9	13	20						615
ENV	ALFYRLDVV	202	9	11	17						616
ENV	VQNNNSNT	218	9	01	20						617
ENV	RLINCNTSA	236	9	17	27						618
ENV	LINCNTSAI	237	9	15	23						619
ENV	AITQACPKV	244	9	13	20						620
ENV	VITQACPKV	244	9	15	23						621
ENV	KVSFEPIPI	252	9	30	47						622
ENV	CAPAGFAIL	264	9	29	45	0.0001					623
ENV	STVQCTHGI	289	9	51	80	0.0001					624
ENV	CTHIGIKPVV	294	9	32	50						625
ENV	CTHIGIRPVV	294	9	26	41	0.0001					626
ENV	PVVSITQLLL	300	9	60	94	0.0001					627
ENV	TOLLNGSL	304	9	57	89						628
ENV	QLLNGSLA	305	9	55	86	0.0001					628

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
ENV	SLAEIEVVI	311	9	13	20	0.0020					629
ENV	NAKTIIVQL	329	9	14	22						630
ENV	ATGDIIGDI	369	9	12	19						631
ENV	DIIGDIRQA	372	9	12	19						632
ENV	EIIGDIRQA	372	9	09	15						633
ENV	GTAGNSSRA	375	9	01	33						634
ENV	NTSPRSRA	376	9	01	33						635
ENV	TAGNSSRAA	376	9	01	33						636
ENV	DIRQAHCNI	380	9	15	23						637
ENV	DIRQAHCNV	380	9	10	16						638
ENV	TLPCRKQI	484	9	26	41						639
ENV	QINMWQEV	491	9	17	27	0.0026					640
ENV	NMWQEVGKA	494	9	15	23	0.0022					641
ENV	QAMYPPI	501	9	14	22						642
ENV	QIRCSSNI	511	9	11	17	0.0001					643
ENV	QIRCSSNIT	512	9	11	17						644
ENV	NTETNKTET	537	9	01	17						645
ENV	NTTGNTTET	537	9	01	17						646
ENV	VVKIEPLGV	566	9	23	36	0.0001					647
ENV	PLGVAPTKA	571	9	23	36	0.0001					648
ENV	PTKAKRRVV	576	9	22	34	0.0001					649
ENV	RVVEREKRA	587	9	32	50	0.0001					650
ENV	RVVQREKRA	587	9	17	27						651
ENV	VVEREKRAV	588	9	25	39						652
ENV	VVQREKRAV	588	9	16	25						653
ENV	AVGIGAVFL	595	9	11	17	0.0950					654
ENV	ALFLGFLGA	602	9	11	17						655
ENV	AMFLGFLGA	602	9	12	19						656
ENV	AVFLGFLGA	602	9	19	30						657
ENV	FLGAAGSTM	608	9	55	86	0.0190					658
ENV	GAAAGSTMGA	610	9	55	86	0.0009					659
ENV	AAGSTMGAA	611	9	45	70	0.0001					660
ENV	STMGAASIT	614	9	39	61						661
ENV	TMGAASITL	615	9	39	61						662
ENV	GAASITLV	617	9	36	56						663
ENV	TLTVQARQL	622	9	37	58						664
ENV	LTVQARQLL	623	9	36	56						665
ENV	QARQLLSGI	626	9	38	59						666
ENV	GIVQQQNLL	633	9	26	41	0.0001					667
ENV	GIVQQQSNL	633	9	32	50						668
ENV	IVQQQNLL	634	9	26	41	0.0001					669
ENV	IVQQQSNL	634	9	32	50						670
ENV	QQQNLLRA	636	9	25	39						671
ENV	QQQNLLRA	636	9	26	41						672
ENV	QQNLLRAI	637	9	26	41						673
ENV	QQSNLLRAI	637	9	26	41						674
ENV	RAIEAQHLL	643	9	45	70						675
ENV	AIEAQHILL	644	9	48	75						676
ENV	EAQQHLLKL	646	9	12	19						677
ENV	EAQQHLLQL	646	9	35	56						678

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
ENV	AQQHLLKLT	647	9	13	20						679
ENV	AQQHLLQLT	647	9	34	53						680
ENV	AQQHMLQLT	647	9	10	16						681
ENV	QQHLLKLT	648	9	13	20						682
ENV	QQHLLQLTV	648	9	34	53						683
ENV	LLKLTWGI	651	9	13	20						684
ENV	LLQLTVWGI	651	9	34	53	0.5100	0.0200	0.2300	0.1500	0.0620	685
ENV	MLQLTVWGI	651	9	10	16	0.2500					686
ENV	LTWVGIGQL	651	9	59	92	0.0001					687
ENV	GKLOQARV	658	9	40	63	0.0001					688
ENV	KQLQARVLA	660	9	41	64						689
ENV	QLQARVLAV	661	9	33	52	0.0085					690
ENV	RVLAVERYL	665	9	33	52	0.0009					691
ENV	GIWGCSSKL	680	9	48	75	0.0011					692
ENV	QQEKNEODL	747	9	16	25						693
ENV	QQEKNEQEL	747	9	18	28						694
ENV	DLALDKWA	754	9	15	23						695
ENV	ELLELDKWA	754	9	18	28						696
ENV	LALDKWASL	756	9	11	17						697
ENV	SLWNWFDIT	763	9	13	20	0.0002					698
ENV	DTTNWLWYI	769	9	10	16						699
ENV	WLWYIKIFI	773	9	49	77	0.0360					700
ENV	YKIFIMIV	776	9	39	61	0.0001					701
ENV	FIMIVGGIL	780	9	35	55						702
ENV	MIVGGILGL	782	9	36	56						703
ENV	LIGLRIFA	787	9	16	25						704
ENV	LIGLRIFA	787	9	21	33						705
ENV	GLRIIFAVL	789	9	17	27						706
ENV	GLRIIFAVL	789	9	28	44	0.0009					707
ENV	RIIFAVLSI	791	9	14	22						708
ENV	RIIFAVLSI	791	9	19	30	0.0002					709
ENV	IFAVLSIV	792	9	15	23						710
ENV	IVFAVLSIV	792	9	18	28						711
ENV	AVLSIVNRV	795	9	31	48	0.0012					712
ENV	RVRQGYSP	802	9	55	86	0.0130					713
ENV	SIRLVSGFL	842	9	11	17	0.0005					714
ENV	SIRLVSGFL	842	9	13	20						715
ENV	RLVNGFLAL	844	9	12	19						716
ENV	RLVSGFLAL	844	9	19	30						717
ENV	LVSGFLALA	845	9	16	25						718
ENV	FLALAWDDL	849	9	25	39						719
ENV	LAWDDLRLS	852	9	20	31						720
ENV	LIAARTVEL	873	9	12	19						721
ENV	IAARTVELL	874	9	11	17						722
ENV	LLGRRGWEA	882	9	10	16						723
ENV	GLRLGWEG	892	9	10	32						724
ENV	LLQYVVSQEL	906	9	16	25						725
ENV	GOELKNSAI	911	9	12	19	0.0270					726
ENV	SOELKNSAV	911	9	10	16						727
ENV	ELKNSAINL	913	9	10	16						728

Table VII HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
ENV	ELKNSAISL	913	9	10	16						729
ENV	ELKNSAVSL	913	9	12	19						730
ENV	SAVSLNAT	917	9	11	17	0.0001					731
ENV	AVSLNATA	918	9	11	17						732
ENV	SLLNATAIA	920	9	14	22						733
ENV	LLNATAIAV	921	9	15	23						734
ENV	IAIAVAEGT	925	9	10	16						735
ENV	TAIAVAEGT	925	9	22	34						736
ENV	AAVEGTDRI	928	9	16	25						737
ENV	AAVEGTDRI	928	9	14	22	0.0008					738
ENV	AAVEGTDRI	928	9	18	28						739
ENV	VAEGTDRII	929	9	16	25	0.0001					740
ENV	VAEGTDRI	929	9	12	19						741
ENV	AIHIPRI	946	9	34	53	0.0003					742
ENV	RIRQGLERA	953	9	34	53						743
ENV	RQGLERALL	955	9	34	53						744
ENV	ILGLVICS	26	10	10	16						745
ENV	LLGMLMCSA	26	10	10	16						746
ENV	QLYATVYAGV	34	10	01	50	0.0150					747
ENV	KLWTVVYGV	44	10	11	17	0.0160					748
ENV	NLWTVVYGV	44	10	34	54	0.0009					749
ENV	WTVVYGVIP	46	10	55	86	0.0001					750
ENV	GVPVWKEATT	52	10	22	34	0.0001					751
ENV	PVWKEATITL	54	10	22	34	0.0001					752
ENV	KTLFCASDA	60	10	12	19						753
ENV	TTTLFCASDA	60	10	24	38	0.0001					754
ENV	TLFCASDAKA	64	10	46	72	0.0006					755
ENV	CASDAKAYDT	67	10	19	30	0.0001					756
ENV	KAYDTEVINV	72	10	17	27	0.0013					757
ENV	DTEVHNWAT	75	10	18	28	0.0001					758
ENV	EVIINVWATIA	77	10	35	55	0.0001					759
ENV	PTDNPQEVV	89	10	13	20						760
ENV	NMVEQMIEDI	112	10	20	31	0.0001					761
ENV	MVEQMIEDII	113	10	23	36	0.0001					762
ENV	EQMHIEDIISL	115	10	22	34						763
ENV	DIISLWDQSL	120	10	38	59	0.0001					764
ENV	DVSLWDQSL	120	10	10	16						765
ENV	DQSLKPCVKL	126	10	47	73						766
ENV	CVKLTPLCVT	132	10	53	83	0.0001					767
ENV	STSNSNSST	159	10	01	50						768
ENV	VTSTGNSAGT	161	10	01	20						769
ENV	EIKNCSFNIT	181	10	12	19						770
ENV	SVQNNNSNT	217	10	01	33						771
ENV	RLINCNTSAI	236	10	15	24						772
ENV	LINCNTSAIT	237	10	14	22						773
ENV	SAITQACPKV	243	10	13	20						774
ENV	SVITQACPKV	243	10	15	23						775
ENV	PIPIHYCAPA	258	10	36	56	0.0002					776
ENV	PIPIHYCTPA	258	10	18	28						777
ENV	GTGFCIKNVST	281		12	19						778
ENV	CINVS:VQCT	285	10	13	20						779

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
ENV	VQCTHIGIKPV	292	10	32	50						779
ENV	VQCTHIGIRPV	292	10	25	39						780
ENV	GIRPVVSTQL	297	10	33	52						781
ENV	GIRPVVSTQL	297	10	26	41	0.0002					782
ENV	STQLLNGSL	303	10	57	89	0.0001					783
ENV	TQLLLNGSLA	304	10	55	86						784
ENV	RIGPGQTFYA	357	10	10	16						785
ENV	GIGPGQTFYA	360	10	01	33						786
ENV	SIGSGOAFYV	360	10	01	33						787
ENV	YATGDIIGDI	368	10	11	17						788
ENV	GTAGNSSRAA	375	10	01	33						789
ENV	MONGTNTST	458	10	01	17						790
ENV	NANITPCRI	478	10	01	50						791
ENV	ITLPCRIKQI	483	10	25	39						792
ENV	TLPCRIKQI	484	10	15	23						793
ENV	TLPCRIKQIV	484	10	10	16						794
ENV	KQINNMQEV	490	10	17	27						795
ENV	NMQEVGKAM	494	10	15	23	0.0004					796
ENV	WQEVGKAMYA	496	10	18	28						797
ENV	WQEVGQAMYA	496	10	10	16						798
ENV	GQIRCSSNIT	511	10	11	17						799
ENV	EIFRPGGDM	544	10	17	27	0.0001					800
ENV	ETFRPGGDM	544	10	21	33						801
ENV	DMRDNRSEL	552	10	37	58	0.0001					802
ENV	ELYKYKVEI	560	10	13	21						803
ENV	ELYKYKVKVI	560	10	29	46						804
ENV	KVKIEPLGV	565	10	23	36						805
ENV	VVKIEPLGVA	566	10	23	36						806
ENV	KIEPLGVAPT	568	10	23	37						807
ENV	VAPTAKRRV	574	10	17	27	0.0001					808
ENV	STRTHREKRA	586	10	01	50						809
ENV	RVVEREKRAV	587	10	25	39						810
ENV	RVVQREKRAV	587	10	16	25						811
ENV	RAVGIGAVFL	594	10	11	17						812
ENV	GIGAVFLGFL	598	10	11	18						813
ENV	MLGANFLGFL	599	10	04	36						814
ENV	TIGAMFLGFL	599	10	03	27	0.0003					815
ENV	GALFLGFLGA	601	10	11	17						816
ENV	GAMFLGFLGA	601	10	12	19						817
ENV	GAVFLGFLGA	601	10	19	30						818
ENV	ALFLGFLGAA	602	10	11	17	0.5000					819
ENV	AMFLGFLGAA	602	10	12	19						820
ENV	AVFLGFLGAA	602	10	19	30						821
ENV	GAAGSTMGAA	610	10	42	66	0.0004					822
ENV	STMGAASITL	614	10	39	61						823
ENV	TMGAAASITL	615	10	39	61						824
ENV	AASITLTVQA	618	10	28	44						825
ENV	ITLTVQARQL	621	10	27	42						826
ENV	TLTVQARQLL	622	10	35	55						827
ENV	VQARQLLSGI	625	10	36	56						828

Table VIII
HIV-1 AD2 Super Motif Peptides With Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
ENV	QARQLLSGIV	626	10	38	59						829
ENV	GIVQQNNLL	633	10	26	41	0.0002					830
ENV	GIVQQSNLL	633	10	32	50						831
ENV	VQQQNLLRA	635	10	25	39						832
ENV	VQQQNLLRA	635	10	26	41						833
ENV	QQQNLLRAI	636	10	25	39						834
ENV	QQQNLLRAI	636	10	26	41						835
ENV	QQQNLLRAI	643	10	44	69						836
ENV	RAIEAQHILL	646	10	12	19						837
ENV	EAQQHLLKLT	646	10	34	54						838
ENV	EAQQHLLQLT	647	10	13	20						839
ENV	AOQHLLKLT	647	10	34	53						840
ENV	AOQHLLQLT	650	10	13	20						841
ENV	HLLKLTWGI	650	10	34	53						842
ENV	HLLKLTWGI	653	10	13	20						843
ENV	KLTVWGIKQL	653	10	44	69	0.0015					844
ENV	KLTVWGIKQL	655	10	49	77	0.0150					845
ENV	TVWGIKQLQA	658	10	40	63	0.0002					846
ENV	GIKQLOARVL	660	10	33	52						847
ENV	KQLQARVLAV	672	10	27	42						848
ENV	YLRDQQLGI	672	10	18	28						849
ENV	YLRDQQLGI	680	10	48	75	0.0004					850
ENV	GIWGSCKLI	721	10	12	19						851
ENV	MTWMEWEREI	746	10	13	20						852
ENV	NQEKNEQDL	746	10	15	23						853
ENV	NQEKNEQEL	746	10	16	25						854
ENV	QOEKNEQDL	747	10	18	28						855
ENV	QOEKNEQEL	747	10	11	17						856
ENV	LLALDKWASL	755	10	18	28	0.0024					857
ENV	WASLWNVFDI	755	10	17	27						858
ENV	ITKWLWYIKI	761	10	15	23						859
ENV	ITNWLWYIKI	770	10	14	22	0.0002					860
ENV	WLVWYIKIFIM	773	10	43	67	0.0001					861
ENV	KIFIMIVGGL	778	10	38	59	0.0003					862
ENV	IMIVGGLIGL	781	10	34	54						863
ENV	IVGGLIGLRI	783	10	42	66						864
ENV	GLIGLRIIFA	786	10	15	23						865
ENV	GLIGLRIIFA	786	10	21	33						866
ENV	LIGLRIIFAV	787	10	16	25						867
ENV	LIGLRIIFAV	787	10	21	33						868
ENV	RIIFAVLSIV	791	10	14	22	0.0007					869
ENV	RIIFAVLSIV	791	10	17	27	0.0002					870
ENV	FAVLSTVNRV	794	10	31	48						871
ENV	FAVLSTVNRV	842	10	12	19						872
ENV	SIRLVSGFLA	844	10	16	25						873
ENV	RLVSGFLALA	851	10	19	30						874
ENV	ALAWDDLRLSL	851	10	11	17						875
ENV	NLCFLSYHRL	859	10	31	48						876
ENV	SLCLFSYHRL	859	10	11	17						877
ENV	LIAARTVELL	873	10	11	17						878
ENV	ELLGR3GWEA	881	10	10	16						878

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
ENV	LLGRRGWEAL	882	10	09	15						879
ENV	RLGWGLKYL	894	10	09	29						880
ENV	NLLQYWSQEL	905	10	16	25	0.0059					881
ENV	ELKNSAVSL	913	10	10	16						882
ENV	SAVSLLNATA	917	10	11	17						883
ENV	AVSLLNATAI	918	10	11	17						884
ENV	SLLNATAIIV	920	10	14	22	0.0650	0.0074	0.0390	0.0600	0.0390	885
ENV	LLNATAIAVA	921	10	14	22	0.0740					886
ENV	ATAIAVAEGT	924	10	14	22						887
ENV	IAVAEGTDRI	927	10	16	25	0.0001					888
ENV	IAVAEGTDRV	927	10	14	22						889
ENV	AVAEGTDRII	928	10	15	23						890
ENV	AVAEGTDRVI	928	10	14	22	0.0004					891
ENV	RAIHIPRRI	945	10	12	19						892
ENV	IIIPRRIRQGL	949	10	13	21						893
ENV	NIPRRIRQGL	949	10	11	17						894
ENV	RIRQGLERAL	953	10	34	53						895
ENV	LILGLVIICSA	21	11	09	15						896
ENV	KQLYATVYSGV	34	11	01	50	0.0001					897
ENV	GVFVWKEATT	52	11	22	34						898
ENV	ATTLFCASDA	59	11	23	36						899
ENV	TTLFCASDA	61	11	44	69						900
ENV	NVWATHIACVPT	80	11	48	75						901
ENV	CVPTDNPQEI	87	11	25	39						902
ENV	CVPTDNPQEV	87	11	21	33						903
ENV	PTDNPQEVVL	89	11	12	19						904
ENV	NMWNKNMVEQM	107	11	30	47						905
ENV	NMVEQMVEDII	112	11	20	31						906
ENV	SLWDOSLPCV	123	11	47	75						907
ENV	DQSLKPCVKLT	126	11	47	73						908
ENV	SLKPCVKLTPL	128	11	54	84						909
ENV	CVKLITLVCVTL	132	11	52	81						910
ENV	LTPLCVTLNCT	135	11	22	34						911
ENV	EIKNCSFNITT	181	11	11	17						912
ENV	RLINCNTSAIT	236	11	14	22						913
ENV	QACPKVSFEPI	248	11	30	47						914
ENV	PIIHYCAPAGFA	260	11	27	42						915
ENV	PIHYCTPAGFA	260	11	10	16						916
ENV	GTGPKNVSTV	281	11	12	19						917
ENV	NVSTVQCTHGI	287	11	51	80						918
ENV	TVQCTHGIKPV	290	11	28	44						919
ENV	TVQCTHGIKPV	290	11	22	34						920
ENV	VQCTHGIKPVV	292	11	31	48						921
ENV	VQCTHGIKPVV	292	11	25	39						922
ENV	CTHGHKPVVST	294	11	32	50						923
ENV	CTHGHKPVVST	294	11	26	41						924
ENV	GIRPVVSTQLL	297	11	33	52						925
ENV	GIRPVVSTQLL	297	11	26	41						926
ENV	STQLLNGSLA	303	11	55	86						927
ENV	LLNGSLAEEV	307	11	16	25						928

Table VII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
ENV	EINCTRPNNNT	342	11	10	16						929
ENV	RIGPGQTFYAT	357	11	10	16						930
ENV	GIGPGQTFYAT	360	11	01	33						931
ENV	SIGSQAFYVT	360	11	01	33						932
ENV	EMHTNYSNDT	458	11	01	17						933
ENV	NITLPCRKQI	482	11	11	17						934
ENV	TITLPCRKQI	482	11	13	20						935
ENV	ITLPCRKQII	483	11	15	23						936
ENV	IINMWQEVGKA	492	11	12	19						937
ENV	EVGKAMYAPPI	498	11	18	28						938
ENV	RVGQAMYAPPI	498	11	10	16						939
ENV	QIRCSSNITGL	512	11	11	17						940
ENV	KVKIEPLGVA	565	11	23	36						941
ENV	GVAPTKAKRRV	573	11	17	27						942
ENV	VAPTKAKRRV	574	11	17	27						943
ENV	NIITPIREKRA	586	11	01	50						944
ENV	STRTHIREKRAV	586	11	11	17						945
ENV	VVEREKRAVGI	588	11	11	17						946
ENV	GALFLGFLGAA	601	11	11	17						947
ENV	GAMFLGFLGAA	601	11	12	19						948
ENV	GAVFGLGAA	601	11	19	30						949
ENV	FLGFLGAAAGST	604	11	48	75						950
ENV	FLGAAGSTTMGA	608	11	55	86						951
ENV	AAGSTMGAASI	611	11	34	53						952
ENV	TMGAASITLTV	614	11	39	61						953
ENV	TMGAASITLTV	615	11	36	56						954
ENV	GAASITLTVQA	617	11	28	44						955
ENV	SITLTVQARQL	620	11	27	42						956
ENV	ITLTVQARQL	621	11	27	42						957
ENV	TVQARQLLSGI	624	11	36	56						958
ENV	VQARQLLSGIV	625	11	36	56						959
ENV	IVQQNNLLRA	634	11	25	39						960
ENV	IVQQNNLLRA	634	11	26	41						961
ENV	VQQNNLLRAI	635	11	25	39						962
ENV	VQQS'NLLRAI	635	11	26	41						963
ENV	QQNNLLRAIEA	637	11	26	41						964
ENV	QQSNL'RAIEA	637	11	23	36						965
ENV	LLRAIEAQHIIL	641	11	45	70						966
ENV	AIEAQHLLKL	644	11	12	19						967
ENV	AIEAQHLLQL	644	11	35	55						968
ENV	EAQQHLLKLT	646	11	12	19						969
ENV	EAQQHLLQLTV	646	11	34	54						970
ENV	LQLTVWGKQL	652	11	44	69						971
ENV	LTVWGKQLQA	654	11	49	77						972
ENV	GKQLQARVLA	658	11	40	63						973
ENV	QARVLAVERYL	663	11	33	52						974
ENV	AVERYLKDQQL	668	11	23	36						975
ENV	AVERYLRDQQL	668	11	11	17						976
ENV	LLGIW'GCSGKL	678	11	46	72						977
ENV	NMTWMEWEREI	720	11	12	19						978

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
ENV	NQEKNEQDLL	746	11	13	20						979
ENV	NQEKNEQELL	746	11	15	23						980
ENV	QOEKNEODLLA	747	11	16	25						981
ENV	EQDLLALDKWA	752	11	12	19						982
ENV	EQELLELDKWA	752	11	11	17						983
ENV	ELLELDKWASL	754	11	15	23						984
ENV	WASLWNWFDIT	761	11	13	20						985
ENV	WLWYKIFIMI	773	11	43	67						986
ENV	KIFIMVGGLI	778	11	31	48						987
ENV	FIMVGGGLGL	780	11	34	53						988
ENV	MIVGGGLGLRI	782	11	36	56						989
ENV	IVGGGLGLRII	783	11	12	19						991
ENV	IVGGGLGLRIV	783	11	30	47						992
ENV	GLGLRIIFAV	786	11	15	23						993
ENV	GLGLRIVFAV	786	11	21	33						994
ENV	LIGLRIFAVL	787	11	15	23						995
ENV	LIGLRIFAVL	787	11	20	31						996
ENV	GLRIIFAVLSI	789	11	14	22						997
ENV	GLRIVFAVLSI	789	11	19	30						998
ENV	ROGYSPISFQT	804	11	45	70						999
ENV	SIRLVSGFLAL	842	11	11	17						1000
ENV	LAWDDLRLSL	850	11	19	30						1001
ENV	CLFSYHRLRDL	852	11	20	31						1002
ENV	ELLGRRGWEL	861	11	20	31						1003
ENV	SOELKNSAVSL	881	11	09	15						1004
ENV	SAVSLLNATAI	911	11	10	16						1005
ENV	AVSLLNATAIA	917	11	11	17						1006
ENV	SLNATAIAVA	918	11	11	17						1007
ENV	NATAIAVAEGT	920	11	13	20	0.2700					1008
ENV	AIAVAEGTDRI	923	11	13	20						1009
ENV	AIAVAEGTDRI	926	11	16	25						1010
ENV	AIAVAEGTDRI	926	11	14	22						1011
ENV	IAVAEGTDRII	927	11	15	23						1012
ENV	IAVAEGTDRII	927	11	14	22						1013
ENV	PTRIROGLERA	951	11	11	17						1014
ENV	RUROGLERALL	953	11	33	52						1015
GAG	SVLSGGEL	6	8	11	17						1016
GAG	SVLSGGKL	6	8	28	44						1017
GAG	KLDWWEKI	12	8	18	28						1018
GAG	KLDKWEKI	12	8	10	16						1019
GAG	DAWEKIRL	14	8	17	27						1020
GAG	KLKHVWA	31	8	13	20						1021
GAG	RLKHLVWA	31	8	17	27						1022
GAG	IVWASREL	35	8	21	33						1023
GAG	LVWASREL	35	8	36	56						1024
GAG	FALNPGLL	46	8	22	34						1025
GAG	FAVNPGLL	46	8	16	25						1026
GAG	QLQPALQT	65	8	17	27						1027
GAG	QLQPSLOT	65	8	15	23						1028
GAG	LQTGSEEL	70	8	17	27						

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HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
GAG	GTELRSL	73	8	12	19						1029
GAG	ELRSLNT	76	8	17	27						1030
GAG	SLFNTVAT	79	8	16	25						1031
GAG	SLYNTVAT	79	8	22	34						1032
GAG	TVATLYCV	83	8	41	64						1033
GAG	DVKDTKEA	95	8	11	17						1034
GAG	EVDTKFA	95	8	22	34						1035
GAG	AQQAADT	119	8	10	16						1036
GAG	AQQAADT	132	8	01	33						1037
GAG	AQQAADT	148	8	15	27						1038
GAG	KVSQNYPI	148	8	27	48						1039
GAG	QVSQNYPI	156	8	21	33						1040
GAG	VQNLQGGM	156	8	29	45						1041
GAG	QMVHQAI	161	8	28	44						1042
GAG	IQALSPRT	165	8	29	45						1043
GAG	IQALSPRT	165	8	11	17						1044
GAG	QALSPRTL	166	8	29	45						1045
GAG	QALSPRTL	166	8	61	95						1046
GAG	TLNAWVKV	172	8	50	78						1047
GAG	KAFSPFVI	183	8	46	72						1048
GAG	EVIPMFSA	188	8	14	22						1049
GAG	EVIPMFSA	188	8	46	72						1050
GAG	VIPMFSA	189	8	14	22						1051
GAG	VIPMFSA	189	8	15	23						1052
GAG	FTALSEGA	193	8	44	69						1053
GAG	SALSEGAT	194	8	15	23						1054
GAG	TALSEGAT	194	8	15	23						1055
GAG	ATPQDLNM	200	8	12	19						1056
GAG	ATPQDLNT	200	8	42	66						1057
GAG	PDQLNTML	202	8	12	19						1058
GAG	PDQLNTML	202	8	43	67						1059
GAG	DLNMLINI	204	8	12	19						1060
GAG	DLNTMLNT	204	8	44	69						1061
GAG	NIVGGHQA	210	8	12	19						1062
GAG	IVGGHQA	210	8	47	73						1063
GAG	IVGGHQA	211	8	12	19						1064
GAG	TVGGHQA	211	8	47	73						1065
GAG	HQAAMQML	215	8	61	95						1066
GAG	AMQMLKDT	218	8	33	52						1067
GAG	AMQMLKET	218	8	26	41						1068
GAG	AMQMLKET	219	8	33	52						1069
GAG	MQMLKDTI	219	8	26	41						1070
GAG	MQMLKETI	219	8	33	52						1071
GAG	DTINSEAA	224	8	22	34						1072
GAG	ETINSEAA	224	8	39	61						1073
GAG	EAAEWDRV	229	8	15	23						1074
GAG	EAAEWDRV	229	8	30	48						1075
GAG	PVHAGPIA	238	8	19	30						1076
GAG	DIAGTTST	256	8	55	86						1077
GAG	IAGTTSTL	257	8	48	75						1078
GAG	STLQEQIA	262	8	12	19						1079

Table A11
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
GAG	LQEQIAWM	264	8	14	22						1079
GAG	LQEQIGWM	264	8	29	45						1080
GAG	WMTNPPPI	270	8	20	31						1081
GAG	WMTSNPPI	270	8	16	25						1082
GAG	DIYKRWII	284	8	17	27						1083
GAG	EYKRWII	284	8	39	61						1084
GAG	IILGLNKI	290	8	57	89						1085
GAG	ILGLNKIV	291	8	58	91						1086
GAG	GLNKIVRM	293	8	60	94						1087
GAG	IVRMYSPV	297	8	15	23						1088
GAG	IVRMYSPV	297	8	42	66						1089
GAG	RMYSPTS	299	8	14	22						1090
GAG	RMYSPTS	299	8	40	63						1091
GAG	YVDREFFKT	320	8	28	44						1092
GAG	YVDREFFKT	320	8	28	44						1093
GAG	YVDREFFKT	320	8	28	44						1094
GAG	YVDREFFKT	320	8	28	44						1095
GAG	YVDREFFKT	320	8	28	44						1096
GAG	YVDREFFKT	320	8	28	44						1097
GAG	YVDREFFKT	320	8	28	44						1098
GAG	YVDREFFKT	320	8	28	44						1099
GAG	YVDREFFKT	320	8	28	44						1100
GAG	YVDREFFKT	320	8	28	44						1101
GAG	YVDREFFKT	320	8	28	44						1102
GAG	YVDREFFKT	320	8	28	44						1103
GAG	YVDREFFKT	320	8	28	44						1104
GAG	YVDREFFKT	320	8	28	44						1105
GAG	YVDREFFKT	320	8	28	44						1106
GAG	YVDREFFKT	320	8	28	44						1107
GAG	YVDREFFKT	320	8	28	44						1108
GAG	YVDREFFKT	320	8	28	44						1109
GAG	YVDREFFKT	320	8	28	44						1110
GAG	YVDREFFKT	320	8	28	44						1111
GAG	YVDREFFKT	320	8	28	44						1112
GAG	YVDREFFKT	320	8	28	44						1113
GAG	YVDREFFKT	320	8	28	44						1114
GAG	YVDREFFKT	320	8	28	44						1115
GAG	YVDREFFKT	320	8	28	44						1116
GAG	YVDREFFKT	320	8	28	44						1117
GAG	YVDREFFKT	320	8	28	44						1118
GAG	YVDREFFKT	320	8	28	44						1119
GAG	YVDREFFKT	320	8	28	44						1120
GAG	YVDREFFKT	320	8	28	44						1121
GAG	YVDREFFKT	320	8	28	44						1122
GAG	YVDREFFKT	320	8	28	44						1123
GAG	YVDREFFKT	320	8	28	44						1124
GAG	YVDREFFKT	320	8	28	44						1125
GAG	YVDREFFKT	320	8	28	44						1126
GAG	YVDREFFKT	320	8	28	44						1127
GAG	YVDREFFKT	320	8	28	44						1128

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
GAG	PLASLKSL	548	8	15	23						1129
GAG	PLTSLKSL	548	8	12	19						1130
GAG	PLTSLRSL	548	8	12	19						1131
GAG	SLFGNDPL	554	8	12	19						1132
GAG	SLFGSDPL	554	8	11	17						1133
GAG	VLSGGKLLDA	7	9	15	23						1134
GAG	HIVWASREL	34	9	21	33						1135
GAG	HLVWASREL	34	9	36	56						1136
GAG	ALNPGLLET	47	9	19	30						1137
GAG	AVNPGLLET	47	9	14	22						1138
GAG	ETSEGRQI	54	9	16	25						1139
GAG	ILGQLQPSL	62	9	11	17						1140
GAG	GQLQPSLQT	64	9	11	17						1141
GAG	LQPALQTGT	66	9	14	22						1142
GAG	SLQTGSEEL	69	9	14	22						1143
GAG	ELRSLYNTV	76	9	15	23						1144
GAG	SLFNIVATL	79	9	16	25	0.0037	0.0012	0.2000	0.0001	0.0004	1145
GAG	SLYNTVATL	79	9	22	34	0.0053					1146
GAG	NTVATLYCV	82	9	41	64						1147
GAG	TLYCVHQI	86	9	12	19						1148
GAG	TLYCVHQRI	86	9	15	23						1149
GAG	HQREVKDT	91	9	10	16						1150
GAG	DVKDTKEAL	95	9	11	17						1151
GAG	DVKDTKEAL	95	9	20	31						1152
GAG	DTKEALDKI	98	9	32	50						1153
GAG	DTKEALEKI	98	9	10	16						1154
GAG	EQNKSKKKA	109	9	17	27						1155
GAG	KAQAQAADT	118	9	10	16						1156
GAG	QVSNQYPI	146	9	22	44						1157
GAG	QVSNQYPI	148	9	15	27						1158
GAG	QVSNQYPI	148	9	27	48						1159
GAG	IVQNAQQQM	155	9	21	33	0.0001					1160
GAG	IVQNLQQQM	155	9	29	45						1161
GAG	VQNAQGMV	156	9	14	22						1162
GAG	VQNLQQQM	156	9	29	45						1163
GAG	AQGQMVIIQA	159	9	12	19						1164
GAG	LQQQMVIIQA	159	9	21	33						1165
GAG	HQAISPTL	165	9	29	45						1166
GAG	HQAISPTL	165	9	11	17						1167
GAG	ALSPRTLNA	167	9	29	45						1168
GAG	RTLNAAWVKV	171	9	10	16						1169
GAG	TLNAWVKV	172	9	30	95	0.0012					1170
GAG	TLNAWVKV	172	9	61	47	0.0032					1171
GAG	WVKVIEKA	176	9	31	48	0.0005					1172
GAG	WVKVIEKA	176	9	25	39						1173
GAG	WVKVIEKA	176	9	28	44						1174
GAG	EVIPMFSA	188	9	46	72	0.0001					1175
GAG	EVIPMFSA	188	9	14	22						1176
GAG	FTALSEGAT	193	9	15	23						1177
GAG	GATPQDLNM	199	9	12	19						1178

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Λ^*0201	Λ^*0202	Λ^*0203	Λ^*0206	Λ^*6802	SEQ ID NO
GAG	GATPQDLNT	199	9	42	66						1179
GAG	ATPQDLNMM	200	9	12	19						1180
GAG	ATPQDLNTM	200	9	42	66						1181
GAG	DLNMLNIV	204	9	12	19						1182
GAG	DLNTMLNTV	204	9	42	66	0.0001					1183
GAG	NIVGGHQAA	210	9	12	19						1184
GAG	NTVGGHQAA	210	9	47	73						1185
GAG	IVGGHQAA	211	9	12	19						1186
GAG	TVGGHQAA	211	9	47	73						1187
GAG	AAMQMLKDT	217	9	33	52						1188
GAG	AAMQMLKET	217	9	26	41						1189
GAG	AMQMLKDTI	218	9	33	52						1190
GAG	AMQMLKETI	218	9	26	41						1191
GAG	DIAGTTSTL	256	9	48	75	0.0001					1192
GAG	TTSTLQEQI	260	9	45	71						1193
GAG	TLQEQIAWM	263	9	12	19						1194
GAG	TLQEQIGWM	263	9	27	42						1195
GAG	LQEQIAWMT	264	9	14	22						1196
GAG	LQEQIGWMT	264	9	29	45						1197
GAG	MTNNPPIPV	271	9	20	31	0.0300	0.0006	0.3000	0.0023	3.3000	1198
GAG	MTSNPPIPV	271	9	16	25						1199
GAG	DIYKRWIL	284	9	17	27						1200
GAG	EIYKRWIL	284	9	37	58	0.0001					1201
GAG	WILGLNKI	289	9	57	89	0.0091					1202
GAG	IILGLNKIV	290	9	57	89	0.0003					1203
GAG	KIVRMYSPT	296	9	15	23						1204
GAG	KIVRMYSPIV	296	9	41	64	0.0007					1205
GAG	RMYSPTSIL	299	9	14	22						1206
GAG	RMYSPIV	299	9	40	63						1207
GAG	YVDRFFKTL	320	9	27	42						1208
GAG	YVDRFFKTL	320	9	28	44	0.0010					1209
GAG	KTLRAEQAT	326	9	34	53						1210
GAG	RAEQASQEV	329	9	12	19						1211
GAG	RAEQATQDV	329	9	15	23						1212
GAG	RAEQATQEV	329	9	27	42						1213
GAG	ATQDVKNWM	333	9	15	23						1214
GAG	ATQDVKNWM	333	9	18	28						1215
GAG	ATQDVKNWM	334	9	11	17						1216
GAG	SOEVKNWMT	334	9	15	23						1217
GAG	TQDVKNWMT	334	9	18	28						1218
GAG	TQDVKNWMT	336	9	12	19						1219
GAG	DVKNWMTET	336	9	12	19						1220
GAG	EKNWMTET	336	9	25	39						1221
GAG	NANPDCKSI	349	9	11	17						1222
GAG	NANPDCKII	349	9	45	70						1223
GAG	TILKALGPA	356	9	16	25						1224
GAG	ILKALGPA	357	9	16	25	0.0001					1225
GAG	ILRALGPGA	357	9	18	28						1226
GAG	KALGPAATL	359	9	16	25	0.0001					1227
GAG	PAATLEEMM	363	9	16	25						1228

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
GAG	NAQGQMVHQA	158	10	12	19						1279
GAG	NLQQQMVHQA	158	10	21	33						1280
GAG	LQQQMVHQA	159	10	15	23						1281
GAG	MVLIQAISPR	163	10	27	42						1282
GAG	QAISPRTLNA	166	10	29	45						1283
GAG	QALSPTLNA	166	10	10	16						1284
GAG	RTLNAWVKVI	171	10	30	47						1285
GAG	RTLNAWVKVV	171	10	31	48	0.0003					1286
GAG	KAFSPVIM	183	10	50	78						1287
GAG	PMFSALSEGA	191	10	45	70						1288
GAG	PMFTALSEGA	191	10	15	23						1289
GAG	GATPQDLNMM	199	10	12	19						1290
GAG	GATPQDLNMM	199	10	42	66						1291
GAG	GATPQDLNMM	199	10	12	19						1292
GAG	ATPQDLNMM	200	10	42	66						1293
GAG	ATPQDLNMM	200	10	11	17						1294
GAG	PQDLNMMMLNI	202	10	43	67						1295
GAG	PQDLNMMMLNI	202	10	12	19						1296
GAG	MLNIVGGHQA	208	10	47	73						1297
GAG	MLNTVGGHQA	208	10	12	19						1298
GAG	NIVGGHQAAM	210	10	47	73	0.0022					1299
GAG	NIVGGHQAAM	210	10	33	52						1300
GAG	QAAMQMLKDT	216	10	26	41						1301
GAG	QAAMQMLKET	216	10	33	52						1302
GAG	QAAMQMLKDTI	217	10	26	41						1303
GAG	QAAMQMLKETI	217	10	32	50						1304
GAG	MLKDTINEEA	221	10	22	34						1305
GAG	MLKETINEEA	221	10	34	53						1306
GAG	AAEWDRVHPV	230	10	14	22						1307
GAG	AAEWDRVHPV	230	10	22	34						1308
GAG	RLHPVHAGPI	235	10	14	22						1309
GAG	RVHPVHAGPI	235	10	18	28						1310
GAG	HAGPIAPGQM	240	10	17	27						1311
GAG	HAGPIAPGQM	240	10	44	69						1312
GAG	QMRPRGSDI	248	10	45	70						1313
GAG	GTSTLQEQI	259	10	11	17						1314
GAG	TSTLQEQIA	260	10	12	19						1315
GAG	STLQEQIAWM	262	10	27	42						1316
GAG	STLQEQIGWM	262	10	12	19						1317
GAG	TLOEQIAWMT	263	10	27	42						1318
GAG	TLQEQIGWMT	263	10	20	31	0.0510	0.0014	0.5900	0.0002	0.0180	1319
GAG	WMTNPPPIV	270	10	16	25						1320
GAG	WMTNPPPIV	270	10	01	50						1321
GAG	GANSIPVGD	276	10	17	27						1322
GAG	PVGDIYKRWI	281	10	40	63						1323
GAG	PVGEYKRWI	281	10	57	89	0.0009					1324
GAG	WILGLNKIV	289	10	14	22	0.0010					1325
GAG	ILGLNKIVRM	291	10	14	22						1326
GAG	IVRMYSPVSI	297	10	40	63						1327
GAG	IVRMYSPVSI	297	10	11	17						1328
GAG	QASQEVKNWM	332	10								

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
GAG	QATQDVVKNMW	332	10	15	23						1329
GAG	QATQEVKNWM	332	10	18	28						1330
GAG	ATQDVKNWMT	333	10	15	23						1331
GAG	ATQEVKNWMT	333	10	18	28						1332
GAG	DVKNWMTDTL	336	10	12	19						1333
GAG	DVKNWMTETL	336	10	11	17						1334
GAG	EVKNWMTETL	336	10	25	39						1335
GAG	MTDTLLVQNA	341	10	22	34						1336
GAG	MTETLLVQNA	341	10	36	56						1337
GAG	VQNPDPCKT	347	10	45	70						1338
GAG	NANPDCKSIL	349	10	11	17						1339
GAG	NANPDCKTIL	349	10	45	70						1340
GAG	KTLKALGPA	355	10	16	25						1341
GAG	TILKALGPAA	356	10	16	25						1342
GAG	TILRALGPGA	356	10	13	20						1343
GAG	ILKALGPAAT	357	10	16	25						1344
GAG	PAATLEEMMT	363	10	16	25						1346
GAG	AATLEEMMTA	364	10	16	25						1347
GAG	GASLEEMMTA	364	10	10	16						1348
GAG	GATLEEMMTA	364	10	28	44						1349
GAG	RVLAEAMSPA	385	10	16	25						1350
GAG	RVLAEAMSVQ	385	10	33	52	0.0058					1351
GAG	VLAEMSQT	386	10	20	31						1352
GAG	EAMSVQVNSA	389	10	11	17						1353
GAG	AMSVQVNSAT	390	10	10	16						1354
GAG	QMKDCTERQA	455	10	49	77						1355
GAG	FLQNRPEPTA	486	10	10	16						1356
GAG	FLQSRPEPTA	486	10	28	44						1357
GAG	PAESFRPEET	511	10	02	67						1358
GAG	TTPSOKOEPI	522	10	09	45						1359
GAG	ETIDKDLPL	537	10	01	25						1360
GAG	PIDKELYPLT	538	10	01	25						1361
GAG	RTENSLYPPL	538	10	01	25						1362
GAG	TIDKDLPLA	538	10	01	25						1363
GAG	WASRELERFAL	37	11	22	34						1364
GAG	WASRELERFAV	37	11	17	27						1365
GAG	ELERFALNPGL	42	11	14	22						1366
GAG	ELERFAVNPGL	42	11	15	23						1367
GAG	LLETSEGCRQI	52	11	16	25						1368
GAG	ROILOLOPSL	60	11	11	17						1369
GAG	LQTGSELRSL	70	11	11	17						1370
GAG	ELRSLYNTVAT	76	11	13	20						1371
GAG	VATLYCVHQKI	84	11	15	23						1372
GAG	VATLYCVHQRI	84	11	15	23						1373
GAG	RIEVKDTKEAL	93	11	12	19						1374
GAG	PIVQNAQQQMV	154	11	14	22						1375
GAG	PIVQNLQQQMV	154	11	29	45						1376
GAG	NLQGMVHQAI	158	11	15	23						1377
GAG	QMVHQAIQSPRT	162	11	27	42						1378
GAG	QMVHQAIQSPRTL	163	11	27	42						1378

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HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
GAG	HQAIPTLNA	165	11	29	45						1379
GAG	HQALSPRTLNA	165	11	10	16						1380
GAG	AIPTLNAWV	167	11	29	45						1381
GAG	ALSPRTLNAWV	167	11	10	16						1382
GAG	NAWVKVIEKA	174	11	25	39						1383
GAG	NAWVKVVEEKA	174	11	27	42						1384
GAG	VIEEKAFSPEV	179	11	20	31						1385
GAG	VVEEKAFSPEV	179	11	28	44						1386
GAG	PMFSALSEGAT	191	11	44	69						1387
GAG	PMFTALSEGAT	191	11	15	23						1388
GAG	ALSEGATPQDL	195	11	58	91						1389
GAG	GATPQDLNML	199	11	12	19						1390
GAG	GATPQDLNML	199	11	42	66						1391
GAG	PQDLNMLNIV	202	11	11	17						1392
GAG	PQDLNMLNTV	202	11	41	64						1393
GAG	MMLNIVGGIIQA	207	11	12	19						1394
GAG	TMLNTVGGIIQA	207	11	43	67						1395
GAG	MLNIVGGIIQA	208	11	12	19						1396
GAG	MLNTVGGIIQA	208	11	47	73						1397
GAG	IVGGIIQAAMQM	211	11	11	17						1398
GAG	TVGGIIQAAMQM	211	11	47	73						1399
GAG	HQAAMQMLKDT	215	11	33	52						1400
GAG	HQAAMQMLKET	215	11	26	41						1401
GAG	QAAMQMLKETI	216	11	33	52						1402
GAG	QAAMQMLKETI	216	11	26	41						1403
GAG	QMLKDTINEEA	220	11	32	50						1404
GAG	QMLKDTINEEA	220	11	22	34						1405
GAG	MLKDTINEEA	221	11	32	50						1406
GAG	MLKDTINEEA	221	11	22	34						1407
GAG	MLKETINEEA	221	11	34	53						1408
GAG	EAAEWDRVHPV	229	11	15	23						1409
GAG	EAAEWDRVHPV	229	11	44	69						1410
GAG	RLHPVIAIGPIA	235	11	15	23						1411
GAG	GOMREPFGSDI	247	11	44	69						1412
GAG	QMRPFGSDIA	248	11	44	69						1413
GAG	GTTSTLQEQIA	259	11	11	17						1414
GAG	STLQEQIAWMT	262	11	12	19						1415
GAG	STLQEQIGWMT	262	11	27	42						1416
GAG	QIGWMTNPPPI	267	11	18	29						1417
GAG	QIGWMTSNPPI	267	11	10	16						1418
GAG	PVGDIYKRWII	281	11	17	27						1419
GAG	PVGEIYKRWII	281	11	39	61						1420
GAG	DIYKRWIILGL	284	11	17	27						1421
GAG	EIYKRWIILGL	284	11	37	58						1422
GAG	IILGLNKIVRM	290	11	56	88						1423
GAG	KIVRMYSPTSIL	296	11	14	22						1424
GAG	KIVRMYSPTSIL	296	11	39	61						1425
GAG	IVRMYSPTSIL	297	11	14	22						1426
GAG	IVRMYSPTSIL	297	11	40	63						1427
GAG	RMYSPTSILDI	299	11	13	20						1428
GAG	RMYSPTSILDI	299	11	38	59						1428

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
GAG	YVDRFFKTLRA	320	11	27	42						1429
GAG	YVDRFYKTLRA	320	11	28	44						1430
GAG	TLRAEQASQEV	327	11	12	19						1431
GAG	TLRAEQATQDV	327	11	11	17						1432
GAG	TLRAEQATQEV	327	11	24	38						1433
GAG	EQASQEVKNWM	331	11	11	17						1434
GAG	EQATQDVKNWM	331	11	15	23						1435
GAG	EQATQEVKNWM	331	11	18	28						1436
GAG	QASQEVKNWMT	332	11	11	17						1437
GAG	QATQDVKNWMT	332	11	15	23						1438
GAG	QATQEVKNWMT	332	11	18	28						1439
GAG	SQEVKNWMTET	334	11	11	17						1440
GAG	TQDVKNWMTDT	334	11	14	22						1441
GAG	TOEVKNWMTET	334	11	12	19						1442
GAG	DVKNWMTDTLL	336	11	11	17						1443
GAG	DVKNWMTETLL	336	11	25	39						1444
GAG	EVKNWMTETLL	336	11	22	34						1445
GAG	WMTDTLLVQNA	340	11	35	55						1446
GAG	WMTETLLVQNA	340	11	45	70						1447
GAG	LVQNAVPCDKT	346	11	10	16						1448
GAG	VQNAVPCDKSI	347	11	45	70						1449
GAG	VQNAVPCDKTI	347	11	16	25						1450
GAG	KTILKALGPAA	355	11	13	20						1451
GAG	KTILRALGPAA	355	11	16	25						1452
GAG	TILKALGPAAT	356	11	16	25						1453
GAG	ILKALGPAATL	357	11	16	25						1454
GAG	ALGPAATLEEM	360	11	16	25						1455
GAG	ALGPGATLEEM	360	11	17	27						1456
GAG	PAATLEEMMTA	363	11	16	25						1457
GAG	CQGVGGPGHKA	374	11	36	56						1458
GAG	CQGVGGPGSHKA	374	11	23	36						1459
GAG	GVGGPGHKARV	376	11	36	56						1460
GAG	GVGGPGSHKARV	376	11	19	30						1461
GAG	RVLAEAMSQVT	385	11	20	31						1462
GAG	EAMSVTNSAT	389	11	10	16						1463
GAG	SAQQDLKGGYT	393	11	01	50						1464
GAG	TAQQDLKGGYT	393	11	01	50						1465
GAG	HQMKDCTERQA	454	11	49	77						1466
GAG	PAEPTAPPAEI	492	11	01	50						1467
GAG	PAESRFEET	511	11	02	67						1468
GAG	SQKQEPIDKEL	529	11	09	15						1469
GAG	ETIDKDLPLA	537	11	01	25						1470
GAG	RTENSLYPLT	538	11	01	25						1471
GAG	SLKSLFGNDPL	551	11	12	19						1472
NEF	RAQAEPAA	32	8	01	17						1473
NEF	AQAEPAAA	33	8	01	17						1474
NEF	PAADGVGA	41	8	15	23						1475
NEF	PAAEGVGA	41	8	21	33						1476
NEF	AADGVGAV	42	8	11	18						1477
NEF	AAEGVGAA	42	8	10	16						1478

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Λ^*0201	Λ^*0202	Λ^*0203	Λ^*0206	Λ^*6802	SEQ ID NO
NEF	AAEGVGAV	42	8	17	28						1479
NEF	DLEKHGAI	57	8	14	22						1480
NEF	GAITSSNT	62	8	32	50						1481
NEF	GALTSSNT	62	8	10	16						1482
NEF	AITSSNTA	63	8	27	42						1483
NEF	ITSSNTAA	64	8	15	23						1484
NEF	AATNADCA	70	8	12	22						1485
NEF	EAQEEEEV	82	8	16	25						1486
NEF	PVRPQVPL	95	8	48	75						1487
NEF	PQVPLRPM	99	8	56	88						1488
NEF	QVPLRPMT	100	8	57	89	0.0001					1489
NEF	ALDLSHFL	111	8	11	17						1490
NEF	AVDLSIIFL	111	8	15	23						1491
NEF	FLKEKGGL	117	8	56	88						1492
NEF	SOKRODIL	177	8	12	19						1493
NEF	QTEPAAGV	32	9	01	17						1494
NEF	RAEPAADGV	32	9	01	17						1495
NEF	RAQAEPAAA	32	9	01	17						1496
NEF	RTEPAAGV	32	9	01	17						1497
NEF	QAEPAAEV	33	9	01	17						1498
NEF	QAPTAAKGV	33	9	01	17						1499
NEF	QAEPAAGV	34	9	01	33						1500
NEF	PAADGVGAV	41	9	11	17						1501
NEF	PAAEVGAV	41	9	12	19						1502
NEF	GVGAASQDL	45	9	11	17						1503
NEF	GVGAVSQDL	45	9	21	33						1504
NEF	GVGAVSRDL	45	9	17	27	0.0001					1505
NEF	DLEKHGAI	57	9	14	22						1506
NEF	GAITSSNTA	62	9	27	42						1507
NEF	AITSSNTAA	63	9	14	22						1508
NEF	ITSSNTAAT	64	9	13	20						1509
NEF	TAATNADCA	69	9	12	19						1510
NEF	ATNACAWL	71	9	12	22						1511
NEF	NADCAWLEA	73	9	17	27						1512
NEF	PQVPLRPMT	99	9	56	88						1513
NEF	PLRPMTYKA	102	9	21	33						1514
NEF	MTYKGAFDL	106	9	12	19						1515
NEF	GAFDLSFEL	110	9	10	16						1516
NEF	RQDILDLWV	182	9	31	55						1517
NEF	ROEILDLWV	182	9	35	55						1518
NEF	ILDWVYHT	186	9	34	53						1519
NEF	ILDWVYNT	186	9	19	30						1520
NEF	LTFGWCFKL	221	9	39	61	0.1400	0.1300	0.0022	0.0180	7.2000	1521
NEF	LVPVDPREV	229	9	11	17						1522
NEF	KQAEPAAGV	32	10	01	17						1523
NEF	RQAPTAAKGV	32	10	01	17						1524
NEF	AQAEPAAGV	33	10	01	17						1525
NEF	GAITSSNTAA	62	10	14	22						1526
NEF	AITSSNTAAT	63	10	13	20						1527
NEF	NTAATNADCA	68	10	12	19						1528

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0201	Δ^*0202	Δ^*0203	Δ^*0206	Δ^*6802	SEQ ID NO
NEF	AATNADCAWL	70	10	12	22						1529
NEF	WLEAQEEVEV	79	10	15	24						1530
NEF	EVGFVRTPQV	91	10	40	63						1531
NEF	PLRPMITYKAA	102	10	20	31						1532
NEF	PLRPMITYKGA	102	10	25	39						1533
NEF	PMITYKGAFDL	105	10	12	19						1534
NEF	LIYSKKRQEI	174	10	18	28						1535
NEF	SQKRQDILD	177	10	12	19						1536
NEF	DILDLVVYHT	185	10	12	19						1537
NEF	EILDLVVYHT	185	10	22	34						1538
NEF	EILDLVVYNT	185	10	11	17						1539
NEF	WQNYTPGPGI	204	10	18	29						1540
NEF	WQNYTPGPGT	204	10	21	33						1541
NEF	WQNYTPGPGV	204	10	11	17						1542
NEF	PLTFGWCFKL	219	10	39	61	0.0350	0.0058	0.0021	0.0010	0.8400	1543
NEF	LTFGWCFKL	221	10	35	55	0.0170	0.0880	0.0540	0.0640	6.5000	1544
NEF	KLVPVDPREV	228	10	11	17						1545
NEF	LHPIQIHGM	257	10	10	16						1546
NEF	LHPIQIHGM	257	10	12	19						1547
NEF	QTEPAAVGVA	32	11	01	17						1548
NEF	RAEPAAAGVGA	32	11	01	17						1549
NEF	RAQAEPAAGV	32	11	01	17						1550
NEF	RTEPAAVGVA	32	11	01	17						1551
NEF	QAEPAAGVGA	33	11	01	17						1552
NEF	QAPTAAKGVGA	33	11	01	17						1553
NEF	QAEPAAGVGA	34	11	01	33						1554
NEF	AVSRDLEKHA	48	11	11	17						1555
NEF	GAITSSNTAAT	62	11	13	20						1556
NEF	ITSSNTAATNA	64	11	12	19						1557
NEF	TAATNADCAWL	69	11	12	19						1558
NEF	ATNADCAWLEA	71	11	12	22						1559
NEF	AQEEEEVGFPV	83	11	17	27						1560
NEF	PVRPQVPLRPM	95	11	47	73						1561
NEF	QVPLRPMITYKA	100	11	20	31						1562
NEF	FLKEKGGLDGL	117	11	26	41						1563
NEF	FLKEKGGLGL	117	11	29	45						1564
NEF	GLYSKKRQEI	173	11	18	28						1565
NEF	LIYSKKRQEI	174	11	18	28						1566
NEF	YTPGPGIRYPL	207	11	16	25						1567
NEF	YTPGPGTRFPL	207	11	13	20						1568
NEF	PLTFGWCFKL	219	11	35	55						1569
NEF	CLLHPMSQHGM	256	11	10	16						1570
POL	LAFPIQGEA	6	8	12	19						1571
POL	LAFPIQGEA	6	8	12	19						1572
POL	LAFQGEA	6	8	16	25						1573
POL	QTRANSPT	21	8	28	45						1574
POL	PTRELOV	30	8	14	22						1575
POL	QTRANSPT	35	8	01	33						1576
POL	PTRELOV	36	8	01	33						1577
POL	GADRQGV	70	8	01	20						1578

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
POL	GTLNCPQI	80	8	01	33						1579
POL	PTFNFPQI	80	8	01	33						1580
POL	ITLWQRPL	90	8	47	73						1581
POL	TLWQRPLV	91	8	49	77						1582
POL	WQRPLVTI	93	8	21	33						1583
POL	WQRPLVTV	93	8	19	30						1584
POL	TIKIGGOL	99	8	17	27						1585
POL	TVKIGGQL	99	8	11	17						1586
POL	GQIEALL	104	8	10	16						1587
POL	GQLKEALL	104	8	34	53						1588
POL	LIEALLDT	106	8	10	16						1589
POL	EALLDTGA	108	8	61	95						1590
POL	DTGADDTV	112	8	63	98						1591
POL	TVLEDINL	118	8	13	20						1592
POL	TVLEENL	118	8	15	23						1593
POL	GIGGFIKV	136	8	64	100						1594
POL	KVROYDQI	142	8	41	64						1595
POL	QYDQILI	144	8	20	31						1596
POL	QYDQIPI	144	8	20	31						1597
POL	EICGHKAI	152	8	13	20						1598
POL	EICOKKAI	152	8	19	30						1599
POL	KAIGTVLV	157	8	24	38						1600
POL	GTVLVGPT	160	8	48	75						1601
POL	VLVGPTPV	162	8	60	94						1602
POL	NIGRNLL	170	8	53	83						1603
POL	NIGRNML	171	8	26	41						1604
POL	IIGRNMLT	171	8	26	41						1605
POL	LLTQIGCT	176	8	30	47						1606
POL	MLTQIGCT	176	8	21	33						1607
POL	MLTQIGCT	176	8	18	28						1608
POL	MLTQIGCT	177	8	10	16						1609
POL	LTQIGCTL	177	8	42	66						1610
POL	LTQIGCTL	177	8	15	23						1611
POL	PISPIETV	187	8	57	89						1612
POL	PVKLKPGM	195	8	56	88						1613
POL	KVKQWPLT	207	8	56	88						1614
POL	LTEEKIKA	213	8	49	77						1615
POL	KIKALTEI	217	8	56	88						1616
POL	KIKALVEI	217	8	28	44						1617
POL	KALTEICT	219	8	15	23						1618
POL	LVEICTEM	221	8	12	19						1619
POL	EMEKEGKI	229	8	15	24						1620
POL	AIKKKDSI	251	8	15	24						1621
POL	STKWRKLV	257	8	42	66						1622
POL	KLVDREL	262	8	59	92						1623
POL	RTQDFWEV	272	8	59	92						1624
POL	QLGIPHPA	280	8	63	98						1625
POL	GIPHPAGL	282	8	55	86						1626
POL	GLKKKSV	288	8	56	89						1627
POL	GLKKKSV	288	8	52	81						1628

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HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
POL	TVLDVGDA	296	8	58	91						1629
POL	DAYFSVPL	302	8	55	86						1630
POL	TAFTIPSI	317	8	37	58						1631
POL	TAFTIPST	317	8	13	20						1632
POL	GIRYQYNV	330	8	52	81						1633
POL	PAIFQSSM	346	8	42	66						1634
POL	AIQSSMTI	347	8	39	61						1635
POL	FQSSMTKI	349	8	38	59						1636
POL	KQNTDIVI	362	8	14	22						1637
POL	DIVIQYQM	366	8	18	28						1638
POL	EIVVQYQM	366	8	24	38						1639
POL	DLVYVGSDL	375	8	63	98						1640
POL	YVGSDLLEI	377	8	58	91						1641
POL	HLLKWGFT	397	8	22	34						1642
POL	HLLRWGFT	397	8	25	39						1643
POL	LLKWGFTT	398	8	23	36						1644
POL	LLRWGFTT	398	8	24	38						1645
POL	HOKEPPFL	410	8	62	97						1646
POL	FLWMGYEL	416	8	64	100						1647
POL	ELHPDKWT	422	8	60	94						1648
POL	WTVQPIQL	428	8	28	44						1649
POL	WTVQPIVL	428	8	13	20						1650
POL	TVNDIQKL	442	8	62	97						1651
POL	IQKLVGKL	446	8	62	97						1652
POL	LVGKLNWA	449	8	61	95						1653
POL	KLNWASOI	452	8	61	95						1654
POL	QIYAGIKV	458	8	27	43						1655
POL	QIYPGIKV	458	8	27	43						1656
POL	KVKQLCKL	464	8	29	45						1657
POL	KVRQLCKL	464	8	19	30						1658
POL	KLLRGAKA	470	8	25	40						1659
POL	KLLRGTKA	470	8	24	38						1660
POL	LLRGAKAL	471	8	30	47						1661
POL	LLRGTKAL	471	8	24	38						1662
POL	GAKALTDI	474	8	25	39						1663
POL	GTKALTEV	474	8	19	30						1664
POL	ALTDIVPL	477	8	21	33						1665
POL	ALTEVIPL	477	8	16	25						1666
POL	LTDIVPLT	478	8	23	36						1667
POL	LTEVIPLT	478	8	16	25						1668
POL	IVPLTEEA	481	8	13	20						1669
POL	VIPLTEEA	481	8	11	17						1670
POL	PLTEEAEL	483	8	30	47						1671
POL	ELAENREI	491	8	57	89						1672
POL	LAENREIL	492	8	57	89						1673
POL	KQGQDQWT	523	8	15	23						1674
POL	KQGQGWWT	523	8	25	39						1675
POL	YQEPFKNL	534	8	43	67						1676
POL	NLTKGYA	540	8	58	92						1677
POL	KTGKYAKM	542	8	19	30						1678

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0201	Δ^*0202	Δ^*0203	Δ^*0206	Δ^*6802	SEQ ID NO
POL	KTGKYARM	542	8	13	21						1679
POL	RTAHINDV	550	8	11	17						1680
POL	HTNDVKQL	553	8	49	77						1681
POL	DKVQLTEA	556	8	33	52						1682
POL	LTEAVQKI	560	8	34	53						1683
POL	EAVQKIAT	562	8	11	17						1684
POL	KIATESIV	566	8	14	22						1685
POL	IATESIVI	567	8	14	22						1686
POL	SIVIVGKT	571	8	42	66						1687
POL	KLPIQKET	582	8	20	31						1688
POL	RLPIQKET	582	8	26	41						1689
POL	IQKETWEA	585	8	15	23						1691
POL	IQKETWET	585	8	27	42						1692
POL	ETWEAWWT	588	8	11	17						1693
POL	ETWETWWT	588	8	22	34						1694
POL	WTDYWQAT	594	8	15	23						1695
POL	WIPEWFEV	602	8	24	38						1696
POL	FVNTPLV	608	8	54	86						1697
POL	NTPLVVKL	610	8	57	89						1698
POL	LVKLWYQL	614	8	58	91						1699
POL	KLWYQLET	616	8	12	19						1700
POL	YQLEKDPH	619	8	14	22						1701
POL	YQLEKEPI	619	8	31	48						1702
POL	YQLETEPI	619	8	11	17						1703
POL	OLEKEPIV	620	8	16	25						1704
POL	ETFYVDGA	630	8	55	86						1705
POL	ANRETKL	637	8	30	47						1706
POL	KLKGAGYV	643	8	36	56						1707
POL	RQKVVSLE	655	8	19	30						1708
POL	KVVSLETT	657	8	11	17						1709
POL	VVSLTDTT	658	8	10	16						1710
POL	VVSLTETT	658	8	11	17						1711
POL	TTNOKTEL	664	8	55	86						1712
POL	NQKTELIA	666	8	12	19						1713
POL	NQKTELQA	666	8	42	66						1714
POL	ELQAIHLA	670	8	16	25						1715
POL	ELQAIYLA	670	8	12	19						1716
POL	LOAHILAL	671	8	16	25						1717
POL	LQAIYLA	671	8	12	19						1718
POL	LALQDSGL	676	8	27	42						1719
POL	LQDSGLEV	678	8	27	42						1720
POL	LQDSGSEV	678	8	25	39						1721
POL	GLEVNIVT	682	8	26	41						1722
POL	IVTDSQYA	687	8	61	95						1723
POL	VTDSQYAL	688	8	59	92						1724
POL	SOYALGII	691	8	59	92						1725
POL	YALGIIQA	693	8	58	91						1726
POL	NQIEQLI	711	8	24	38						1727
POL	SQIEQLI	711	8	20	31						1728

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
POL	QLIKKEKV	716	8	28	44						1729
POL	WVPAILKGI	727	8	63	98						1730
POL	GIGGNEQV	733	8	59	92						1731
POL	QVDKLVSA	739	8	16	25						1732
POL	SAGIRKVL	745	8	15	23						1733
POL	GIRKVLFL	747	8	51	80						1734
POL	KVFLDGI	750	8	50	78						1735
POL	FLDGIDKA	753	8	55	86						1736
POL	AMASDFNL	773	8	45	70						1737
POL	PIVAKEIV	782	8	26	41						1738
POL	PVVAKEIV	782	8	28	44						1739
POL	IVAKEIVA	783	8	26	41						1740
POL	VVAKEIVA	783	8	31	48						1741
POL	CQLKGEAM	795	8	53	83						1742
POL	QVDCSPGI	805	8	57	89						1743
POL	GIWQLDCT	811	8	59	92						1744
POL	WQLDCTHL	813	8	61	95						1745
POL	CTHLEGGI	817	8	35	55						1746
POL	CTHLEGGV	817	8	26	41						1747
POL	HLEGGKIL	819	8	31	48						1748
POL	HLEGGKVL	819	8	23	36						1749
POL	HLVAVHV	824	8	30	47						1750
POL	VILVAVHV	824	8	24	38						1751
POL	ILVAVHVA	825	8	54	84						1752
POL	VASGYIEA	831	8	52	81						1753
POL	PAETQGET	842	8	58	91						1754
POL	GOETAYFI	846	8	31	48						1755
POL	GOETAYFL	846	8	26	41						1756
POL	TAYFLKL	849	8	32	50						1757
POL	TAYFLKL	849	8	27	42						1758
POL	KLGRWPV	855	8	59	92						1759
POL	FTSAAVKA	873	8	28	44						1760
POL	FTSTTVKA	873	8	14	22						1761
POL	AACWVAGI	880	8	32	50						1762
POL	GIQGEFGI	886	8	22	34						1763
POL	GIQGEFGI	886	8	11	17						1764
POL	SQGVVESM	899	8	53	83						1765
POL	DOAEHLKT	919	8	46	72						1766
POL	EQAEHLKT	919	8	13	20						1767
POL	QAEHLKTA	920	8	59	92						1768
POL	HLKTAQVM	923	8	57	89						1769
POL	KTAVQMAV	925	8	57	89						1770
POL	AVQMAVFI	927	8	60	94						1771
POL	RIDIIAT	951	8	29	45						1772
POL	RIVDIAT	951	8	12	19						1773
POL	IIASDIQT	955	8	15	23						1774
POL	IIATDIQT	955	8	41	64						1775
POL	LOKQIHKI	965	8	13	20						1776
POL	LQKQITKI	965	8	36	56						1777
POL	LLWKGEKA	993	8	62	97						1778

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HIV A02 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0201	Δ^*0202	Δ^*0203	Δ^*0206	Δ^*6802	SEQ ID NO
POL	VIQNSDI	1003	8	37	58						1779
POL	VIQNSEI	1003	8	12	19						1780
POL	KVIRKKA	1011	8	52	81						1781
POL	KVIRRKV	1011	8	11	17						1782
POL	QMAQDDCV	1027	8	44	69						1783
POL	MAGDDCVA	1028	8	44	69						1784
POL	NLAFQGEA	5	9	10	16						1785
POL	NLAFQGEA	5	9	16	25						1786
POL	EQTRANSPT	20	9	26	41						1787
POL	EQTRANSPT	34	9	01	33						1788
POL	QTRANSPTT	35	9	01	33						1789
POL	QTRANSPTT	64	9	10	16						1790
POL	EAGADROGT	69	9	01	17						1791
POL	GQRQGTSL	79	9	01	17						1792
POL	GTTLNFPQI	80	9	01	33						1793
POL	ATSLSPQI	80	9	01	33						1794
POL	GTLCNCPQIT	80	9	01	33						1795
POL	PTNFPQIT	80	9	47	73						1796
POL	QITLWQRPL	89	9	47	73						1797
POL	ITLWQRPLV	90	9	47	73						1798
POL	TLWQRPLV	91	9	39	61	0.0185	0.0002	0.0040	0.0002	0.0140	1799
POL	VTIKGGQL	98	9	17	27						1800
POL	VTIKGGQL	98	9	11	17						1801
POL	VTIKGGQL	98	9	23	36						1802
POL	KIGGQLKEA	101	9	10	16						1803
POL	OLIEALLDT	105	9	34	53						1804
POL	QLKEALLDT	105	9	63	98						1805
POL	LLDTGADDT	110	9	61	95						1806
POL	DTGADDTVL	112	9	13	20						1807
POL	DTVLEEDNL	117	9	14	22						1808
POL	DTVLEEDNL	117	9	62	97	0.0025					1809
POL	MIGGIGGFI	133	9	21	33	0.0001					1810
POL	KVRQYDQIL	142	9	10	16						1811
POL	LIEICGHKA	150	9	13	20						1812
POL	LIEICGHKA	150	9	53	83						1813
POL	TVLVGPTFV	161	9	54	84	0.0047	0.0280	0.5200	0.0013	0.5900	1814
POL	LVGPTFVNI	163	9	26	41	0.0110					1815
POL	PVNIIGRNL	168	9	24	38	0.0001					1816
POL	PVNIIGRNM	168	9	24	38						1817
POL	NIIGRNLLT	170	9	26	41						1818
POL	NIIGRNMLT	170	9	30	47						1819
POL	NLLTQIGCT	175	9	21	33						1820
POL	NMLTQIGCT	175	9	18	28						1821
POL	NMLTQIGCT	175	9	10	16	0.0002					1822
POL	MLTQIGCTL	176	9	21	33						1823
POL	MLTQIGCTL	176	9	18	28						1824
POL	MLTQIGCTL	176	9	10	16						1825
POL	MLTQIGCTL	176	9	61	97	0.0660	0.0029	9.3000	0.0019	0.7000	1826
POL	TLNFPISPI	183	9	53	83	0.0001					1827
POL	PIETVPVKL	190	9	54	84						1828
POL	PLTEEKIKA	212	9	56	88						1829
POL	LTEEKIKAL	213	9	15	23	0.0230	0.0230	0.0710	0.0140	0.0140	1830
POL	ALVEICTEM	220	9	15	23						1831

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
POL	FAIKKKDST	250	9	59	92						1829
POL	TQDFWEVQL	273	9	55	86						1830
POL	VQLGPIHPA	279	9	54	84						1831
POL	GLKKKKSST	288	9	49	77						1832
POL	VTVDVGDGA	295	9	57	89						1833
POL	DVGDAYFSV	299	9	54	84						1834
POL	YTAFTIPSI	316	9	37	58	0.0005	0.7100	1.1000	0.5300	2.4000	1835
POL	YTAFTIPST	316	9	13	20	0.1900					1836
POL	TIPSNNET	320	9	37	58						1837
POL	TIPSTNNET	320	9	14	22						1838
POL	SINNETPGI	323	9	32	50						1839
POL	STNETPGI	323	9	11	17						1840
POL	GIRYQYNVL	330	9	52	81	0.0001					1841
POL	PQGWKGSPA	339	9	59	92						1842
POL	PAIFQSSMT	346	9	39	61						1843
POL	FQSSMTKIL	349	9	38	59						1844
POL	VIYQYMDL	368	9	51	80	0.0004					1845
POL	YQYMDLLYV	370	9	61	95						1846
POL	DLEIGQHIRA	381	9	28	44						1847
POL	DLEIGQHRT	381	9	21	33						1848
POL	EIGQIRAKI	383	9	26	41						1849
POL	EIGQIRTKI	383	9	21	33						1850
POL	KIEELREHL	390	9	19	30						1851
POL	KIEELRQHL	390	9	17	27	0.0001					1852
POL	HLLKWGFTT	397	9	22	34						1853
POL	HLRWGFTT	397	9	24	38						1854
POL	ELHPDKWTV	422	9	60	94	0.0001					1855
POL	QLPEKDSWT	434	9	13	20						1856
POL	VLPEKDSWT	434	9	13	20						1857
POL	WTVNDIQKL	441	9	62	97	0.0001					1858
POL	TVNDIQKLV	442	9	61	95	0.0001					1859
POL	DIQKLVGKL	445	9	62	97	0.0001					1860
POL	KLVGKLNWA	448	9	61	95	0.0001	0.3400	1.7000	0.0930	0.0130	1861
POL	WASQIYAGI	455	9	27	42	0.0840					1862
POL	WASQIYPGI	455	9	29	45	0.0020					1863
POL	SOIYAGIKV	457	9	27	42						1864
POL	SOIYPGIKV	457	9	27	42						1865
POL	YAGIKVKQL	460	9	18	28						1866
POL	KVKQLCKLL	464	9	28	44						1867
POL	KVRQLCKLL	464	9	19	30						1868
POL	QLCKILRGA	467	9	25	39						1869
POL	QLCKLLRGT	467	9	21	33						1870
POL	KLLRGAKAL	470	9	25	40						1871
POL	KLLRGTKAL	470	9	24	38	0.0069					1872
POL	LLRGAKALT	471	9	30	47						1873
POL	LLRGTKALT	471	9	24	38						1874
POL	GAKALTDIV	474	9	24	38						1875
POL	GTKALTEVI	474	9	11	17						1876
POL	KALTDIVPL	476	9	21	33						1877
POL	KALTEVIPL	476	9	16	25						1878

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
POL	ALTDIVPLT	477	9	21	33						1879
POL	ALTEVIPLT	477	9	16	25						1880
POL	DIVPLTEEA	480	9	13	20						1881
POL	EVIPLTEEA	480	9	11	17						1882
POL	LTEEALELE	484	9	37	58						1883
POL	ELAEAREIL	491	9	57	89						1884
POL	ILKEPVHGV	498	9	41	64	0.0001					1885
POL	GQDQWYQI	525	9	13	20	0.0055					1886
POL	GQGWYQI	525	9	25	39						1887
POL	YAKMRTAHT	546	9	10	16						1888
POL	YARMRGAIHT	546	9	13	20						1889
POL	IITNDVKQLT	553	9	43	67						1890
POL	DKVQLTEAV	556	9	33	52						1891
POL	QLTEAVQKI	559	9	34	53	0.0001					1892
POL	LTEAVQKIA	560	9	26	41	0.0007					1893
POL	VQKIATESI	564	9	14	22						1894
POL	KIATESIVI	566	9	14	22						1895
POL	KTPKFKLPI	577	9	17	27						1896
POL	KTPKFKLPI	577	9	29	45						1897
POL	PIQKETWEA	584	9	15	23						1898
POL	PIQKETWET	584	9	15	42						1899
POL	PLVKLWYQL	613	9	54	84	0.0002					1900
POL	YQLEKEPIV	619	9	16	25						1901
POL	IVGAETFYV	626	9	28	44	0.0099					1902
POL	ETFYVDGAA	630	9	51	80						1903
POL	GAANRETKL	636	9	30	47						1904
POL	KLKGAGYVT	643	9	36	56						1905
POL	VTDGRQKV	650	9	30	47	0.0002					1906
POL	KVSLTETT	657	9	11	17						1907
POL	LTDITNQKT	661	9	19	30						1908
POL	LTDITNQKT	661	9	25	39						1909
POL	DITNQKT	663	9	26	41						1910
POL	ETINQKT	663	9	29	45						1911
POL	NQKTELHAI	666	9	12	19						1912
POL	NQKTELOAI	666	9	42	66						1913
POL	KTELQAIHL	668	9	15	23						1914
POL	KTELQAIHL	668	9	12	19						1915
POL	ELQAIHLAL	670	9	16	25	0.0001					1916
POL	ELQAIHLAL	670	9	12	19						1917
POL	HLALQDSGL	675	9	15	23	0.0005					1918
POL	ALQDSGLEV	677	9	27	42	0.0083					1919
POL	ALQDSGSEV	677	9	25	39						1920
POL	NIVTDSQYA	686	9	61	95	0.0024					1921
POL	IVTDSQYAL	687	9	59	92						1922
POL	LVNCHIEQL	709	9	19	30						1923
POL	LVSQIEQL	709	9	19	30						1924
POL	EQLIKKEKV	715	9	28	44						1925
POL	LIKKEKVYL	717	9	35	55	0.0001					1926
POL	KVYLAWVPA	722	9	20	32						1927
POL	KVYLSWVPA	722	9	23	37						1928

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Λ^*0201	Λ^*0202	Λ^*0203	Λ^*0206	Λ^*6802	SEQ ID NO
POL	EQVDKLVSA	738	9	16	25						1929
POL	LYSAGIRKV	743	9	15	23	0.0001					1930
POL	LVSSGIRKV	743	9	26	41						1931
POL	RAMASDFNL	772	9	41	64	0.0230	0.0370	0.0004	0.0710	0.0130	1932
POL	PIVAKEIVA	782	9	25	39						1933
POL	PVVAKEIVA	782	9	28	44						1934
POL	VASCDKCQL	789	9	43	67						1935
POL	GQVDCSPGI	804	9	57	89						1936
POL	CTHLEGGKII	817	9	35	55						1937
POL	CTHLEGGKVI	817	9	26	41	0.0010					1938
POL	HLEGGKILV	819	9	31	48	0.0006					1939
POL	HLEGGKILV	819	9	23	36	0.0002					1940
POL	KIILVAVHV	823	9	30	47	0.0001					1941
POL	KIILVAVHV	823	9	23	36						1942
POL	ILVAVHVA	824	9	30	47						1943
POL	VILVAVHVA	824	9	23	36						1944
POL	AVHVASGYI	828	9	53	83						1945
POL	HVASGYIEA	830	9	52	81						1946
POL	YIEAEVIPA	835	9	53	83						1947
POL	EAETPAET	837	9	62	98						1948
POL	PAETGQETA	842	9	58	91						1949
POL	GOETAYFIL	846	9	31	48						1950
POL	GOETAYFLL	846	9	26	41						1951
POL	ETAYFILKL	848	9	31	48						1952
POL	ETAYFLLKL	848	9	27	42						1953
POL	TAYFILKLA	849	9	32	50						1954
POL	TAYFLLKLA	849	9	27	42						1955
POL	LAGRWVPKT	856	9	14	22						1956
POL	LAGRWVPKV	856	9	30	47						1957
POL	HTDNGSNFT	866	9	49	77						1958
POL	FTSAAVKAA	873	9	27	42						1959
POL	FTSTTVKAA	873	9	14	22						1960
POL	AVKAAACWVA	877	9	32	50						1961
POL	TVKAAACWVA	877	9	23	36						1962
POL	KAACVWAGI	879	9	31	49	0.0180	0.0040	0.1200	0.0230	0.0150	1963
POL	VVESMINKEL	902	9	48	75						1964
POL	SMNKELKKI	905	9	53	83	0.0001					1965
POL	ELKKIIGQV	909	9	57	89						1966
POL	IIGQVRDQA	913	9	44	69						1967
POL	IIGQVREQA	913	9	13	20	0.0001					1968
POL	QVRDQAEHL	916	9	48	75						1969
POL	QVREQAEHL	916	9	13	20						1970
POL	DQAEHLKTA	919	9	46	72						1971
POL	EQAEHLKTA	919	9	13	20						1972
POL	QAEHLKTAV	920	9	59	92						1973
POL	HLKTAVQMA	923	9	57	89	0.0033					1974
POL	TAVOMAVFI	926	9	59	92						1975
POL	SAGERIDI	947	9	41	64						1976
POL	SAGERIVDI	947	9	14	22						1977
POL	IIDIASDI	952	9	12	19						1978

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
POL	IIDIIATDI	952	9	29	45						1979
POL	IVDIATDI	952	9	12	19						1980
POL	DIASDIQT	954	9	15	23						1981
POL	DIATDIQT	954	9	40	63						1982
POL	ATDIQTKEI	957	9	35	55						1983
POL	QTKELQKQI	961	9	46	72						1984
POL	ELQKQIKI	964	9	13	21						1985
POL	ELQKQITKI	964	9	34	54						1986
POL	IKIQNFRV	969	9	12	19						1987
POL	ITIKIQNFRV	969	9	36	57						1988
POL	PIWKGPAPKL	985	9	36	56						1989
POL	PLWKGPAPKL	985	9	19	30						1990
POL	KLLWKGEA	992	9	60	94	0.0002					1991
POL	LLWKGEAV	993	9	62	97	0.0230					1992
POL	VVIQDNSDI	1002	9	37	58	0.0001					1993
POL	VVIQDNSEI	1002	9	12	19						1994
POL	IQDNSDIKV	1004	9	38	59						1995
POL	IQDNSEIKV	1004	9	12	19						1996
POL	VVPRIRKAKI	1012	9	51	80						1997
POL	VVPRIRKVKI	1012	9	11	17						1998
POL	IKDYGKQM	1020	9	11	17						1999
POL	IRDYGKQM	1020	9	50	78						2000
POL	KQAGDDCV	1026	9	44	69						2001
POL	QMGDDCVA	1027	9	44	69	0.0001					2002
POL	KAREFSEQT	12	10	10	16						2003
POL	RANSPTREL	26	10	16	25						2004
POL	RANSPTSREL	26	10	10	16						2005
POL	STNSPTSREL	32	10	01	33						2006
POL	SQTRANSPTT	34	10	01	33						2007
POL	RANSPTSREL	35	10	01	33						2008
POL	RANSPTTREL	37	10	01	50						2009
POL	GAISLSLPQI	79	10	01	17						2010
POL	GTTLNFPQIT	79	10	01	17						2011
POL	AIISLSLPQIT	80	10	01	33						2012
POL	GTILNCPQITL	80	10	01	33						2013
POL	PTFNPQITL	80	10	01	33						2014
POL	PQITLWQRPL	88	10	47	73						2015
POL	QITLWQRPLV	89	10	47	73						2016
POL	ITLWQRPLVT	90	10	37	58						2017
POL	TLWQRPLVTI	91	10	21	33						2018
POL	TLWQRPLVTV	91	10	18	28						2019
POL	WORPLVTIKI	93	10	14	22						2020
POL	WORPLVTIKI	93	10	12	19						2021
POL	LVTIKIGGQI	97	10	13	20						2022
POL	KIGGOLKEAL	101	10	23	36						2023
POL	QGLIEALLDT	104	10	10	16						2024
POL	QGLKEALLDT	104	10	34	53						2025
POL	LIEALLDTGA	106	10	10	16						2026
POL	ALLDTGADDT	109	10	61	95						2027
POL	LLDTGADDTV	110	10	63	98	0.0005					2028

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
POL	GADDTVLEDI	114	10	15	23						2029
POL	GADDTVLEEI	114	10	18	28						2030
POL	GADDTVLEEM	114	10	11	17						2031
POL	NLPGWKPKM	124	10	35	55						2032
POL	KMIGGIGGF	132	10	62	97						2033
POL	FIKVRQYDQI	140	10	41	64	0.0290	0.0790	2.1000	0.0048	0.0120	2034
POL	KVRQYDQIPI	142	10	20	31						2035
POL	KVRQYDQIPI	142	10	13	20						2036
POL	ROYDQILIEI	144	10	20	31						2037
POL	ROYDQILIEI	144	10	12	19						2038
POL	ROYDQILIEI	144	10	13	20						2039
POL	ILIEICGKKA	149	10	10	16						2040
POL	LIEICGKKA	150	10	10	20						2041
POL	LIEICGKKA	150	10	13	20						2042
POL	EICGHKAIGT	152	10	19	30						2043
POL	EICGHKAIGT	152	10	24	38						2044
POL	EICGHKAIGT	152	10	52	81						2045
POL	AGTVLVGPT	158	10	53	83						2046
POL	GTVLVGPTTV	160	10	53	83	0.0025					2047
POL	VLVGPTTVNI	162	10	53	83	0.0015					2048
POL	LVGPTTVNII	163	10	52	81	0.0002					2049
POL	PVNIIGRNLL	168	10	26	41						2050
POL	PVNIIGRNLL	168	10	24	38						2051
POL	PVNIIGRNLL	168	10	21	33						2052
POL	IIGRNLLTQI	171	10	18	28						2053
POL	IIGRNLLTQI	171	10	11	17						2054
POL	IIGRNLLTQI	171	10	21	33	0.0007					2055
POL	NULLTQIGCTL	175	10	18	28						2056
POL	NMLTQIGCTL	175	10	10	16						2057
POL	NMLTQIGCTL	175	10	10	16	0.0025					2058
POL	QIGCTLNFI	179	10	41	64						2059
POL	QIGCTLNFI	179	10	16	25	0.0340	0.1800	0.3300	0.4400	0.4000	2060
POL	QIGCTLNFI	182	10	60	94	0.0002					2061
POL	CTLNFIPI	187	10	56	88						2062
POL	PISPIETVPV	193	10	54	84						2063
POL	TPVVKLKPGM	209	10	56	88	0.0002					2064
POL	KQWPLTEEKI	212	10	54	84						2065
POL	PLTEEKIKAL	213	10	37	58						2066
POL	LTEEKIKALT	213	10	15	23						2067
POL	LTEEKIKALV	217	10	12	19						2068
POL	KIKALTEICT	217	10	15	23						2069
POL	KIKALVEICT	219	10	15	24						2070
POL	KALVEICTEM	225	10	27	42						2071
POL	CTEMEKEGKI	238	10	50	78						2072
POL	KIGPENPYNT	238	10	10	16						2073
POL	RIGPENPYNT	238	10	53	83						2074
POL	RTQDFWEVQL	272	10	54	84	0.0002					2075
POL	EVQLGIPHPA	280	10	56	89						2076
POL	QLGIPHPAGL	286	10	50	78						2077
POL	PAGLKKKKSIV	288	10	49	77	0.0002					2078
POL	GLKKKKSIV	294	10	57	89						2079
POL	SVTLVDVGDA	308	10	19	30						2080
POL	PLDKDFRKYT	319	10	37	58						2081
POL	FTIPSINNET		10								2082

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
POL	FTIPSTNNET	319	10	13	20						2079
POL	PQGWKGSPI	339	10	59	92						2080
POL	AFQSSMTKI	347	10	36	56						2081
POL	IVVQYMDL	367	10	42	66						2082
POL	DLVYGSLEI	375	10	58	91	0.0007					2083
POL	GQHRAKIEEL	385	10	25	39	0.0001					2084
POL	GQHRKIEEL	385	10	20	31						2085
POL	KIEELREHLL	390	10	19	30						2086
POL	KIEELRQHLL	390	10	17	27	0.0002					2087
POL	RQHLLRWGFT	395	10	12	19						2088
POL	HQKEPFLWM	410	10	62	97						2089
POL	IQLEKDSWT	433	10	13	20						2090
POL	IVLEKDSWT	433	10	13	20						2091
POL	QLPEKDSWT	434	10	13	20						2092
POL	VLPEKDSWT	434	10	13	20						2093
POL	WTVNDIQKLV	441	10	61	95	0.0056					2094
POL	KLNWASQIYA	452	10	27	42	0.0001	0.0011	0.0250	0.0006	0.0130	2095
POL	GKVKQLCKL	462	10	28	44						2096
POL	GKVRQLCKL	462	10	18	28						2097
POL	KQLCKLLRGA	466	10	12	19						2098
POL	KQLCKLLRGT	466	10	14	22						2099
POL	ROLCKLLRGA	466	10	13	21						2100
POL	KLRLGAKALT	470	10	25	40						2101
POL	KLRLGTAKALT	470	10	24	38						2102
POL	KALTDIVPLT	476	10	21	33						2103
POL	KALTEVIPLT	476	10	16	25						2104
POL	IVPLTEEAEL	481	10	13	20						2105
POL	VIPLTEEAEL	481	10	11	17						2106
POL	PLTEEAEL	483	10	30	47						2107
POL	LTEEALELA	484	10	36	56						2108
POL	ELLEAENREI	489	10	53	83						2109
POL	EILKEPIVIGV	497	10	41	64	0.0007					2110
POL	GVYYDPSKDL	508	10	38	59						2111
POL	IQKQGQDQWT	521	10	12	19						2112
POL	IQKQGQDQWT	521	10	15	23						2113
POL	QIYQEPKNL	532	10	40	63						2114
POL	YQEPKNLKT	534	10	43	67	0.0002					2115
POL	NLKTGKYAKM	540	10	18	29						2116
POL	NLKTGKYARM	540	10	13	21						2117
POL	KTGKYAKMRT	542	10	10	16						2118
POL	RMRGAIITNDV	548	10	12	19						2119
POL	GAITNDVKQL	551	10	19	30						2120
POL	SAITNDVKQL	551	10	16	25						2121
POL	TAITNDVKQL	551	10	11	17						2122
POL	KQLTEAVQKI	558	10	32	51						2123
POL	QLTEAVQKIA	559	10	26	41						2124
POL	LTEAVQKIAT	560	10	11	17						2125
POL	AVQKIATESI	563	10	10	16						2126
POL	VQKIATESIV	564	10	14	22						2127
POL	ETWWTIDYWQA	591	10	10	16						2128

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Λ^*0201	Λ^*0202	Λ^*0203	Λ^*0206	Λ^*6802	SEQ ID NO
POL	WTDYWQATWI	594	10	14	22						2129
POL	WTEYWOATWI	594	10	24	38						2130
POL	ATWPEWFEV	600	10	51	80	0.0013					2131
POL	WIPEWFEVNT	602	10	50	81						2132
POL	FVNTPLVLKL	608	10	54	86	0.0002					2133
POL	LVKLWYQLET	614	10	11	17						2134
POL	QLEKEPIVGA	620	10	16	25						2135
POL	PIVGAETFYV	625	10	28	44	0.0002					2136
POL	GAETFYVDGA	628	10	48	75						2137
POL	YVDGAANRET	633	10	45	70						2138
POL	ETKLGKAGYV	641	10	35	55						2139
POL	YVTDGRQKVV	649	10	29	45	0.0002					2140
POL	VTDGRQKVV	650	10	28	44						2141
POL	RQKVYSLTET	655	10	10	16						2142
POL	SLTDTTNQKT	660	10	11	17						2143
POL	SLTETTNQKT	660	10	19	30						2144
POL	TTNQKTELHA	664	10	12	19						2145
POL	TTNQKTELQA	664	10	42	66						2146
POL	KTELQAIHILA	668	10	15	23						2147
POL	KTELQAIYLA	668	10	12	19						2148
POL	LALQDSGLEV	676	10	27	42						2149
POL	LALQDSGSEV	676	10	25	39	0.0006					2150
POL	LQDSGLEVNI	678	10	27	42						2151
POL	LQDSGSEVNI	678	10	25	39						2152
POL	NIVTDSQYAL	686	10	59	92	0.0004					2153
POL	VTDQYALGI	688	10	58	91						2154
POL	SOYALGIQA	691	10	58	91						2155
POL	AQPKSESEL	700	10	36	56						2156
POL	ELVNQIEQL	708	10	18	28						2157
POL	ELVSQIEQL	708	10	19	30						2158
POL	LVNQIEQL	709	10	19	30						2159
POL	LVSQIEQL	709	10	19	30						2160
POL	QLIKKEKVYL	716	10	28	44	0.0006					2161
POL	LIKKEKVYLA	717	10	20	31						2162
POL	LAWVFAIKGI	725	10	22	34						2163
POL	QVDKLYSAGI	739	10	15	23						2164
POL	QVDKLYSSGI	739	10	29	45						2165
POL	KLVSSGIRKV	742	10	15	23	0.0074					2166
POL	KLVSSGIRKV	742	10	26	41						2167
POL	LVSSGIRKVL	743	10	15	23	0.0002					2168
POL	LVSSGIRKVL	743	10	26	41						2169
POL	SAGIRKVLFL	745	10	15	23						2170
POL	VLFIDGDKA	751	10	51	80	0.0007					2171
POL	MASDFNLPI	774	10	22	34						2172
POL	MASDFNLPPV	774	10	25	39	0.0800	0.1900	0.1800	0.1100	2.2000	2173
POL	NLPPVVAKEI	779	10	26	41						2174
POL	NLPPVVAKEI	779	10	27	42	0.0007					2175
POL	IVASCDKCCQL	788	10	43	67	0.0006					2176
POL	GIWQLDCTHL	811	10	59	92	0.0003					2177
POL	CTHLEGKIIL	817	10	31	48						2178

Table VIII
HIV A02 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Λ^*0201	Λ^*0202	Λ^*0203	Λ^*0206	Λ^*6802	SEQ ID NO
POL	CTHLEGGKVL	817	10	23	36						2179
POL	HLEGGKILVA	819	10	31	48						2180
POL	HLEGGKILVA	819	10	23	36						2181
POL	KHLVAVHVA	823	10	30	47						2182
POL	KVLVAVHVA	823	10	22	34						2183
POL	VAVHVASGYI	827	10	53	83						2184
POL	VASGYIEAEV	831	10	52	81						2185
POL	VIPAETGGQET	840	10	58	91						2186
POL	ETGQETAYFI	844	10	31	48						2187
POL	ETGQETAYFL	844	10	26	41						2188
POL	ETAYFILKLA	848	10	31	48						2189
POL	ETAYFLKLA	848	10	27	42						2190
POL	ILKLAGRWPV	853	10	34	53						2191
POL	LLKLAGRWPV	853	10	25	39						2192
POL	KLGRWPVKV	855	10	14	22						2193
POL	KLGRWPVKV	855	10	30	47						2194
POL	LAGRWPVKTI	856	10	13	20						2195
POL	LAGRWPVKVI	856	10	22	34						2196
POL	AAVKAACWVA	876	10	28	44						2197
POL	TTVKAACWVA	876	10	14	22						2198
POL	WAGIKQEFGI	884	10	21	33						2199
POL	WAGIKQEFGI	884	10	11	17						2200
POL	POSQGVVSM	897	10	53	83						2201
POL	GVVESMKNEL	901	10	48	75						2202
POL	SMNKKELKII	905	10	53	83						2203
POL	KIIGQVRDQA	912	10	43	67						2204
POL	KIIGQVREQA	912	10	13	20						2205
POL	QVVRDQAEHL	915	10	44	69						2206
POL	QVVRDQAEHL	915	10	13	20						2207
POL	QVVRDQAEHL	915	10	46	72						2208
POL	EQAEHLKTAV	919	10	13	20						2209
POL	HLKTAVQMAV	923	10	57	89						2210
POL	KTAVQMAVFI	925	10	56	88	0.0005					2211
POL	SAGERIIDII	947	10	41	64	0.0002					2212
POL	SAGERIVDII	947	10	14	22						2213
POL	RIIDIIASDI	951	10	12	19						2214
POL	RIIDIIATDI	951	10	29	45						2215
POL	RIVDIIATDI	951	10	12	19						2216
POL	IASDIQTKEL	956	10	14	22						2217
POL	IATDIQTKEL	956	10	35	55						2218
POL	IOTKELQKQI	960	10	44	69						2219
POL	QTKELQKQII	961	10	10	16						2220
POL	QTKELQKQIT	961	10	32	50						2221
POL	QIHKIQNFRV	968	10	12	19						2222
POL	QITKIQNFRV	968	10	35	55	0.0002					2223
POL	PIWKGPAKLL	985	10	35	55						2224
POL	PLWKGPAKLL	985	10	18	28						2225
POL	KLLWKGEFAG	992	10	60	94	0.0006					2226
POL	LLWKGEFAGV	993	10	61	95	0.0360					2227
POL	AVVIQDNSDI	1000	10	37	58						2228

Table VIII
HIV A02 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Λ^*0201	Λ^*0202	Λ^*0203	Λ^*0206	Λ^*6802	SEQ ID NO
POL	AVVIQDNSEI	1000	10	12	19						2229
POL	VIQDN-SDIKV	1003	10	37	58						2230
POL	VIQDN-SEIKV	1003	10	12	19	0.0013					2231
POL	IQDNSEIKVV	1004	10	38	59						2232
POL	IQDNSEIKVV	1004	10	12	19						2233
POL	DIKVVPRRKA	1009	10	39	61						2234
POL	EIKVVPRRKA	1009	10	13	20						2235
POL	KVVPRRKAKI	1011	10	51	80						2236
POL	KVVPRRKVKI	1011	10	11	17						2237
POL	VVPRKAKII	1012	10	50	78						2238
POL	VVPRKVKII	1012	10	11	17						2239
POL	KIKDYGKQM	1019	10	11	17						2240
POL	KIIRDYGKQM	1019	10	50	78						2241
POL	IKDYGKQMA	1020	10	11	17						2242
POL	IIRDYGKQMA	1020	10	49	77						2243
POL	KQMAGDDCVA	1026	10	44	69						2244
POL	GAISLSPQIT	79	11	01	17						2245
POL	AISLSLPQITL	80	11	01	33						2246
POL	POITLWQRPLV	88	11	47	73						2247
POL	QITLWQRPLVT	89	11	37	58						2248
POL	ITLWQRPLVTI	90	11	19	30						2249
POL	ITLWQRPLVTI	90	11	18	28						2250
POL	PLVTIKIGGQL	96	11	13	20						2251
POL	TIKIGGQLKEA	99	11	17	27						2252
POL	KIGGQLKEALL	101	11	23	36						2253
POL	QLJEALLDTGA	105	11	10	16						2254
POL	QLKEALLDTGA	105	11	34	53						2255
POL	EALLDTGADDT	108	11	60	94						2256
POL	ALLDTGADDTV	109	11	61	95						2257
POL	LLDTGADDTVL	110	11	61	95						2258
POL	NLPGRKWKPKMI	124	11	35	55						2259
POL	MIGGIGGFKV	133	11	62	97						2260
POL	FIKVRQYDQIL	140	11	21	33						2261
POL	QILIEICGKKA	148	11	13	20						2262
POL	ILIEICGKKAI	149	11	13	20						2263
POL	EICGHKAIGTV	152	11	19	30						2264
POL	EICGKKAIGTV	152	11	23	36						2265
POL	KAIGTVLYGPT	157	11	48	75						2266
POL	TVLVGPTPVNI	161	11	53	83						2267
POL	VLVGPPTPVNI	162	11	51	80						2268
POL	PTPVNIIGNRM	166	11	26	41						2269
POL	PTPVNIIGNRM	166	11	24	38						2270
POL	PVNIIGNRMILT	168	11	26	41						2271
POL	PVNIIGNRMILT	168	11	23	36						2272
POL	NIIGNRMILTQI	170	11	21	33						2273
POL	NIIGNRMILTQI	170	11	18	28						2274
POL	NIIGNRMILTQI	170	11	11	17						2275
POL	NIIGNRMILTQI	178	11	41	64						2276
POL	TQLGCTLNFI	178	11	15	23						2277
POL	TLNFIPIPIET	183	11	54	86						2278

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HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SIFQ ID NO
POL	ETVPVKLKPGM	192	11	51	80						2279
POL	KLKPGMDGPKV	197	11	47	73						2280
POL	PLTEEKIKALT	212	11	35	55						2281
POL	PLTEEKIKALV	212	11	15	23						2282
POL	EMEKEGKISKI	229	11	32	50						2283
POL	PIFAIKKKDST	248	11	22	34						2284
POL	PVFAIKKKDST	248	11	37	58						2285
POL	LVDFRELKRT	263	11	60	94						2286
POL	TQDFWEVQLGI	273	11	55	86						2287
POL	VQLGIPIHAGL	279	11	54	84						2288
POL	PAGLKKKKSVT	286	11	47	73						2289
POL	GLKKKKSIVL	288	11	49	77						2290
POL	VLDVGDYFSV	297	11	53	83						2291
POL	DVGDAYFSVPL	299	11	54	84						2292
POL	PLDKDFRKYTA	308	11	19	30						2293
POL	ETGIRYQYNV	327	11	51	80						2294
POL	VLPQGWKGSFA	337	11	58	92						2295
POL	PAIFQSSMTKI	346	11	36	56						2296
POL	AIQSSMTKIL	347	11	36	56						2297
POL	DIVIQYMDL	366	11	18	28						2298
POL	EIVIQYMDL	366	11	24	38						2299
POL	VIQYMDLYV	368	11	51	80						2300
POL	YMDDLTVGSDL	372	11	61	95						2301
POL	DLEIGQIRAKI	381	11	26	41						2302
POL	DLEIGQIRTKI	381	11	20	31						2303
POL	RAKIEELREHL	388	11	13	20						2304
POL	RTKIEELROHL	388	11	14	22						2305
POL	RQHLLRWGFTT	395	11	12	19						2306
POL	PIQLPEKDSWT	432	11	13	20						2307
POL	PIVLPEKDSWT	432	11	13	20						2308
POL	IQLEPKDSWT	433	11	13	20						2309
POL	IVLPEKDSWT	433	11	13	20						2310
POL	IQKLVGKLNWA	446	11	61	95						2311
POL	LVGKLNWASQI	449	11	60	94						2312
POL	WASQIYAGIKV	455	11	26	41						2313
POL	WASQIYPGKIV	455	11	27	42						2314
POL	QIYAGIKVKQL	458	11	18	29						2315
POL	QIYPGKIVKQL	458	11	11	17						2316
POL	QIYPGKIVRQL	458	11	14	22						2317
POL	GKVKQLCKLL	462	11	27	42						2318
POL	GKIVRQLCKLL	462	11	18	28						2319
POL	QLCKLLRGAKA	467	11	24	38						2320
POL	QLCKLLRGTKA	467	11	21	33						2321
POL	LLRGAKALTDI	471	11	22	34						2322
POL	LLRGTKALTEV	471	11	18	28						2323
POL	GAKALTDIVPL	474	11	17	27						2324
POL	GTKALTEVIPL	474	11	11	17						2325
POL	LTDIVPLTEEA	478	11	13	20						2326
POL	LTEVIPLTEEA	478	11	11	17						2327
POL	DIVPLTEEAEL	480	11	13	20						2328

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
POL	EVIPLTEAEAL	480	11	11	17						2329
POL	PLTEAELELA	483	11	29	45						2330
POL	ELELAENREIL	489	11	53	83						2331
POL	GVYDPSKDLI	508	11	31	48						2332
POL	EIQKQGQDQWT	520	11	12	19						2333
POL	EIQKQGQGWIT	520	11	15	23						2334
POL	KQGQDQWTYQI	523	11	13	20						2335
POL	KQGQDQWTYQI	523	11	25	39						2336
POL	YQIQEPEKNL	531	11	40	63						2337
POL	KTGKYAKMRTA	542	11	10	16						2338
POL	KTGKYARMRGA	542	11	13	21						2339
POL	GAHTNDVKQLT	551	11	18	28						2340
POL	SAHTNDVKQLT	551	11	12	19						2341
POL	TAHTNDVKQLT	551	11	10	16						2342
POL	HTNDVKQLTEA	553	11	32	50						2343
POL	KQLTEAVQKIA	558	11	24	38						2344
POL	QLTEAVQKIAT	559	11	11	17						2345
POL	EAVQKIATESI	562	11	10	16						2346
POL	AVQKIATESIV	563	11	10	16						2347
POL	VQKIATESIVI	564	11	14	22						2348
POL	ATESIVIWGKT	568	11	16	25						2349
POL	VIWGTKTPKFL	573	11	17	27						2350
POL	VIWGTKTPKRL	573	11	29	45						2351
POL	RLPIQKETWET	582	11	18	28						2352
POL	IQKETWEAWWT	585	11	11	17						2353
POL	IQKETWETWWT	585	11	21	33						2354
POL	ETWWTDYWQAT	591	11	10	16						2355
POL	QATWIPEWFEV	599	11	51	81						2356
POL	KLWYQLEKDPI	616	11	14	22						2357
POL	KLWYQLEKEPI	616	11	31	48						2358
POL	KLWYQLETEPI	616	11	11	17						2359
POL	YQLEKEPIVGA	619	11	16	25						2360
POL	GAETFFYVDGAA	628	11	44	69						2361
POL	AANRETCLGKA	637	11	30	47						2362
POL	ETKLGKAGYVT	641	11	35	55						2363
POL	YVTDGRQKVV	649	11	27	42						2364
POL	RQKVVSLETT	655	11	10	16						2365
POL	LTDTTNQKTEL	661	11	19	30						2366
POL	LTETTNQKTEL	661	11	25	39						2367
POL	DTTNQKTELQA	663	11	25	39						2368
POL	ETTNQKTELHA	663	11	11	17						2369
POL	ETTNQKTELQA	663	11	17	27						2370
POL	TTNOKTELHAI	664	11	12	19						2371
POL	TTNOKTELQAI	664	11	42	66						2372
POL	NQKTELQAIHL	666	11	15	23						2373
POL	NQKTELQAIYL	666	11	12	19						2374
POL	KTELQAIHLAL	668	11	15	23						2375
POL	KTELQAIYLLAL	668	11	12	19						2376
POL	AIHLALQDSGL	673	11	15	23						2377
POL	HLALQDSGLEV	675	11	15	23						2378

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
POL	ALQDSGLEVNI	677	11	27	42						2379
POL	ALQDSGSEVNI	677	11	25	39						2380
POL	LQDSGLEVNIV	678	11	27	42						2381
POL	LQDSGSEVNIV	678	11	25	39						2382
POL	EVNIVTDSQYA	684	11	59	92						2383
POL	IVTDSQYALGI	687	11	58	91						2384
POL	VTDSQYALGII	688	11	58	91						2385
POL	QAQPKSESEL	699	11	36	56						2386
POL	AQPKSESEL	700	11	36	56						2387
POL	ELVNQIEQLI	708	11	18	28						2388
POL	ELVSIIEQLI	708	11	19	30						2389
POL	IEQLIKKEKV	713	11	28	44						2390
POL	EQLIKKEKYYL	715	11	28	44						2391
POL	QLIKKEKYYLA	716	11	19	30						2392
POL	YLAWVPAIKGI	724	11	22	34						2393
POL	YLSWVPAIKGI	724	11	37	58						2394
POL	GIGGNEQVDKL	733	11	58	91						2395
POL	EQVDKLVSSGI	738	11	15	23						2396
POL	EQVDKLVSSGI	738	11	29	45						2397
POL	KLVSAGIRKVL	742	11	15	23						2398
POL	KLVSAGIRKVL	742	11	26	41						2399
POL	KLVSAGIRKVL	742	11	49	77						2400
POL	GIRKVLFLDGI	747	11	48	75						2401
POL	KVLFLDGDICA	750	11	18	28						2402
POL	AMASDFNLPI	773	11	25	39						2403
POL	AMASDFNLPI	773	11	20	31						2404
POL	MASDFNLPI	774	11	25	39						2405
POL	MASDFNLPI	774	11	26	41						2406
POL	NLPPIVAKIV	779	11	27	42						2407
POL	NLPPIVAKIV	779	11	43	67						2408
POL	ELVASCDCQCL	787	11	53	83						2409
POL	QLKGEAMHIGQV	796	11	56	88						2410
POL	QVDCSFGIWQL	805	11	33	52						2411
POL	QLDCTHLEGI	814	11	26	41						2412
POL	QLDCTHLEGI	814	11	31	48						2413
POL	CTHLEGIILV	817	11	23	36						2414
POL	CTHLEGIILV	817	11	31	48						2415
POL	HLEGIILVAV	819	11	23	36						2416
POL	HLEGIILVAV	819	11	47	73						2417
POL	LVAVHVASGYI	826	11	52	81						2418
POL	AVIVASGYIEA	828	11	52	81						2419
POL	HVAVGYIEAEV	830	11	52	81						2420
POL	VASGYIEAEVI	831	11	52	81						2421
POL	YIEAEVIPAET	835	11	58	91						2422
POL	EVIPAETQET	839	11	58	91						2423
POL	VIPAETQETA	840	11	31	48						2424
POL	ETQETAYFIL	844	11	26	41						2425
POL	ETQETAYFIL	844	11	26	41						2426
POL	QGETAYFILKL	846	11	26	41						2427
POL	QGETAYFILKL	846	11	32	50						2428
POL	FILKLAGRWPV	852	11								

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
REV	GTQSQGT	97	8	10	16						2479
REV	PGTETGV	101	8	05	18						2480
REV	SQGTETGV	101	8	05	18						2481
REV	LVEPAVL	114	8	11	17						2482
REV	SISERILST	58	9	10	16						2483
REV	CLGRPAEPV	67	9	10	16						2484
REV	PAEPVPLQL	71	9	21	33						2485
REV	SAEPVPLQL	71	9	12	19						2486
REV	PVPLQLPPI	74	9	11	17						2487
REV	PVPLQLPPL	74	9	35	55						2488
REV	LQLPPIERL	77	9	11	17						2489
REV	LQLPPIERL	77	9	36	56						2490
REV	QLPPIERLT	78	9	18	28						2491
REV	TOGVGSPQI	98	9	11	18						2492
REV	RARQRHISI	50	10	10	16						2493
REV	PLQLPPIERL	76	10	11	17						2494
REV	PLQLPPIERL	76	10	34	53						2495
REV	LQLPPIERLT	77	10	17	27						2496
REV	QLPPIERLT	78	10	18	28						2497
REV	GTQGVGSPQI	97	10	11	18						2498
REV	PLQLPPIERLT	76	11	15	23						2499
REV	LQLPPIERLT	77	11	17	27						2500
REV	LQLPPIERLT	77	11	10	16						2501
REV	GTSGTQSQGT	94	11	10	16						2502
TAT	SQPKTACT	19	8	13	20						2503
TAT	FLNKGLGI	41	8	14	22						2504
TAT	SQPRGDPT	80	8	13	20						2505
TAT	KVERETET	97	8	12	19						2506
TAT	PTGPKESKKKV	88	11	12	19						2507
VIF	QVMVWQV	6	8	43	67						2508
VIF	IVWQVDRM	9	8	59	92						2509
VIF	WQVDRMKI	11	8	13	20						2510
VIF	WQVDRMRI	11	8	48	75						2511
VIF	KIRTWNSL	17	8	12	19						2512
VIF	RIRTWNSL	17	8	15	23						2513
VIF	RIRTWNSL	17	8	15	23						2514
VIF	LVKIHMYI	24	8	19	30						2515
VIF	IMYVSKKA	28	8	21	33						2516
VIF	KISSEVII	50	8	13	20						2517
VIF	KISSEVII	50	8	15	23						2518
VIF	RISSEVII	50	8	20	31						2519
VIF	PLGDARLV	58	8	15	23						2520
VIF	PLGEARLV	58	8	11	17						2521
VIF	VIKTYWGL	67	8	19	30						2522
VIF	VITYWGL	67	8	10	16						2523
VIF	VVRTYWGL	67	8	22	34						2524
VIF	VVTYWGL	67	8	10	16						2525
VIF	VTYWGLHT	69	8	11	17						2526
VIF	HLGHGVS	83	8	24	38						2527
VIF	HLGGQVSI	83	8	25	39						2528

0.0001

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HIV A02 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
POL	FLKLAGRPVP	852	11	25	39						2429
POL	KLGRWPVKTI	855	11	13	20						2430
POL	KLGRWPVKVI	855	11	22	34						2431
POL	TIHTDNGSNFT	864	11	13	20						2432
POL	VIHTDNGSNFT	864	11	23	36						2433
POL	HTDNGSNFTSA	866	11	33	52						2434
POL	HTDNGSNFTST	866	11	11	17						2435
POL	SAAVKAACWVA	875	11	28	44						2436
POL	STTVKAACWVA	875	11	14	22						2437
POL	AVKAACWWAGI	877	11	10	16						2438
POL	TVKAACWWAGI	877	11	20	31						2439
POL	GIPYNFQSGV	892	11	63	98						2440
POL	QVRDQAEHLKT	916	11	43	67						2441
POL	QVREQAEHLKT	916	11	13	20						2442
POL	QAEHLKTAVQM	920	11	57	89						2443
POL	FIHNFKRKGGI	933	11	58	91						2444
POL	GIGGYSAGERI	942	11	57	89						2445
POL	SAGERIIDIHA	947	11	40	63						2446
POL	SAGERIIVDIIA	947	11	14	22						2447
POL	IDIHIAIDIQT	952	11	12	19						2448
POL	IDIHIAIDIQT	952	11	27	42						2449
POL	IVDIIATDIQT	952	11	12	19						2450
POL	IASDIQTKEL	955	11	14	22						2451
POL	IATDIQTKEL	955	11	34	53						2452
POL	DIQTKELQKQI	959	11	44	69						2453
POL	IQTKELQKQII	960	11	10	16						2454
POL	IQTKELQKQIT	960	11	30	47						2455
POL	KQIKIQNFRV	967	11	12	19						2456
POL	KQIKIQNFRV	967	11	34	54						2457
POL	RVYYRDSRDP	976	11	34	53						2458
POL	RVYYRDSRDP	976	11	14	22						2459
POL	PAKLLWKGEA	990	11	59	92						2460
POL	KLLWKGEAVV	992	11	59	92						2461
POL	LLWKGEAVVI	993	11	59	92						2462
POL	GAVVIQDNDI	999	11	37	58						2463
POL	GAVVIQDNDSEI	999	11	12	19						2464
POL	VVIQDNDSEI	1002	11	37	58						2465
POL	VVIQDNDSEI	1002	11	12	19						2466
POL	VVIQDNDSEI	1003	11	37	58						2467
POL	VVIQDNDSEI	1003	11	12	19						2468
POL	VVIQDNDSEI	1003	11	50	78						2469
POL	KVPRRKAKII	1011	11	11	17						2470
POL	KVPRRKAKII	1011	11	11	17						2471
POL	KIIRDYQKQMA	1019	11	49	77						2472
POL	KIIRDYQKQMA	1019	11	11	17						2473
REV	LLKTVRLI	12	8	11	17						2474
REV	AVRIKIL	17	8	13	20						2475
REV	RQRQHSI	52	8	11	17						2476
REV	QLPIERL	78	8	14	22						2477
REV	QLPIERL	78	8	37	58						2478
REV	GTSGTQGV	94	8	21	33						2479

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
VIF	GVSIEWRL	87	8	18	28						2529
VIF	STQIDPDL	100	8	12	19						2530
VIF	STQVDPGL	100	8	11	17						2531
VIF	TQIDPDLA	101	8	12	19						2532
VIF	TQVDPDLA	101	8	11	17						2533
VIF	TQVDPGLA	101	8	16	25						2534
VIF	LADQLIHL	107	8	25	39						2535
VIF	LADQLIHM	107	8	17	27						2536
VIF	SAIRKAIL	123	8	35	55						2537
VIF	SAIRNAIL	123	8	12	19						2538
VIF	YQAGHINKV	140	8	38	59						2539
VIF	KVGSLOYL	146	8	52	81						2540
VIF	SLQYLALA	149	8	12	19						2541
VIF	SLQYLALT	149	8	31	48						2542
VIF	LOYLALAA	150	8	12	19						2543
VIF	LQYLALKA	150	8	11	17						2544
VIF	LQYLALTA	150	8	34	53						2545
VIF	YLALTALI	152	8	28	44						2546
VIF	ALIKPKKI	157	8	10	16						2547
VIF	PLPSVKKL	168	8	21	33						2548
VIF	PLPSVRKL	168	8	14	22						2549
VIF	WQVMIVWQV	5	9	43	67						2550
VIF	MIVWQVDRM	8	9	46	72						2551
VIF	QVDRMKIRT	12	9	12	19						2552
VIF	QVDRMRINT	12	9	10	16						2553
VIF	QVDRMRIRT	12	9	31	48						2554
VIF	KIRTWNSLV	17	9	12	19						2555
VIF	RIRTWKSIV	17	9	15	23						2556
VIF	RIRTWNSLV	17	9	15	23						2557
VIF	SLVKIHIMYI	23	9	19	30						2558
VIF	SLVKIHIMYV	23	9	21	33						2559
VIF	EVHIFLGDA	54	9	24	38						2560
VIF	EVHIFLGEA	54	9	25	39						2561
VIF	HPLCDARL	56	9	13	20						2562
VIF	HPLGEARL	56	9	20	31						2563
VIF	PLGEARLVI	58	9	10	16						2564
VIF	LVKITWGL	66	9	10	16						2565
VIF	LVITTYWGL	66	9	22	34						2566
VIF	ITTYWGLIIT	68	9	16	25						2567
VIF	HITGERDWHL	75	9	21	33						2568
VIF	QTGERDWHL	75	9	12	19						2569
VIF	STQIDPDLA	100	9	12	19						2570
VIF	STQVDPGLA	100	9	11	17						2571
VIF	DLADQLIHL	106	9	18	28						2572
VIF	GLADQLIHM	106	9	15	23						2573
VIF	KVGSLOQLA	146	9	52	81						2574
VIF	SLQYLALAA	149	9	12	19						2575
VIF	SLQYLALKA	149	9	11	17						2576
VIF	SLQYLALTA	149	9	31	48						2577
VIF	LQYLALAAAL	150	9	12	19						2578

0.0031

Table VIII
HIV A02 Super-Motif Peptides with Bridging Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
VIF	LQYLAKAL	150	9	11	17						2579
VIF	LQYLALAL	150	9	33	52						2580
VIF	KIKPLPSV	164	9	19	30						2581
VIF	KTKEPLPSV	164	9	12	19						2582
VIF	PLPSVKKLT	168	9	13	20						2583
VIF	VMVWQVDRM	7	10	44	69						2584
VIF	IVWQVDRMKI	9	10	12	19						2585
VIF	IVWQVDRMRI	9	10	47	73						2586
VIF	WQVDRMKIRT	11	10	12	19						2587
VIF	WQVDRMRINT	11	10	10	16						2588
VIF	WQVDRMRIRT	11	10	31	48						2589
VIF	RMKIRTWNSL	15	10	12	19						2590
VIF	RMKIRTWKS	15	10	15	23						2591
VIF	RMKIRTWNSL	15	10	15	23						2592
VIF	KISSEVHIPL	50	10	14	22						2593
VIF	KISSEVHIPL	50	10	19	30						2594
VIF	RISSEVHIPL	50	10	13	20						2595
VIF	HIPLGDARLV	56	10	10	16						2596
VIF	HIPLGEARLV	56	10	19	30						2597
VIF	RLVITTYWGL	65	10	12	19						2598
VIF	VITTYWGLHT	67	10	16	25						2599
VIF	LQTGERDWHL	74	10	12	19						2600
VIF	QIDPDLADQL	102	10	10	16						2601
VIF	QVDPGLADQL	102	10	14	22						2602
VIF	IVSPRCEYQA	133	10	11	17						2603
VIF	QAGHNKVGSL	141	10	38	59						2604
VIF	KVGSQVYAL	146	10	51	80						2605
VIF	SLQYLALAL	149	10	12	19						2606
VIF	SLQYLAKAL	149	10	11	17						2607
VIF	SLQYLALAL	149	10	31	48						2608
VIF	LQYLALAL	150	10	28	44						2609
VIF	KTGHRGSHT	188	10	16	25						2610
VIF	QVMVWQVDRM	6	11	43	67						2611
VIF	MVWQVDRMRI	8	11	43	67						2612
VIF	RMKIRTWNSLV	15	11	12	19						2613
VIF	RMKIRTWNSLV	15	11	15	23						2614
VIF	RMKIRTWNSLV	15	11	15	23						2615
VIF	RTWKSLSVKHHM	19	11	14	22						2616
VIF	RTWKSLSVKHHM	19	11	24	38						2617
VIF	EVHPLGDARL	54	11	13	20						2618
VIF	EVHPLGEARL	54	11	20	31						2619
VIF	HIPLGEARLV	56	11	10	16						2620
VIF	LVTITYWGLHT	66	11	16	25						2621
VIF	GLHTGERDWHL	73	11	21	33						2622
VIF	GLTGERDWHL	73	11	12	19						2623
VIF	TQIDPDLADQL	101	11	10	16						2624
VIF	TQVDPGLADQL	101	11	13	20						2625
VIF	QIDPDLADQL	102	11	10	16						2626
VIF	QVDPGLADQL	102	11	14	22						2627
VIF	YQAGHNKVGSL	140	11	38	59						2628

0.0008

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
VIF	KVGSLOYLALA	146	11	12	19						2629
VIF	KVGSLOYLALT	146	11	28	44						2630
VIF	SLQYLALTALI	149	11	27	42						2631
VIF	LKPKKIKPPL	158	11	10	16						2632
VIF	KTKGHRGSHIM	188	11	15	23						2633
VPR	ALELEEL	19	8	10	16						2634
VPR	LELELEEL	19	8	44	69						2635
VPR	AVRHFPRI	30	8	14	22						2636
VPR	ETYGDTWA	48	8	16	25						2637
VPR	ETYGDTWT	48	8	11	17						2638
VPR	DTWAGVEA	52	8	16	25						2639
VPR	DTWEGVEA	52	8	23	36						2640
VPR	WAGVEAII	54	8	16	25						2641
VPR	GVEAIRI	56	8	34	53						2642
VPR	IIRILQQL	60	8	42	66						2643
VPR	ILOQLLFI	63	8	37	58						2644
VPR	LLFHFRI	67	8	44	69						2645
VPR	LLFVHFRI	67	8	12	19						2646
VPR	CQHSRIGI	77	8	45	70						2647
VPR	WALELEEL	18	9	09	15	0.0035					2648
VPR	WTLELEEL	18	9	42	69						2649
VPR	LLEELKNEA	22	9	17	27						2650
VPR	LLEELKSEA	22	9	16	25						2651
VPR	EAVRHFPRI	29	9	14	22	0.0001					2652
VPR	WLHGLQHI	38	9	20	31						2653
VPR	HIYETYGDT	45	9	17	27						2654
VPR	HIYNTYGDT	45	9	14	22						2655
VPR	YIYETYGDT	45	9	14	22						2656
VPR	DTWAGVEAI	52	9	16	25						2657
VPR	DTWEGVEAI	52	9	20	31						2658
VPR	GVEAIRIL	56	9	34	53						2659
VPR	AIRILQQL	59	9	39	61	0.0150	0.1900	0.2400	0.0960	0.0730	2660
VPR	IIRILQQL	60	9	42	66	0.0004					2661
VPR	RILQQLFI	62	9	36	56	0.2600	0.0028	0.0800	0.1000	0.0220	2662
VPR	QLLFHFRI	66	9	44	69	0.0530	0.0002	0.0004	0.0023	0.0840	2663
VPR	QLLFVHFRI	66	9	10	16						2664
VPR	RIGCQHSRI	74	9	47	73						2665
VPR	RIGCFIISRI	74	9	12	19						2666
VPR	CQHSRIGI	77	9	16	25						2667
VPR	CQHSRIGIT	77	9	14	22						2668
VPR	RQRARNGA	90	9	13	20						2669
VPR	PQREPYNEWI	10	10	29	45						2670
VPR	ELLEEKNEA	21	10	16	25						2671
VPR	ELLEEKSEA	21	10	16	25						2672
VPR	LLEELKNEAV	22	10	17	27						2673
VPR	LLEELKSEAV	22	10	16	25						2674
VPR	AVRHFPRIWL	30	10	14	22	0.0002					2675
VPR	AVRHFPRIWL	30	10	34	53						2676
VPR	ETYGDTWAGV	48	10	16	25	0.0009					2677
VPR	ETYGDTWTGV	48	10	11	17						2678

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0201	Δ^*0202	Δ^*0203	Δ^*0206	Δ^*6802	SEQ ID NO
VPR	NTYGDITWEGV	48	10	16	25						2679
VPR	DTWAGVEAH	52	10	16	25						2680
VPR	DTWEGVEAH	52	10	19	30						2681
VPR	WAGVEAIIRI	54	10	15	23						2682
VPR	EAIIRILOQL	58	10	33	52						2683
VPR	AIIRILOQLL	59	10	39	61						2684
VPR	QQLLFHFR	65	10	44	69	0.0014					2685
VPR	QQLLFHFR	65	10	10	16						2686
VPR	PQREPNWTL	10	11	29	45						2687
VPR	ELLEELKNEAV	21	11	16	25						2688
VPR	ELLEELKSEAV	21	11	16	25						2689
VPR	EAVRHFRPWL	29	11	14	22						2690
VPR	EAVRHFRPWL	29	11	34	53						2691
VPR	GQHIYETYGDT	43	11	17	27						2692
VPR	GQHIYNTYGDT	43	11	13	20						2693
VPR	GQIYETYGDT	43	11	13	20						2694
VPR	WAGVEAIRIL	54	11	15	23						2695
VPR	EAIIRILOQL	58	11	33	52						2696
VPR	HIRLQQLLF	60	11	33	52						2697
VPR	LQQLLFHFR	64	11	44	69						2698
VPR	LQQLLFHFR	64	11	10	16						2699
VPR	RIGCOHSRIGI	74	11	45	70						2700
VPR	RIGCRHSRIGI	74	11	11	17						2701
VPR	#LPGRGRNGA	85	11	01	50						2702
VPU	LAKVDYRI	5	8	01	25						2703
VPU	LAKVDYRL	5	8	01	25						2704
VPU	KVDYRIVI	7	8	01	33						2705
VPU	KVDYRLGV	7	8	01	33						2706
VPU	RIDYRLGV	7	8	01	33						2707
VPU	LAIALV	12	8	12	19						2708
VPU	LAIALVV	13	8	12	20						2709
VPU	AIVALVA	14	8	12	19						2710
VPU	IAIVVWT	27	8	23	36						2711
VPU	IAIVVWTI	28	8	23	36						2712
VPU	AIVVWTIV	29	8	29	45						2713
VPU	VVVTVFI	31	8	15	23						2714
VPU	KILRQKI	45	8	15	23						2715
VPU	RQRKIDRL	48	8	20	31						2716
VPU	QDELSAL	79	8	13	22						2717
VPU	GVEMGHHA	91	8	01	50						2718
VPU	LAKVDYRIV	5	9	01	25						2719
VPU	KVDYRIVIV	7	9	01	33						2720
VPU	LAIALVVA	12	9	11	17						2721
VPU	IAIVVWTI	13	9	09	15						2722
VPU	IAIVVWTIV	27	9	23	36						2723
VPU	IVVTVTFI	28	9	31	31						2724
VPU	IVFIEYRKI	30	9	15	23						2725
VPU	RQRKIDRLI	36	9	12	19						2726
VPU	KIDRLIDRI	48	9	17	27						2727
VPU		52	9	14	22						2728

Table VIII
HIV A02 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0201	A*0202	A*0203	A*0206	A*6802	SEQ ID NO
VPU	LIDRIRERA	58	9	12	19						2729
VPU	DQEELSALV	79	9	11	18						2730
VPU	VTLLSSKL	94	9	01	50						2731
VPU	LAKVDYRIVI	5	10	01	25						2732
VPU	LAKVDYRLGV	5	10	01	25						2733
VPU	KVDYRIVIVA	7	10	01	33						2734
VPU	KVDYRLGVGA	7	10	01	33						2735
VPU	RIDYRLGVGA	7	10	01	33						2736
VPU	IIAIVVWTVI	27	10	20	31						2737
VPU	AIVVWTVIFI	29	10	14	22						2738
VPU	ILRQKKIDRL	46	10	15	23						2739
VPU	LVTLSSSKL	91	10	01	50						2740
VPU	LAKVDYRIVIV	5	11	01	25						2741
VPU	KVDYRLGVGAL	7	11	01	33						2742
VPU	RIDYRLGVGAL	7	11	01	33						2743
VPU	KILRQKKIDRL	45	11	15	23						2744
VPU	ILRQKKIDRLI	46	11	13	20						2745

Table IX
HIV A03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Λ^*0301	Λ^*1101	Λ^*3101	Λ^*3301	Λ^*6801	SEQ ID NO
ENV	SLWDQSLK	123	8	47	75						2746
ENV	QSLKPCVK	127	8	48	75						2747
ENV	AITQACPK	244	8	14	22						2748
ENV	TITQACPK	244	8	11	17						2749
ENV	VITQACPK	244	8	17	27						2750
ENV	PAGFAILK	266	8	38	59						2751
ENV	PAGYAILK	266	8	15	23						2752
ENV	AILKCNDK	270	8	20	31						2753
ENV	ILKCNDKK	271	8	12	19						2754
ENV	SVEINCTR	340	8	13	20						2755
ENV	GTAGNSSR	375	8	01	33						2756
ENV	TTHSFNCR	432	8	12	19						2757
ENV	ITLPCRIK	483	8	26	41						2758
ENV	NMWQEVGK	494	8	15	23						2759
ENV	ITGLLLTR	520	8	37	58						2760
ENV	RSLEYKYK	558	8	54	84						2761
ENV	PLGVAPTK	571	8	26	41						2762
ENV	PLGVAPTR	571	8	10	16						2763
ENV	GVAPTKAK	573	8	19	30						2764
ENV	VAPTKAKR	574	8	19	30						2765
ENV	VISTRTHR	584	8	01	50						2766
ENV	STRTHIREK	586	8	01	50						2767
ENV	RVVEREKR	587	8	32	50	0.0003					2768
ENV	RVVQREKR	587	8	17	27		0.0001				2769
ENV	ITLTVQAR	621	8	32	50						2770
ENV	EAQQHLLK	646	8	12	19						2771
ENV	KLTWVGIK	653	8	13	20						2772
ENV	QLTVWVGK	653	8	44	69						2773
ENV	GIKOLQAR	658	8	49	77						2774
ENV	LAVERYLK	667	8	26	41						2775
ENV	LAVERYLR	667	8	11	17						2776
ENV	GIWGCSGK	680	8	52	81						2777
ENV	MTWMEWER	721	8	12	19						2778
ENV	ESONQQEK	743	8	27	42						2779
ENV	AVLSIVNR	795	8	31	48						2780
ENV	LSIVNRVR	797	8	38	59						2781
ENV	ALAWDDLK	851	8	25	39						2782
ENV	RIVELLGR	878	8	22	34						2783
ENV	IVELLGRR	879	8	22	34						2784
ENV	RLGWEGLK	894	8	10	32						2785
ENV	AVAFEGTDR	928	8	31	48						2786
ENV	RAILHIPIR	945	8	13	20						2787
ENV	AILHIPRR	946	8	13	20						2788
ENV	RIRQGLER	953	8	44	69						2789
ENV	TLFCASDAK	64	9	52	81	0.0930	0.5300	0.0017	0.0013	0.0420	2790
ENV	VTENFMWIK	102	9	31	48						2791
ENV	ISLWDQSLK	122	9	47	73	0.0048	0.0890	0.0017	0.0013	0.0021	2792
ENV	SAITQACPK	243	9	14	22						2793
ENV	STITQACPK	243	9	10	16						2794
ENV	SVITQACPK	243	9	17	27						2795

Table IX
HIV A03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	A*1101	A*3101	A*3301	A*6801	SEQ ID NO
ENV	FAILKCN DK	269	9	14	22	0.0002	0.0002	0.0004	0.0015	0.0027	2796
ENV	AILKCN DKK	270	9	12	19						2797
ENV	TVQCTHG IK	290	9	28	44	0.0021	0.0460	0.0042	0.0017	0.0190	2798
ENV	TVQCTHG IR	290	9	23	36	0.0008	0.0008	0.0880	0.0330	0.0120	2799
ENV	LAEEVVIR	312	9	12	19	0.0002	0.0002	0.0004	0.0007	0.0002	2800
ENV	CTRPNNTR	345	9	28	44						2801
ENV	ITHSFNCR	431	9	11	17						2802
ENV	NANITPCR	478	9	01	50						2803
ENV	NITLPCRIK	482	9	11	17						2804
ENV	TITLPCRIK	482	9	14	22						2805
ENV	NITGLLLTR	519	9	35	55		0.0001				2806
ENV	STNGTETFR	537	9	01	17						2807
ENV	ELYKYKVVK	560	9	32	51						2808
ENV	GVAPTAKRR	573	9	19	30						2809
ENV	VAPTKAKRR	574	9	17	27	0.0002	0.0002	0.0004	0.0006	0.0002	2810
ENV	KAKRRVVQR	579	9	13	20	0.0002	0.0002	0.0800	0.0095	0.0002	2811
ENV	IINHTPHR	584	9	01	50						2812
ENV	ISTRTHREK	585	9	01	50						2813
ENV	NIHTPHREK	586	9	01	50						2814
ENV	STRTHREKR	586	9	01	50						2815
ENV	SITLTVOAR	620	9	32	50						2816
ENV	QARVLAVER	663	9	33	52	0.0009	0.0003	0.0320	0.0320	0.0007	2817
ENV	VLAVERYLK	666	9	18	28						2818
ENV	VLAVERYLR	666	9	11	17						2819
ENV	NMTWMIEWER	720	9	12	19						2820
ENV	ISNWLWYIK	770	9	11	17						2821
ENV	ITNWLWYIK	770	9	16	25						2822
ENV	IVGGJGLR	783	9	15	23						2823
ENV	FAVLSIVNR	794	9	31	42						2824
ENV	VLSIVNRVR	796	9	38	48						2825
ENV	GIEEGGER	829	9	12	19						2826
ENV	LALAWDDL	850	9	25	39						2827
ENV	NLCFSYHR	859	9	11	17						2828
ENV	SLCLFSYIIR	859	9	31	48						2829
ENV	CLFSYHRLR	861	9	42	66						2830
ENV	RIVELLGRR	878	9	22	34	0.0550	0.0100	0.1300	0.0021	0.0180	2831
ENV	IAVAEGTDR	927	9	31	48	0.0004	0.0003	0.0003	0.0004	0.0030	2832
ENV	RAILJIIPRR	945	9	13	20						2833
ENV	ILHIPRRIR	947	9	13	20						2834
ENV	TVYYGVVVK	48	10	41	64	3.8000	7.8000				2835
ENV	TTLFCASDAK	61	10	50	78	0.0920	0.2200	0.0019	0.0020	0.0570	2836
ENV	NVTENFNMAWK	101	10	31	48						2837
ENV	IISLWDQSLK	121	10	38	59	0.0410	0.0540	0.0017	0.0020	0.0029	2838
ENV	TSATOACPK	242	10	14	22						2839
ENV	TSVITOACPK	242	10	14	22						2840
ENV	CAPACFAILK	264	10	29	45						2841
ENV	FAILKCN DKK	269	10	10	16						2842
ENV	STVQCTHG IK	289	10	28	44						2843
ENV	STVQCTHG IR	289	10	23	36						2844
ENV	STVQCTHG IR	289	10	23	36						2845

Table IX
HIV A03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	A*1101	A*3101	A*3301	A*6801	SEQ ID NO
ENV	SLAEVVIR	311	10	12	19						2846
ENV	CTRPNNTRK	345	10	22	34						2847
ENV	ATGDIIGDIR	369	10	12	19						2848
ENV	EITTIISFNCR	430	10	11	17						2849
ENV	IINMWQEVGK	492	10	12	19						2850
ENV	GSENGTETFR	538	10	02	18						2851
ENV	PLGVAPTAK	571	10	19	30						2852
ENV	GVAPTAKARR	573	10	17	27						2853
ENV	VISTRTHREK	584	10	01	50						2854
ENV	ISTRTHREKR	585	10	01	50						2855
ENV	NIITPIREKR	586	10	01	50						2856
ENV	ASITLTQVAR	619	10	28	44						2857
ENV	IVQQNNLLR	634	10	25	39	0.0024	0.0190	0.0130	0.0072	0.0035	2858
ENV	IVQQSNLLR	634	10	26	41						2859
ENV	AIEAQIHLK	644	10	12	19						2860
ENV	LLKLTWVGK	651	10	13	20						2861
ENV	LLQLTVWGIK	651	10	34	53	0.0055	0.0110				2862
ENV	MLQLTVWGIK	651	10	10	16						2863
ENV	RVLAVERYLK	665	10	18	28						2864
ENV	RVLAVERYLR	665	10	10	16						2865
ENV	LLGIWGCCK	678	10	50	78	0.1200	0.0120	0.0017	0.0020	0.0001	2866
ENV	MIVGLIGLR	782	10	36	56						2867
ENV	AVLSIVNRVR	795	10	31	48						2868
ENV	FLALAWDDLRL	849	10	25	39						2869
ENV	RSCLFSYIIR	858	10	31	48						2870
ENV	GLRLGWGLK	892	10	10	32						2871
ENV	LLQYWSELK	906	10	12	19						2872
ENV	AIATAEGTDR	926	10	31	48						2873
ENV	ALIHPRRIR	946	10	12	19						2874
ENV	PTIRQGLER	951	10	12	19						2875
ENV	VTYYGVVVK	47	11	41	64	0.8600	4.1000				2876
ENV	KTTLFCASDAK	60	11	12	19						2877
ENV	TTTLFCASDAK	60	11	22	34						2878
ENV	DIISLWDQSLK	120	11	38	59						2879
ENV	NTSAITQACPK	241	11	14	22						2880
ENV	NTSVITQACPK	241	11	13	20						2881
ENV	VSTVQCTHGK	288	11	28	44						2882
ENV	VSTVQCTHGIR	288	11	23	36						2883
ENV	GSLAEVVR	310	11	12	19						2884
ENV	YATGDIIGDIR	368	11	11	17						2885
ENV	KLREIRQFENK	405	11	01	25						2886
ENV	HTEGNTLQCR	478	11	01	50						2887
ENV	NANITPCRIK	478	11	01	50						2888
ENV	QIINMWQEVGK	491	11	12	19						2889
ENV	SSNITGLLLR	516	11	19	30						2890
ENV	NTETNKTETFR	537	11	01	17						2891
ENV	NTTGNITETFR	537	11	01	17						2892
ENV	EIFRPGGDMR	544	11	15	23						2893
ENV	ETFRPGGDMR	544	11	20	31						2894
ENV	RSELYKYKVK	558	11	29	45						2895

Table IX
HIV A03 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	A*1101	A*3101	A*3301	A*6801	SEQ ID NO
ENV	KIEPLGVAPTK	568	11	15	24						2896
ENV	PLGVAITKAKR	571	11	19	30						2897
ENV	PTKAKRRVVQR	576	11	13	20						2898
ENV	KAKRRVQREK	579	11	13	20						2899
ENV	IINHTHREK	584	11	01	50						2900
ENV	VISTRTHREKR	584	11	01	50						2901
ENV	AASITLTQAR	618	11	28	44						2902
ENV	GIVQQQNLLR	633	11	25	39						2903
ENV	GIVQQSNLLR	633	11	26	41						2904
ENV	HLLKLTWVGK	650	11	13	20						2905
ENV	HLLQLTVWGIK	650	11	34	53						2906
ENV	TVWGIKQLQAR	655	11	48	75						2907
ENV	QLQARVLAVR	661	11	33	52						2908
ENV	QLLGWGCSSGK	677	11	50	78						2909
ENV	NVPWNSSWSNK	693	11	10	16						2910
ENV	LJESQNOQEK	740	11	20	31						2911
ENV	IMVGGGLGLR	781	11	34	54						2912
ENV	IIFAVLSIVNR	792	11	14	22						2913
ENV	IVFAVLSIVNR	792	11	17	27						2914
ENV	FAVLSIVNRVR	794	11	31	48						2915
ENV	GIEEGGERDR	829	11	12	19						2916
ENV	NLCFSYHRLR	859	11	11	17						2917
ENV	SLCLFSYHRLR	859	11	31	48						2918
ENV	LLGRRGWEALK	882	11	09	15						2919
ENV	NLLQYWSQELK	905	11	12	19						2920
ENV	IAIAVAEGTDR	925	11	10	16						2921
ENV	TAIAVAEGTDR	925	11	21	33						2922
ENV	RAILHIPRRIR	945	11	12	19						2923
GAG	GARASILR	2	8	10	16						2924
GAG	ASVLSGGK	5	8	29	45						2925
GAG	RLRPGGKK	20	8	49	77						2926
GAG	WASRELER	37	8	48	75						2927
GAG	QTGSEELR	71	8	12	19						2928
GAG	TLYCVHQK	86	8	12	19						2929
GAG	TLYCVHQK	86	8	15	23						2930
GAG	RIEVKDTK	93	8	13	20						2931
GAG	DTKEALDK	98	8	36	56		0.0001				2932
GAG	DTKEALEK	98	8	12	19						2933
GAG	KIEEQNK	105	8	23	36	0.0003					2934
GAG	PAAADKEK	123	8	01	50						2935
GAG	RTLNAWVK	171	8	63	98	0.0410	0.0560				2936
GAG	WVKVIEEK	176	8	29	45						2937
GAG	WVKVVEEK	176	8	31	48	0.0003	0.0001				2938
GAG	QAAMQMLK	216	8	61	95						2939
GAG	PIAPGQMR	243	8	19	30						2940
GAG	PIPPGQMR	243	8	17	27						2941
GAG	PVAPGQMR	243	8	10	16						2942
GAG	PVGDIYKR	281	8	18	28						2943
GAG	PVGEIYKR	281	8	40	63	0.0003	0.0001				2944
GAG	WILGLNKK	289	8	57	89						2945

Table IX
HIV A03 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	A*1101	A*3101	A*3301	A*6801	SEQ ID NO
GAG	PTSILDIR	303	8	12	19						2946
GAG	PVSILDIR	303	8	16	25						2947
GAG	PVSILDIR	303	8	25	39						2948
GAG	GVGPGHK	376	8	37	58		0.0018				2949
GAG	GVGPGSHK	376	8	23	36	0.0012					2950
GAG	ASAOQDLK	392	8	01	50						2951
GAG	ATAQOQDLK	392	8	01	50						2952
GAG	AAAIMMQK	400	8	04	19						2953
GAG	AAAIMMQK	405	8	01	25						2954
GAG	SATIMMQR	405	8	01	25						2955
GAG	YTAVFMQR	405	8	02	50						2956
GAG	MMQKSNFK	409	8	10	16						2957
GAG	MMQKSNFK	409	8	23	36						2958
GAG	MMQKSNFK	409	8	23	36						2959
GAG	QMKIDCTER	455	8	49	77						2960
GAG	RASVLSGK	4	9	29	45						2961
GAG	KLDAWEKIR	12	9	16	25						2962
GAG	KLDKWEKIR	12	9	10	16						2963
GAG	DAWEKIRLR	14	9	17	27						2964
GAG	KIRLRPGGK	18	9	44	69						2965
GAG	RLRPGGKKK	20	9	34	53						2966
GAG	LLETSEGR	52	9	17	27						2967
GAG	ATLYCVHQK	85	9	12	19						2968
GAG	ATLYCVHQK	85	9	15	23						2969
GAG	MVHQASPR	163	9	27	42	0.0150	0.7100	1.0000	2.1000	0.8400	2970
GAG	PIPVGEYK	279	9	35	55	0.1800	0.0670	0.0006	0.0005	0.0003	2971
GAG	ILGLNKIVR	291	9	58	91	0.0002	0.0012	0.0032	0.0100	0.0004	2972
GAG	ILGLNKIVR	291	9	19	30	0.0008	0.0001				2973
GAG	ILDIRQGP	306	9	42	66	0.0420	0.0048	0.0006	0.0006	0.0002	2974
GAG	ILDIRQGP	306	9	33	33						2975
GAG	NSATIMMQR	404	9	01	16						2976
GAG	IMMQKSNFK	408	9	10	16						2977
GAG	IMMQKSNFK	408	9	20	31						2978
GAG	IMMQKSNFK	408	9	13	20						2979
GAG	IVKCFNCCK	422	9	11	17						2980
GAG	TVKCFNCCK	422	9	11	17						2981
GAG	IANKRAGR	434	9	18	29	0.0009	0.0003	0.0330	0.0500	0.0039	2982
GAG	IANKRAGR	434	9	13	21						2983
GAG	LARNCRAPR	434	9	20	32						2984
GAG	KIWPSSKGR	472	9	22	35	0.0770	0.0005	0.4400	0.0087	0.0001	2985
GAG	KIWPSSKGR	472	9	13	21						2986
GAG	KIWPSSKGR	472	9	10	16						2987
GAG	TAPPIESFR	496	9	15	23						2988
GAG	TAPPIESFR	508	9	02	67						2989
GAG	TAPPIESFR	508	9	01	33						2990
GAG	KIRLRPGGK	18	10	44	69	1.9000	0.0010	0.0008	0.0005	0.0001	2991
GAG	KLKHIVWASR	31	10	13	20						2992
GAG	RLKHLVWASR	31	10	17	27						2993
GAG	IVWASRELER	35	10	20	31	0.0099	0.0066				2994
GAG	LVWASRELER	35	10	26	41						2995
GAG	GLLETSEGR	51	10	16	25						2996

Table IX
HIV A03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	A*1101	A*3101	A*3301	A*6801	SEQ ID NO
GAG	VATLYCVHIQK	84	10	12	19						2996
GAG	VATLYCVHIQR	84	10	15	23						2997
GAG	KIEEQNKSK	105	10	15	23						2998
GAG	QMVLIQASPR	162	10	27	42	0.0260	0.0010	0.0740	0.1000	0.0430	2999
GAG	NAWKVVEEK	174	10	29	45	0.0004	0.0002				3000
GAG	NAWKVVEEK	174	10	30	47						3001
GAG	IAPGQMRPR	244	10	19	30						3002
GAG	PIPVGEYKR	279	10	34	53	0.0003	0.0001	0.0009	0.0010	0.0005	3003
GAG	IILGLNKIVR	290	10	57	89	0.0003	0.0006	0.0110	0.0260	0.0073	3004
GAG	YSPTSILDIR	301	10	12	19						3005
GAG	YSPVSILDIK	301	10	16	25						3006
GAG	YSPVSILDIR	301	10	24	38						3007
GAG	SILDIKQGP	305	10	18	28						3008
GAG	SILDIRQGP	305	10	40	63	0.3100	0.7100	0.0017	0.0020	0.0060	3009
GAG	YVDRFEKTLR	320	10	27	42						3010
GAG	YVDRFYKTLR	320	10	28	44	0.0003	0.0006				3011
GAG	RAEQASQEVK	329	10	12	19						3012
GAG	RAEQATQDVK	329	10	15	23						3013
GAG	RAEQATQEVK	329	10	27	42						3014
GAG	LVQANAPDCK	346	10	59	92	0.0002	0.0110				3015
GAG	GVGGPGIHKAR	376	10	37	58	0.0003	0.0001				3016
GAG	GVGGPSHKAR	376	10	22	34						3017
GAG	TIMMQRGNFR	407	10	12	21						3018
GAG	KTVKCFNCGK	421	10	08	16						3019
GAG	IIAKNCRAPR	433	10	18	28						3020
GAG	IIARNCRAPR	433	10	13	20						3021
GAG	IIARNCRAPR	433	10	20	31						3022
GAG	IAKNCRAPRK	434	10	16	25						3023
GAG	IARNCRAPRK	434	10	13	21						3024
GAG	LARNCRAPRK	434	10	20	32						3025
GAG	RAPRKKGCWK	439	10	51	80						3026
GAG	FLGKIWPSHK	469	10	23	36	0.0200	0.0013				3027
GAG	FLGKIWPSNK	469	10	13	20						3028
GAG	FLGKIWPSK	469	10	10	16						3029
GAG	GTRPGNYVQK	480	10	01	50						3030
GAG	GTRPGNYVQR	480	10	01	50						3031
GAG	PTAPPEESFR	495	10	15	23						3032
GAG	PTAPPAESFR	507	10	02	67						3033
GAG	PTAPPEESFR	507	10	01	33						3034
GAG	ITSLPKQEQK	526	10	01	50						3035
GAG	PSOKQEPIDK	528	10	11	18						3036
GAG	GARASVLSGK	2	11	29	46						3037
GAG	LSGGKLDWEK	8	11	15	23						3038
GAG	KLDWEKIRLR	12	11	16	25						3039
GAG	KLDKWEKIRLR	12	11	10	16						3040
GAG	KIRLRPGGKKK	18	11	30	47						3041
GAG	RLRPGGKKKYK	20	11	12	19						3042
GAG	RLRPGGKKKYR	20	11	19	30						3043
GAG	HIVWASRELER	34	11	20	31						3044
GAG	HLVWASRELER	34	11	26	41						3045

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	A*1101	A*3101	A*3301	A*6801	SEQ ID NO
GAG	TVATLYCVHQK	83	11	12	19						3046
GAG	TVATLYCVHQK	83	11	14	22						3047
GAG	EVKDTKEALDK	95	11	13	20						3048
GAG	ALDKIEEQNK	102	11	17	27						3049
GAG	KIEEQNKSKK	105	11	15	23						3050
GAG	PAAADKEKDSK	123	11	01	50						3051
GAG	ISPRTLNAWVK	168	11	36	56						3052
GAG	LSPRTLNAWVK	168	11	17	27						3053
GAG	TINEEAAEWDR	225	11	53	83						3054
GAG	HAGPIAPGQMR	240	11	18	28						3055
GAG	HAGPIPPGQMR	240	11	17	27						3056
GAG	PIAPGQMREPR	243	11	19	30						3057
GAG	PIPPGQMREPR	243	11	17	27						3058
GAG	WIILGLNKIVR	289	11	57	89						3059
GAG	TSILDIRQGPK	304	11	12	19						3060
GAG	VSILDIKQGPK	304	11	16	25						3061
GAG	VSILDIRQGPK	304	11	25	39						3062
GAG	DIKQGPKEPFR	308	11	19	30						3063
GAG	DIKQGPKEPFR	308	11	41	64						3064
GAG	LLVQNPDPCK	345	11	58	91						3065
GAG	NANPDPCKTILK	349	11	27	42						3066
GAG	NANPDPCKTILR	349	11	18	28						3067
GAG	AAIMMQKSNFK	406	11	06	15						3068
GAG	ATIMMQRGNFR	406	11	11	28						3069
GAG	MMQKGNFRNQR	409	11	15	23						3070
GAG	HIAKNCRAPRK	433	11	16	25						3071
GAG	HIARNCRAPRK	433	11	13	20						3072
GAG	HLARNCRAPRK	433	11	20	31						3073
GAG	IAKNCRAPRK	434	11	14	22						3074
GAG	IARNCRAPRK	434	11	13	21						3075
GAG	LARNCRAPRK	434	11	19	30						3076
GAG	CTERQANFLGK	459	11	52	83						3077
GAG	EITSLPKQEQK	525	11	01	50						3078
NEF	AVSQDLDK	48	8	10	16						3079
NEF	AVSRDLEK	48	8	11	17						3080
NEF	PLRPMITK	102	8	10	16						3081
NEF	PLRPMTYK	102	8	49	77						3082
NEF	LSFELKEK	114	8	22	34	0.0010	0.0003				3083
NEF	LSHFLKEK	114	8	27	42						3084
NEF	GLIYSKKR	173	8	23	36						3085
NEF	YTPGPGIR	207	8	20	31						3086
NEF	YTPGI'GTR	207	8	21	33						3087
NEF	YTPGI'GVR	207	8	12	19						3088
NEF	LTFGWCFK	221	8	39	61						3089
NEF	KLVPV'DPR	228	8	11	17						3090
NEF	ELHP'EFYK	324	8	14	22						3091
NEF	ELHP'EYYK	324	8	22	34						3092
NEF	GAVSQDLDK	47	9	10	16						3093
NEF	GAVSRDLEK	47	9	11	17	0.0002	0.0009	0.0004	0.0006	0.0001	3094
NEF	PVRPQVPLR	95	9	48	75						3095

Table IX
HIV A03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	A*1101	A*3101	A*3301	A*6801	SEQ ID NO
NEF	AVDSLHFLK	111	9	14	22	0.0740	1.1000	0.0009	0.0008	0.0025	3096
NEF	DLSEFLKEK	113	9	22	34						3097
NEF	DLSEFLKEK	113	9	27	42						3098
NEF	GLDGLYSK	125	9	16	25						3099
NEF	GLEGLYSK	125	9	10	16						3100
NEF	PLTFGWCFK	219	9	39	61						3101
NEF	AADGVGAVSR	42	10	09	15						3102
NEF	QVPLRPMTFK	100	10	10	16						3103
NEF	QVPLRPMTYK	100	10	46	72						3104
NEF	GAFDLSFFLK	110	10	10	16						3105
NEF	GLDGLYSK	125	10	14	22						3106
NEF	GVGAVSQDLDK	45	11	10	16	0.6100	0.6300	0.0098	0.0130	0.0600	3107
NEF	GVGAVSRDLEK	45	11	11	17						3108
NEF	AVDSLHFLKEK	111	11	13	20						3109
NEF	GLDGLYSK	125	11	14	22						3110
NEF	GLDGLYSK	125	11	10	16						3111
NEF	MARELIPEYK	321	11	16	25						3112
POL	RANSPTTR	26	8	16	25						3113
POL	RANSPTSR	26	8	17	27						3114
POL	STNSPTSR	32	8	01	33						3115
POL	RANSPTSR	35	8	01	33						3116
POL	RANSPTTR	37	8	01	50						3117
POL	ILIEICGK	149	8	14	22						3118
POL	LIEICGHIK	150	8	10	16						3119
POL	LIEICGKK	150	8	14	22						3120
POL	PIETVPVK	190	8	53	83						3121
POL	ETVPVKLK	192	8	53	83	0.0049	0.0001				3122
POL	GMDGPKVK	201	8	51	80	0.0007	0.0004				3123
POL	PLTEEKIK	212	8	55	86						3124
POL	EICTEMEK	223	8	27	42						3125
POL	NTPIFAIK	246	8	24	38						3126
POL	NTPVFAIK	246	8	37	58	0.0003	0.0003				3127
POL	PIFAIKKK	248	8	25	39						3128
POL	PVFAIKKK	248	8	37	58	0.0003	0.0001				3129
POL	PAGLKKKK	286	8	52	81						3130
POL	PLDKDFRK	308	8	19	30						3131
POL	NVLPQGWK	336	8	63	100	0.0003	0.0012				3132
POL	KILEPERK	355	8	23	36						3133
POL	DLEIGQHR	381	8	52	81						3134
POL	EIGQIRAK	383	8	27	42						3135
POL	EIGQIRTK	383	8	22	34						3136
POL	RAKIEELR	388	8	26	41						3137
POL	RTKIEELR	388	8	22	34						3138
POL	ELREHLLK	393	8	17	27						3139
POL	ELRQHLLR	393	8	15	23						3140
POL	WTVNDIQK	441	8	62	97	0.0003	0.0001				3141
POL	DIQKLVGK	445	8	62	97						3142
POL	ELELAENR	489	8	53	83						3143
POL	GVYYDFSK	508	8	43	67						3144
POL	DLIAEQIK	516	8	28	44						3145
POL	QIQEPFK	532	8	41	64	0.0010	0.0013				

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TABLE III

POSITION

MOTIFS	1° anchor 1	2	3	4	5	1° anchor 6	7	8	9
DR4 preferred	FMYLIVW	M	T		I	VSTCPALIM	MH		MH
deleterious				W			R		WDE
DR1 preferred	MFLIVWY			PAMQ		VMATSPLIC	M		AVM
deleterious		C	CH	FD	CWD		GDE	D	
DR7 preferred	MFLIVWY	M	W	A		IVMSACTPL	M		IV
deleterious		C		G			GRD	N	G
DR Supermotif	MFLIVWY					VMSTACPLI			

(SEQ ID NO:14527)
(SEQ ID NO:14528)

DR3 MOTIFS	1° anchor 1	2	3	1° anchor 4	5	1° anchor 6
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motif a
preferred

LIVMFY

D

motif b
preferred

LIVMFAY

DNQEST

KRH

Italicized residues indicate less preferred or "tolerated" residues.

Table IX
HIV A03 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	A*1101	A*3101	A*3301	A*6801	SEQ ID NO
POL	GAHTNDVK	551	8	19	30						3146
POL	SAHTNDVK	551	8	16	25						3147
POL	TAHTNDVK	551	8	11	17						3148
POL	QLTEAVQK	559	8	37	58						3149
POL	QLTEVVQK	559	8	11	17						3150
POL	ESIVIWGK	570	8	50	79						3151
POL	VIWGTKPK	573	8	48	75						3152
POL	KLWYQLEK	616	8	46	72						3153
POL	YVDGAANR	633	8	50	78	0.0003	0.0001				3154
POL	GAANRETK	636	8	45	70						3155
POL	KAGYVTDI	646	8	42	66						3156
POL	VTDGRQK	650	8	40	63	0.0090	0.0065				3157
POL	LTDITNOK	661	8	19	30						3158
POL	LTETTNOK	661	8	30	47						3159
POL	IIQAQPDK	697	8	40	63						3160
POL	IIQAQPDK	697	8	16	25						3161
POL	IIQAQPDK	697	8	37	58						3162
POL	QIEQLIK	712	8	37	58						3163
POL	IIQLIKK	713	8	22	34						3164
POL	LAWVPAHK	725	8	37	58						3165
POL	LSWVPAHK	725	8	16	25						3166
POL	KLVSAGIR	742	8	29	45						3167
POL	KLVSAGIR	742	8	16	25	0.0091	0.0054				3168
POL	LVSSGIRK	743	8	27	42						3169
POL	LVSSGIRK	743	8	27	43						3170
POL	KAQEEIEK	759	8	16	25						3171
POL	KAQEEIEK	759	8	26	41						3172
POL	NLPPVAK	779	8	27	42						3173
POL	NLPPVAK	779	8	45	70						3174
POL	EIVASCDK	787	8	31	48						3175
POL	ETAYFLK	848	8	27	42	0.0037	0.0430				3176
POL	ETAYFLK	848	8	32	50						3177
POL	FILKLAGR	852	8	25	39						3178
POL	FLKLAGR	852	8	50	78						3179
POL	LAGRWPK	856	8	49	77						3180
POL	GVVESMKN	901	8	53	83						3181
POL	ESMKNELK	904	8	53	83						3182
POL	SMNKLK	905	8	62	97						3183
POL	AVFIHFK	931	8	58	91	0.0280	0.0380				3184
POL	FIHFKRK	933	8	14	22						3185
POL	IASDQTK	956	8	36	56						3186
POL	IATDIQTK	956	8	13	21						3187
POL	ELQKQIK	964	8	35	56						3188
POL	ELQKQITK	964	8	12	19						3189
POL	IKIQNFR	969	8	36	57						3190
POL	ITKIQNFR	969	8	58	91						3191
POL	RVYYRDSR	976	8	35	55						3192
POL	DSRDPWK	981	8	14	22						3193
POL	DSRDPWK	981	8	36	56						3194
POL	PIWKGPAK	985	8	19	30						3195
POL	PLWKGPAK	985	8								

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	A*1101	A*3101	A*3301	A*6801	SEQ ID NO
POL	GIHQAPDR	696	9	16	25	0.0091	0.1600	0.0006	0.0005	0.0120	3246
POL	QIEQLIKK	712	9	37	58	0.0770	0.0570	0.0550	0.8800	4.0000	3247
POL	YLAWVPAHK	724	9	34	58						3248
POL	YLSWVPAHK	724	9	37	58						3249
POL	KLVSAGIRK	742	9	16	25	0.1300	0.0770	0.0017	0.0020	0.0001	3250
POL	KLVSAGIRK	742	9	27	42						3251
POL	KLVSAGIRK	742	9	51	80	0.0380	0.0320	0.0006	0.0006	0.0004	3252
POL	VLFLGIDK	751	9	43	67	0.0027	0.0140	0.0020	0.0009	0.0001	3253
POL	ASCDKQCLK	790	9	50	78	2.7000	0.0690	0.2100	0.0006	0.0002	3254
POL	KLGRWPVK	855	9	50	78	0.0130	0.0470	0.0023	0.0041	0.0014	3255
POL	AACWVAGIK	880	9	21	33						3256
POL	ESMNKELKK	904	9	53	83	0.0170	0.3000	0.0480	0.0560	3.2000	3257
POL	MAVFIHNEK	930	9	60	94	0.1700	1.8000	3.5000	0.2700	1.9000	3258
POL	AVFIHNEK	931	9	62	97						3259
POL	IASDIQTK	955	9	14	22	0.0250	0.0980	0.0007	0.0005	0.0002	3260
POL	IATDIQTK	955	9	35	55	0.0009	0.0006	0.0006	0.0018	0.0001	3261
POL	DIQTELQK	959	9	46	72						3262
POL	QIKIONFR	968	9	12	19	0.0021	0.0045	0.2400	0.0660	0.2600	3263
POL	QITKIQNFR	968	9	35	55	0.0009	0.0068	0.0006	0.0005	0.0001	3264
POL	VIQNSDIK	1003	9	37	58						3265
POL	VIQNSEIK	1003	9	12	19						3266
POL	NSDIKVVPR	1007	9	40	63						3267
POL	NSEIKVVPR	1007	9	12	19	0.0002	0.0001	0.0006	0.0069	0.0065	3268
POL	DIKVVPRK	1009	9	48	75						3269
POL	EIKVVPRK	1009	9	15	23	0.0290	0.0039	0.3100	0.0008	0.0002	3270
POL	KVPRKAK	1011	9	52	81						3271
POL	KVPRKVK	1011	9	11	17						3272
POL	NLAFOQGEAR	5	10	10	16						3273
POL	NLAFOQGEAR	5	10	16	25						3274
POL	QTRANSPTTR	21	10	11	18						3275
POL	QTRANSPTSR	21	10	12	19						3276
POL	PSRANSPTSR	24	10	01	50						3277
POL	QTRANSPTSR	33	10	01	33	0.0370	0.2100	0.0017	0.0025	0.0640	3278
POL	QTRANSPTTR	35	10	01	33						3279
POL	VTIKGGQK	98	10	17	27						3280
POL	VLEENLPGK	119	10	13	20						3281
POL	VLEENLPGK	119	10	12	19	0.0099	0.0550	0.0052	0.0012	0.3100	3282
POL	MIGGIGGFIK	133	10	62	97						3283
POL	QILIEICGKK	148	10	14	22	0.0003	0.0310	0.0017	0.0025	0.0001	3284
POL	ISPIETVPVK	188	10	53	83	0.0002	0.0001	0.0009	0.0009	0.0003	3285
POL	PIETVPVKLK	190	10	53	83	0.3900	0.0760	0.0010	0.0013	0.0024	3286
POL	KLKPGMDGPK	197	10	49	77	0.0002	0.0120	0.0009	0.0009	0.0003	3287
POL	LVEICTEMEK	221	10	15	24	0.0004	0.0001	0.0009	0.0009	0.0003	3288
POL	EMEKEGKISK	229	10	33	52						3289
POL	NTPIFAIKKK	246	10	24	38	0.0006	0.0046	0.0006			3290
POL	NTPVFAIKKK	246	10	37	58	0.0004	0.0002	0.0004			3291
POL	FAIKKDKSTK	250	10	57	89	0.5100	0.0900				3292
POL	KLVDRELNKK	262	10	62	97						3293
POL	LVDFRELNKK	263	10	60	94	0.0110	0.1700	0.0009	0.0009	0.0007	3294
POL	GIPHPAGLKK	282	10	54	86						3295
POL	DAYFSVPLDK	302	10	21	33						

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	A*1101	A*3101	A*3301	A*6801	SEQ ID NO
POL	FSVPLDKDFR	305	10	18	28						3296
POL	SVPLDKDFRK	306	10	18	28						3297
POL	SINNETPGIR	323	10	32	50						3298
POL	STNETPGIR	323	10	11	17						3299
POL	PAIFQSSMTK	346	10	36	56		0.0830	0.0017	0.0025	0.0046	3300
POL	SMTKILEPER	352	10	42	66	0.0760	0.0004				3301
POL	MTKILEPERK	353	10	22	34	0.0004	0.0004	0.0150	0.0060	0.1100	3302
POL	GSDLEIGQHR	379	10	52	81	0.0150	0.0380				3303
POL	DLEIGQHRK	381	10	27	42						3304
POL	DLEIGQHRK	381	10	21	33						3305
POL	FTTPDKKHOK	403	10	51	80	0.0002	0.0150	0.0010	0.0013	0.0273	3306
POL	WMGYELIIPDK	418	10	60	94	0.0005	0.0004	0.0009	0.0016	0.0003	3307
POL	TVQPIQLPEK	429	10	17	27	0.1600	5.6000				3308
POL	DSWTVNDIQK	439	10	13	20	0.0007	0.0002				3309
POL	ESWTVNDIQK	439	10	43	67						3310
POL	WASQIYAGIK	455	10	11	17						3311
POL	WASQIYPGIK	455	10	27	42						3312
POL	KVKQLCKLLR	464	10	28	44						3313
POL	KVRQLCKLLR	464	10	27	42						3314
POL	QLCKLLRGAK	467	10	19	30						3315
POL	QLCKLLRGTK	467	10	25	39						3316
POL	QLCKLLRGTK	467	10	21	33						3317
POL	EAELEIAENR	487	10	53	83						3318
POL	ELAEIREILK	491	10	54	84	0.0002	0.0003				3319
POL	ATESIWIWIK	568	10	19	30						3320
POL	SIVIWGKTPK	571	10	42	66						3321
POL	VIWGTKPKFK	573	10	17	27						3322
POL	VIWGTKPKFR	573	10	29	45						3323
POL	LVKLWYOLEK	614	10	46	72	0.0560	0.0820	0.0075	0.0081	0.0097	3324
POL	AANRETKLGK	637	10	30	47	0.0007	0.0016				3325
POL	KAGYVIDRGR	646	10	39	61						3326
POL	VSLTDITNQK	659	10	10	16						3327
POL	VSLTETITNQK	659	10	20	31						3328
POL	VSQIIEOLIK	710	10	19	30	0.0007	0.0370	0.0017	0.0025	0.0007	3329
POL	IIEQLIKKEK	713	10	30	47	0.0004	0.0003	0.0009	0.0008	0.0003	3330
POL	GIGGNEQVDK	733	10	58	91	0.0005	0.0001	0.0009	0.0009	0.0003	3331
POL	KVFLDGDIDK	750	10	48	75	0.3600	0.7800				3332
POL	VASCDKCOLK	789	10	43	67	0.0004	0.0004				3333
POL	QLDCTHLEK	814	10	60	95	0.0010	0.0003				3334
POL	GSNFTSAVK	870	10	26	41						3335
POL	GSNFTSTTVK	870	10	11	17	0.0300	0.0740	0.0017	0.0025	0.0002	3336
POL	KAACWWAGIK	879	10	20	32						3337
POL	VVESMKNELK	902	10	48	75						3338
POL	ELKKIIGQVR	909	10	56	88	0.0089	0.0093				3339
POL	QVRDQAEHLK	916	10	44	69						3340
POL	QVREQAEHLK	916	10	13	20						3341
POL	QMAVFHIFNK	929	10	60	94	0.6100	0.6400	0.0240	0.0083	0.0610	3342
POL	MAVFIHIFNR	930	10	60	94	0.0068	0.0083				3343
POL	AVFIHIFNRK	931	10	58	91	0.6600	0.8500				3344
POL	GIGGYSAGER	942	10	58	91	0.0003	0.0001	0.0010	0.0029	0.0003	3345

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	A*1101	A*3101	A*3301	A*6801	SEQ ID NO
POL	DIASDIQTK	954	10	14	22						3346
POL	DIATDIQTK	954	10	34	53	0.0056	0.0130	0.0017	0.0025	0.0170	3347
POL	KIQFRVYYR	971	10	52	81	0.0320	0.2100	6.6000	0.0850	0.0380	3348
POL	VVIQDINSIDK	1002	10	37	58	0.0005	0.0210	0.0010	0.0013	0.0018	3349
POL	VVIQDINSEIK	1002	10	12	19						3350
POL	NSDIKVVPRR	1007	10	40	63	0.0007	0.0001				3351
POL	NSEIKVVPRR	1007	10	12	19						3352
POL	KAKIIRYDK	1017	10	41	64	0.0048	0.0018				3353
POL	MAGDDCVAGR	1028	10	24	38						3354
POL	MAGDDCVASR	1028	10	19	30						3355
POL	NSPTSRELQVR	34	11	01	33						3356
POL	NSPSSRELQVR	37	11	01	50						3357
POL	NSPTTRELQVR	39	11	01	50						3358
POL	FSFQITLWOR	85	11	14	22						3359
POL	TLWQRPLVTIK	91	11	17	27						3360
POL	TLWQRPLVTIK	91	11	13	20						3361
POL	LVTKIGGQLK	97	11	13	20						3362
POL	TVLEDINLPK	118	11	13	20						3363
POL	TVLEENLPK	118	11	12	19						3364
POL	DINLPKWKPK	122	11	13	20						3365
POL	EINLPKWKPK	122	11	12	19						3366
POL	KMIGGIGGFIK	132	11	62	97	2.3000	0.7000				3367
POL	PSPIETVPVK	187	11	53	83	0.0750	0.0330				3368
POL	KVKQWPLTEEK	207	11	46	72						3369
POL	ALVEICTEMEK	220	11	15	23						3370
POL	EICTEMEKEGK	223	11	27	42						3371
POL	AIKKKDKTKWR	251	11	57	89						3372
POL	STKWRKLVDFR	257	11	58	91						3373
POL	KLVDRELNKR	262	11	18	94						3374
POL	QLGPHIPAGLK	280	11	56	89						3375
POL	GIPHPAGLKKK	282	11	53	84						3376
POL	FSVPLDKDFRK	305	11	18	28						3377
POL	PSINNETPGIR	322	11	31	48						3378
POL	PSNNETPGIR	322	11	11	17						3379
POL	SMTKILEPFR	351	11	32	50						3380
POL	SMTKILEPFR	352	11	22	34						3381
POL	KIEELREHLK	390	11	13	20						3382
POL	KIEELRQHLR	390	11	15	23						3383
POL	LLKWGFTTDPK	398	11	23	36						3384
POL	LLRWGFTTDPK	398	11	23	36						3385
POL	WTVPQIQLPEK	428	11	17	27						3386
POL	WTVPQIQLPEK	428	11	13	20	0.0011	0.0510				3387
POL	TVNDIQKLVGK	442	11	61	95	0.0400	0.1700				3388
POL	ASQIYAGIKVK	456	11	20	32						3389
POL	ASQIYAGIKVK	456	11	12	19						3390
POL	ASQIYAGIKVK	456	11	14	22						3391
POL	YAGIKYKQCK	460	11	18	28						3392
POL	PVHGIVYDPSK	505	11	39	61						3393
POL	PSKDLIAEIQK	513	11	25	39	0.9200	0.0540				3394
POL	WTYQIYQEPFK	529	11	40	63						3395

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	A*1101	A*3101	A*3301	A*6801	SEQ ID NO
POL	QIQEPPKLNK	532	11	40	63	0.2800	0.2900				3396
POL	NLKTGKYAKMR	540	11	18	29						3397
POL	NLKTGKYARMR	540	11	13	21						3398
POL	RMRGAHTNDVK	548	11	12	19						3399
POL	DVKQLTEAVQK	556	11	33	52	0.0048	0.0240				3400
POL	IATESIVIWGK	567	11	14	22						3401
POL	ESIVIWGKTPK	570	11	41	65						3402
POL	IVIWGKTPKFK	572	11	17	27						3403
POL	IVIWGKTPKFR	572	11	29	45						3404
POL	KTPKFKLPQK	577	11	14	22						3405
POL	KTPKFKLPQK	577	11	22	34						3406
POL	PLVKLWYQLEK	613	11	45	70						3407
POL	ETFYVDGAANR	630	11	43	67						3408
POL	YVDGAANRETK	633	11	44	69						3409
POL	GAANRETKLGK	636	11	30	47						3410
POL	KLKAGYVTDK	643	11	24	38						3411
POL	VVSLTDTTNQK	658	11	10	16						3412
POL	VVSLTDTTNQK	658	11	17	17						3413
POL	VVSLTDTTNQK	694	11	39	61						3414
POL	ALGIQAOQIDR	694	11	15	23						3415
POL	LVNQIEQLIK	709	11	15	23						3416
POL	LVNQIEQLIK	709	11	18	28						3417
POL	VSQIEQLIKK	710	11	19	30						3418
POL	QIEQLIKKEK	712	11	30	47						3419
POL	KVYLAWVPAHK	722	11	20	32	8.6000	2.3000				3420
POL	KVYLSWVPAHK	722	11	23	37						3421
POL	QVDFKLVSAGIR	739	11	15	23						3422
POL	QVDFKLVSAGIR	739	11	29	45						3423
POL	GIDKAOEEHEK	756	11	25	39						3424
POL	GIDKAOEEHEK	756	11	14	22						3425
POL	VAKENVASCDK	784	11	45	71	0.0970	0.1000				3426
POL	IVASCDKCKLK	788	11	43	67						3427
POL	TAYFILKLAGR	849	11	31	48						3428
POL	TAYFLKLAGR	849	11	24	38						3429
POL	ILKLGRWPVK	853	11	30	47						3430
POL	LLKLGRWPVK	853	11	20	31						3431
POL	QSQGVVSMNK	898	11	49	77						3432
POL	GVVSMNKELK	901	11	48	75						3433
POL	VVESMNKELK	902	11	48	75						3434
POL	QMAVFIHFKR	929	11	60	94						3435
POL	MAVFIHFKRK	930	11	57	89						3436
POL	ASDIQTKELQK	957	11	11	17	0.0051	0.1800				3437
POL	ATDIQTKELQK	957	11	35	55						3438
POL	QTKELQKQIK	961	11	10	16						3439
POL	QTKELQKQIK	961	11	32	50	0.0050	0.0100				3440
POL	AVVIQDNDIK	1000	11	37	58	0.0004	0.0150				3441
POL	AVVIQDNDIK	1000	11	12	19						3442
POL	NSDIKVVPRRK	1007	11	40	63						3443
POL	NSEIKVVPRRK	1007	11	11	17						3444
POL	DIKVVPRRKAK	1009	11	39	61						3445

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	A*1101	A*3101	A*3301	A*6801	SEQ ID NO
POL	EIKVPRRKAK	1009	11	13	20						3446
POL	VVPRRKAKIIR	1012	11	42	66						3447
POL	QMGDDDCVAGR	1027	11	24	38						3448
POL	QMGDDDCVASR	1027	11	19	30						3449
REV	DSDELLK	7	8	12	19						3450
REV	QARKNRRR	40	8	17	27						3451
REV	QARNRRR	40	8	38	59						3452
REV	RARQRIIR	50	8	12	19						3453
REV	ILSTCLGR	63	8	12	19						3454
REV	GTETGVGR	103	8	06	19						3455
REV	LLKTVRLIK	12	9	10	16						3456
REV	GTRQARKNR	36	9	15	23						3457
REV	GTRQARNR	36	9	34	53						3458
REV	GTQTRKNR	37	9	01	50						3459
REV	TTRQARNR	37	9	01	50						3460
REV	QARKNRRR	40	9	16	25						3461
REV	QARNRRR	40	9	38	59						3462
REV	RILSTCLGR	62	9	12	19						3463
REV	PLQLPIER	76	9	11	17						3464
REV	PLQLPIER	76	9	35	55						3465
REV	PSPEGTQAR	31	10	13	20						3466
REV	GTRQARKNR	36	10	15	23						3467
REV	GTRQARNR	36	10	34	53						3468
REV	GTQTRKNR	37	10	01	50						3469
REV	TTRQARNR	37	10	01	50						3470
REV	RSQSDDELLK	4	11	11	17						3471
REV	PSPEGTQAR	31	11	13	20						3472
REV	GTRQARKNR	36	11	14	22						3473
REV	GTRQARNR	36	11	34	53						3474
REV	GTQTRKNR	37	11	01	50						3475
REV	TTRQARNR	37	11	01	50						3476
REV	QARKNRRRWR	40	11	16	25						3477
REV	QARNRRRWR	40	11	37	58						3478
REV	PVPLQLPIER	74	11	11	17						3479
REV	PVPLQLPIER	74	11	34	53						3480
TAT	GLGISYGR	45	8	55	87						3481
TAT	GLSYGRKK	47	8	58	91						3482
TAT	ISYGRKKR	48	8	58	91						3483
TAT	PTGPKESK	88	8	20	31						3484
TAT	TACNNCYCK	23	9	17	27						3485
TAT	TACTNCCYCK	23	9	10	16						3486
TAT	GLGISYGRK	45	9	55	87	0.0340	0.0006	0.0017	0.0020	0.0001	3487
TAT	GLSYGRKK	47	9	57	89	0.0008	0.0005	0.0018	0.0014	0.0001	3488
TAT	GLSYGRKKR	47	9	46	72	0.0008	0.0005	0.3900	0.1300	0.0032	3489
TAT	ISYGRKKR	48	9	18	28						3490
TAT	PTGPKESK	88	9	12	19						3491
TAT	ESKKKVESK	93	10	11	17						3492
TAT	PVDPRLPEWK	3	10	11	17						3493
TAT	TACNNCYCK	23	10	11	17						3494
TAT	GLGISYGRKK	45	10	55	87						3495
TAT	GLSYGRKKR	47	10	45	70	0.0003	0.0001				3495

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HIV A03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	A*1101	A*3101	A*3301	A*6801	SEQ ID NO
TAT	PTGPKESKKK	88	10	12	19						3496
TAT	KAGPGGYPRR	101	10	01	50						3497
TAT	GLGISYGRKKR	45	11	54	86						3498
TAT	ISYGRKKRROR	48	11	39	61						3499
TAT	KAGPGGYPRRK	101	11	01	50						3500
VIF	LIVWQVDR	8	8	10	16						3501
VIF	MIVWQVDR	8	8	46	72						3502
VIF	QVDRMKIR	12	8	13	20						3503
VIF	QVDRMRIR	12	8	34	53						3504
VIF	RMINTWK	15	8	10	16						3505
VIF	RMRTWK	15	8	15	23						3506
VIF	RTWKS LVK	19	8	15	23						3507
VIF	RTWNSLVK	19	8	27	42						3508
VIF	HIPLGDAR	56	8	13	20						3509
VIF	HIPLGEAR	56	8	20	31						3510
VIF	GVSEWRK	87	8	16	25						3511
VIF	VSIEWRLR	88	8	15	23						3512
VIF	SIIEWRLR	89	8	11	17						3513
VIF	FSDSAIRK	120	8	13	20						3514
VIF	FSESAIRK	120	8	14	22						3515
VIF	SLQYLALIK	149	8	13	20						3516
VIF	LALTALIK	153	8	16	25						3517
VIF	LTALIKPK	155	8	13	20						3518
VIF	TALIKPKK	156	8	11	17						3519
VIF	LKPKKKIK	158	8	10	16						3520
VIF	LTEDRWNK	178	8	31	48	0.0045					3521
VIF	LVEDRWNK	178	8	11	17						3522
VIF	VMIVWQVDR	7	9	44	69	0.0034	0.0220	4.8000	5.5000	0.0010	3523
VIF	IVWQVDRMK	9	9	12	19						3524
VIF	IVWQVDRMR	9	9	47	73	0.0008	0.0007	0.4500	0.5600	0.0048	3525
VIF	GVSEWRRLR	87	9	14	22						3526
VIF	VSIEWRLR	88	9	11	17						3527
VIF	GSLOYLALIK	148	9	13	20						3528
VIF	YLALTALIK	152	9	16	25						3529
VIF	ALTALIKPK	154	9	13	20						3530
VIF	LTALIKPKK	155	9	11	17						3531
VIF	ALIKPKKKIK	157	9	10	16						3532
VIF	SVKKLTEDR	174	9	13	20						3533
VIF	KLTEDRWNK	177	9	29	45	0.0130	0.2700	0.0680	0.0006	0.0002	3534
VIF	KLVEDRWNK	177	9	11	17						3535
VIF	QVMIVWQVDR	6	10	43	67	0.0062	0.0001				3536
VIF	MIVWQVDRMR	8	10	43	67						3537
VIF	KIRTWNSLVK	17	10	12	19						3538
VIF	RIRTWNSLVK	17	10	15	23						3539
VIF	RIRTWNSLVK	17	10	15	23						3540
VIF	LVKHHMYVSK	24	10	12	19						3541
VIF	EVHIPLGDAR	54	10	13	20						3542
VIF	EVHIPLGEAR	54	10	20	31						3543
VIF	GVSEWRRLR	87	10	10	16						3544
VIF	LALTALIKPK	153	10	13	20						3545

Table IX
HIV A03 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	A*1101	A*3101	A*3301	A*6801	SEQ ID NO
VPU	LIDRIRER	58	8	14	22						3596
VPU	VTLLSSSK	94	8	01	50						3597
VPU	WTIVFIEYR	34	9	10	16						3598
VPU	LVQRKQDRR	43	9	01	50						3599
VPU	ILRQRKIDR	46	9	15	23						3600
VPU	RLIDRIRER	56	9	10	16						3601
VPU	LVTLSSSK	91	9	01	50						3602
VPU	KILRQRKIDR	45	10	15	23	0.0039	0.0001				3603
VPU	KIDRLIDRIR	52	10	10	16						3604
VPU	VVWTIVFIEYR	31	11	10	16						3605

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
ENV	LILGLVII	21	8	09	15		3606
ENV	KLWVTYY	44	8	11	17		3607
ENV	NLWVTYY	44	8	35	56		3608
ENV	VYGVVW	49	8	55	86		3609
ENV	DTEVHNV	75	8	19	30		3610
ENV	NVTENFM	101	8	34	53		3611
ENV	VTFENFM	102	8	34	53		3612
ENV	SLKPCVKL	128	8	55	86		3613
ENV	LTPLCVTL	135	8	54	84		3614
ENV	HYCAPAGF	262	8	27	42		3615
ENV	HYCTPAGF	262	8	11	17		3616
ENV	CTPAGFAI	264	8	10	16		3617
ENV	TVQCTHGI	290	8	51	80		3618
ENV	PVSTQLL	300	8	60	94		3619
ENV	VYSTQLL	301	8	60	94		3620
ENV	QLLLNGSL	305	8	57	89		3621
ENV	NTRKSIRI	351	8	10	16		3622
ENV	RIGPGQTF	357	8	11	17		3623
ENV	GIGPGQTF	360	8	01	33		3624
ENV	SIGSGQAF	360	8	01	33		3625
ENV	FYATGDII	367	8	12	19		3626
ENV	KLREIROF	405	8	01	25		3627
ENV	SPNCGGEF	437	8	36	56		3628
ENV	SPNCGGEF	437	8	16	25		3629
ENV	FYNTSGL	445	8	21	33		3630
ENV	HTEGNITL	478	8	01	50		3631
ENV	NITLPCRI	482	8	11	17		3632
ENV	TITLPCRI	482	8	14	22		3633
ENV	RIKQIINM	488	8	30	47		3634
ENV	RIKQIINM	488	8	12	19		3635
ENV	QIRCSSNI	512	8	11	17		3636
ENV	STNGTETF	537	8	01	17		3637
ENV	KVKIEPL	565	8	25	39		3638
ENV	AVGIGAVF	595	8	11	17		3639
ENV	STMGAASI	614	8	39	61		3640
ENV	LTVQARQL	623	8	38	59		3641
ENV	TVQARQL	624	8	36	56		3642
ENV	IVQQNNL	634	8	26	41		3643
ENV	IVQQSNL	634	8	32	50		3644
ENV	AIEAQQHL	644	8	49	77		3645
ENV	HLKLTW	650	8	13	20		3646
ENV	HLKLTW	650	8	34	53		3647
ENV	HMLQLTVW	650	8	10	16		3648
ENV	TVWGIKQL	655	8	59	92		3649
ENV	RVLAVERY	665	8	33	52		3650
ENV	RVLAVERY	666	8	34	53		3651
ENV	RYLKDOQL	671	8	30	47		3652
ENV	RYLKDOQL	671	8	18	28		3653
ENV	YLDQQL	672	8	31	48		3654
ENV	YLDQQL	672	8	18	28	0.0001	3655

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
ENV	IWGCSCKL	681	8	48	75		3656
ENV	NYPWNSSW	693	8	13	20		3657
ENV	EIWDNMTW	716	8	13	20		3658
ENV	IWDNMTWM	717	8	11	17		3659
ENV	IWNMTWM	717	8	17	27		3660
ENV	WMEWEREI	723	8	12	19		3661
ENV	DLALDKW	754	8	21	33		3662
ENV	ELLELDKW	754	8	20	31		3663
ENV	ALDKWASL	757	8	11	17		3664
ENV	ELDKWASL	757	8	18	28		3665
ENV	KWASLWNW	760	8	26	41		3666
ENV	SLWNWFDI	763	8	17	27		3667
ENV	WFDITNWL	767	8	10	16		3668
ENV	DITNWLWY	769	8	10	16		3669
ENV	ITKWLWYI	770	8	16	25		3670
ENV	ITNWLWYI	770	8	19	30		3671
ENV	KWLWYIKI	772	8	19	30		3672
ENV	NWLWYIKI	772	8	25	39		3673
ENV	WLWYIKIF	773	8	50	78		3674
ENV	WYIKIFI	774	8	49	77		3675
ENV	WYIKIFIM	775	8	43	67		3676
ENV	YIKIFIM	776	8	43	67		3677
ENV	FIMIVGGL	780	8	44	69		3678
ENV	IMIVGGLI	781	8	35	56		3679
ENV	IVGGLIGL	783	8	42	66		3680
ENV	IVGGLVGL	783	8	10	16		3681
ENV	GLIGLRII	786	8	15	23		3682
ENV	LIGLRIIF	787	8	16	25		3683
ENV	LIGLRIVF	787	8	29	45		3684
ENV	IIFAVLSI	792	8	15	23		3685
ENV	IVFAVLSI	792	8	20	31		3686
ENV	PLSFQTLI	809	8	10	16		3687
ENV	SIRLVNGF	842	8	13	20		3688
ENV	SIRLVSGF	842	8	13	20		3689
ENV	LVNGFLAL	845	8	14	22		3690
ENV	LVSGFLAL	845	8	19	30		3691
ENV	AWDDLRLS	853	8	20	31		3692
ENV	DLRNLCLF	856	8	17	27		3693
ENV	DLRSLCLF	856	8	38	59		3694
ENV	CLFSYHRL	861	8	42	66		3695
ENV	SYHRLRDF	864	8	18	28		3696
ENV	SYHRLRDL	864	8	23	36		3697
ENV	KLRDLILI	867	8	13	20		3698
ENV	ELLGHSSL	881	8	09	15		3699
ENV	ELLGRGW	881	8	23	37		3700
ENV	GWEALKYL	896	8	12	19		3701
ENV	GWEGLKYL	896	8	12	19		3702
ENV	YWNLLQY	902	8	15	23		3703
ENV	WNNLLQYW	903	8	15	23		3704
ENV	SLLNATAI	920	8	14	22		3705

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
ENV	ILHIIPRI	947	8	13	20		3706
ENV	PTIRIQGL	951	8	12	19		3707
ENV	TVYGGVPVW	48	9	55	86		3708
ENV	VWKEATTL	55	9	22	34	0.0300	3709
ENV	PTDPNPOEI	89	9	25	39		3710
ENV	NVTENFNMW	101	9	34	53		3711
ENV	NFNWKNNDM	105	9	12	19		3712
ENV	NFNWKNNDM	105	9	18	28		3713
ENV	MVEQMIEDI	113	9	23	36		3714
ENV	QMIEDIISL	116	9	29	45		3715
ENV	IISLWDQSL	121	9	38	59		3716
ENV	VISLWDQSL	121	9	10	16		3717
ENV	KLTPLCVTL	134	9	52	81		3718
ENV	EIKNCFSNI	181	9	13	20		3719
ENV	LINCNTSAI	237	9	15	23		3720
ENV	KVSFEPIPI	252	9	30	47		3721
ENV	SFEPIPIIY	254	9	31	48		3722
ENV	ILKCNDRKKF	271	9	12	19		3723
ENV	STVQCTHGI	289	9	51	80		3724
ENV	PVYSTQLLL	300	9	60	94		3725
ENV	SLAEFEVVI	311	9	13	20		3726
ENV	RIGPGQTFY	357	9	11	17		3727
ENV	GIGPGQTFY	360	9	01	33		3728
ENV	SIGSGQAFY	369	9	01	33		3729
ENV	ATDIIIGDI	380	9	12	19		3730
ENV	DIROAHCNI	428	9	15	23		3731
ENV	DLEITHSF	437	9	21	33		3732
ENV	SFNCGGEFF	437	9	35	55		3733
ENV	SFNCRGEFF	444	9	16	25		3734
ENV	FFYCNTSGL	445	9	21	33		3735
ENV	FYCNTSGLF	484	9	21	33		3736
ENV	TLPCRKQI	488	9	26	41		3737
ENV	RIKQINMW	495	9	30	47		3738
ENV	RIKQINMW	495	9	12	19		3739
ENV	MWQEVGKAM	545	9	15	23		3740
ENV	MWQRYGQAM	545	9	10	16		3741
ENV	IFRPGGGDM	545	9	17	27		3742
ENV	IFRPGGGDM	545	9	25	39		3743
ENV	NWRSELYKY	556	9	54	84		3744
ENV	LYKYKVKVI	561	9	13	20	0.0200	3745
ENV	LYKYKVKVI	595	9	29	45		3746
ENV	AVGIGAVFL	598	9	11	17		3747
ENV	GIGAVFLGF	599	9	11	18		3748
ENV	MLGAMFLGF	599	9	04	36		3749
ENV	TIGAMFLGF	608	9	03	27		3750
ENV	FLGAAGSTM	615	9	55	86		3751
ENV	TMGAASITL	622	9	39	61		3752
ENV	TLTVQARQL	623	9	37	58		3753
ENV	LTVQARQLL	633	9	36	56		3754
ENV	GIVQQNNL		9	26	41		3755

Table X
HIV A24 Super-Void peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
ENV	GIVQQSNL	633	9	32	50		3756.
ENV	IVQQNNLL	634	9	26	41		3757
ENV	IVQQSNLL	634	9	32	50		3758
ENV	AIEAQHLL	644	9	48	75		3759
ENV	LLKLTWGI	651	9	13	20		3760
ENV	LLQLTWGI	651	9	34	53		3761
ENV	MLQLTWGI	651	9	10	16		3762
ENV	LTWGIKQL	654	9	59	92		3763
ENV	RVLAVERYL	665	9	33	52	0.7600	3764
ENV	RYLKDQQL	671	9	29	45	0.2300	3765
ENV	RYLRDQQL	671	9	17	27		3766
ENV	GIWGCCKL	680	9	48	75	0.0270	3767
ENV	IWGCCKLI	681	9	19	30		3768
ENV	LICTTAVPW	688	9	17	27		3769
ENV	LICTTNPW	688	9	12	19		3770
ENV	LICTTTPW	688	9	12	19		3771
ENV	TWMEWEREI	722	9	11	17		3772
ENV	EWEREIDNY	725	9	11	17		3773
ENV	ALDKWASLW	757	9	11	17		3774
ENV	ELDKWASLW	757	9	18	28		3775
ENV	KWASLWNNWF	760	9	26	41		3776
ENV	WFDITNWLW	767	9	10	16		3777
ENV	DTNWLWYI	769	9	10	16		3778
ENV	KWLWYKIF	772	9	16	25		3779
ENV	NWLWYKIF	772	9	25	39		3780
ENV	WLWYKIFI	773	9	49	77		3781
ENV	LWYKIFIM	774	9	43	67		3782
ENV	WYKIFIMI	775	9	43	67		3783
ENV	IFIMVGGI	779	9	41	64		3784
ENV	IFIMVGGI	780	9	35	55		3785
ENV	MIVGGIIGL	782	9	36	56		3786
ENV	GLGLRIIF	786	9	15	23		3787
ENV	GLGLRIIF	786	9	29	45		3788
ENV	GLRIIFAVL	789	9	17	27		3789
ENV	GLRIIFAVL	789	9	28	44		3790
ENV	RIIFAVLSI	791	9	14	22		3791
ENV	RIIFAVLSI	791	9	19	30		3792
ENV	IVNRVROGY	799	9	38	59		3793
ENV	RVROGYSP	802	9	55	86		3794
ENV	SIRLVNGFL	842	9	11	17		3795
ENV	SIRLVSGFL	842	9	13	20		3796
ENV	RLVNGFLAL	844	9	12	19		3797
ENV	RLVSGFLAL	844	9	19	30		3798
ENV	FLALAWDDL	849	9	25	39		3799
ENV	SYHRLRDFI	864	9	13	20		3800
ENV	SYHRLRDL	864	9	14	22		3801
ENV	LIAARTVEL	873	9	12	19		3802
ENV	SLKGLRLGW	889	9	11	18		3803
ENV	SLRGLQRGW	889	9	05	18		3804
ENV	GLRLGWEG	892	9	10	32		3805

Table X

HIV A24: Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
ENV	RLGWEGLKY	894	9	09	29		3806
ENV	KYWNLLQY	901	9	14	22		3807
ENV	YWNLLQYW	902	9	15	23		3808
ENV	LQYWSQEL	906	9	16	25		3809
ENV	ELKNSAINL	913	9	10	16		3810
ENV	ELKNSAISL	913	9	10	19		3811
ENV	ELKNSAVSL	913	9	12	19		3812
ENV	AVAEGETDRI	928	9	16	25		3813
ENV	AILHIPRRI	946	9	12	19		3814
ENV	VTVYGVVPVW	47	10	55	86		3815
ENV	PVWKEATTL	54	10	22	34		3816
ENV	VWKEATTLF	55	10	22	34	0.2700	3817
ENV	LFCASDAKAY	65	10	42	66		3818
ENV	AYDTEVHNWV	73	10	18	28		3819
ENV	MWKNMVEQ	108	10	35	55		3820
ENV	NMVEQMIEDI	112	10	20	31	0.0004	3821
ENV	MVEQMIEDI	113	10	23	36		3822
ENV	QMHEDIISLW	116	10	29	45		3823
ENV	DIISLWDQSL	120	10	38	59		3824
ENV	DVSLWDQSL	120	10	10	16		3825
ENV	RLINCNTSAI	236	10	15	24		3826
ENV	ITQACPVSF	245	10	29	45		3827
ENV	PIHYCTPAGF	260	10	27	42		3828
ENV	HYCAPAGFAI	262	10	10	16		3829
ENV	HYCTPAGFAI	262	10	27	42		3830
ENV	AILKNDKFF	270	10	12	19		3831
ENV	GKPVVSTQL	297	10	33	52		3832
ENV	GIRPVVSTQL	297	10	26	41		3833
ENV	STQLLNGSL	303	10	57	89		3834
ENV	NTSPRSRVAY	376	10	01	33		3835
ENV	SFNCGGEFFY	437	10	35	55		3836
ENV	SFNCGGEFFY	437	10	16	25		3837
ENV	EFFYCNTSGL	443	10	21	33		3838
ENV	FFYCNTSGLF	444	10	21	33		3839
ENV	ITLPCRKQI	483	10	25	39		3840
ENV	TLPCRKQII	484	10	15	23	0.0001	3841
ENV	NMWQEVGKA	494	10	15	23		3842
ENV	MWQEVGKAM	495	10	15	23		3843
ENV	MWQEVGOAM	495	10	15	23		3844
ENV	NTETNKTET	537	10	10	16		3845
ENV	NTTGNITET	537	10	01	17		3846
ENV	EIFRPGGDM	544	10	17	17		3847
ENV	EIFRPGGDM	544	10	21	27		3848
ENV	DMRDNRSEL	552	10	37	58		3849
ENV	ELYKYKVVEI	560	10	13	21		3850
ENV	ELYKYKVVKI	560	10	29	46		3851
ENV	KYKVKIEPL	563	10	25	39		3852
ENV	GIGAVFLGFL	598	10	11	18		3853
ENV	MLGAMFLGFL	599	10	04	36		3854
ENV							3855

HIV A24 Super Motif Peptides with Binding Information

Table X

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
ENV	TIGAMFLGFL	599	10	03	27		3856
ENV	GFLGAAGSTM	606	10	55	86		3857
ENV	STMGAASITL	614	10	39	61		3858
ENV	ITLTVOARQL	621	10	27	42		3859
ENV	TLTVQARQL	622	10	35	55		3860
ENV	GIVQOQNLL	633	10	26	41		3861
ENV	GIVQOQNLL	633	10	32	50		3862
ENV	GIVQOQNLL	633	10	13	20		3863
ENV	HLLQLTVWGI	650	10	34	53		3864
ENV	HLLQLTVWGI	650	10	13	20		3865
ENV	KLTVWGIKQL	653	10	44	69		3866
ENV	KLTVWGIKQL	653	10	40	63		3867
ENV	GIKQLQARVL	658	10	27	42		3868
ENV	YLRDQQLGI	672	10	18	28		3869
ENV	YLRDQQLGI	672	10	48	75		3870
ENV	GIWGCCKLI	680	10	19	30		3871
ENV	KLICTTAVPW	687	10	17	27		3872
ENV	KLICTTAVPW	687	10	12	19		3873
ENV	KLICTTAVPW	687	10	11	17		3874
ENV	TTNVPWNSS	691	10	10	16		3875
ENV	IWNMTWME	717	10	10	16		3876
ENV	MTWMEWRE	721	10	12	19		3877
ENV	LLALDKWASL	755	10	11	17		3878
ENV	LLALDKWASL	755	10	18	28		3879
ENV	WFDITNWLW	767	10	10	16		3880
ENV	ITKWLWYIKI	770	10	15	23		3881
ENV	ITNWLWYIKI	770	10	14	22		3882
ENV	KWLWYIKIFI	772	10	16	25		3883
ENV	NWLWYIKIFI	772	10	25	39		3884
ENV	WLWYIKIFIM	773	10	43	67		3885
ENV	LWYIKIFIMI	774	10	43	67		3886
ENV	KIFIMIVGGL	778	10	38	59		3887
ENV	IFIMIVGGLI	779	10	33	52		3888
ENV	IMVGGIIGL	781	10	34	54		3889
ENV	IVGGLIGLRI	783	10	42	66		3890
ENV	SIVNRVQGY	798	10	36	56		3891
ENV	GYSPLSFQTL	806	10	29	45		3892
ENV	LVSGFLALAW	845	10	16	25		3893
ENV	GFLALAWDDL	848	10	25	39		3894
ENV	ALAWDDLRLS	851	10	19	30		3895
ENV	AWDDLRLSL	853	10	20	31		3896
ENV	DLRNLCLFSY	856	10	16	25		3897
ENV	DLRNLCLFSY	856	10	35	55		3898
ENV	NLCCLFSYHRL	859	10	11	17		3899
ENV	SLCLFSYHRL	859	10	31	48		3900
ENV	LFSYHRLRDL	862	10	18	28		3901
ENV	LFSYHRLRDL	862	10	22	34		3902
ENV	SYHRLRDLFI	864	10	13	20		3903
ENV	SYHRLRDLFI	864	10	12	19		3904
ENV	LIAARTVELL	873	10	11	17		3905
ENV	IVELLGRRGW	879	10	22	34		

Table X
HIV A24 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*240I	SEQ ID NO
ENV	LLGRRGWEAL	882	10	09	15		3906
ENV	RLGWEGKYL	894	10	09	29		3907
ENV	KYWNLLQY	901	10	14	22		3908
ENV	NLLQYWSQEL	905	10	16	25		3909
ENV	ELKNSAYSL	913	10	10	16		3910
ENV	AVSLLNATAI	918	10	11	17		3911
ENV	AVAEGTDRII	928	10	15	23		3912
ENV	AVAEGTDRVI	928	10	14	22		3913
ENV	HIPRIRQGL	949	10	13	21		3914
ENV	NIPRIRQGL	949	10	11	17		3915
ENV	RIRQGLERAI	953	10	34	53		3916
ENV	WVTVYGVVPV	46	11	55	86		3917
ENV	PVWKEATTL	54	11	22	34		3918
ENV	TLFCASDAKA	64	11	40	63		3919
ENV	PTDPNPQEI	87	11	25	39		3920
ENV	CVPTDPNPQEI	89	11	12	19		3921
ENV	NMWKNMVE	107	11	30	47		3922
ENV	NMVEQMIIEDII	112	11	20	31		3923
ENV	SLKPCVKLTPL	128	11	54	84		3924
ENV	CVKLTPLCVT	132	11	52	81		3925
ENV	VITQACPVSF	244	11	14	22		3926
ENV	KVSPEPIPIHY	252	11	28	44		3927
ENV	HYCAPAGFAIL	262	11	27	42		3928
ENV	NVSTVQCTHGI	287	11	51	80		3929
ENV	GIRPVVSTQLL	297	11	33	52		3930
ENV	GIRPVVSTQLL	297	11	26	41		3931
ENV	FYATGDIIGDI	367	11	11	17		3932
ENV	GTAGNSSRAA	375	11	01	33		3933
ENV	TTHSFNCGGE	432	11	16	25		3934
ENV	TTHSFNCGGE	432	11	12	19		3935
ENV	VMHSFNCGGE	432	11	13	20		3936
ENV	EFFYCNTSGLF	443	11	21	33		3937
ENV	NITLPCRKQI	482	11	11	17		3938
ENV	TITLPCRKQI	482	11	13	20		3939
ENV	ITLPCRKQII	483	11	15	23		3940
ENV	NMWQEVGKA	494	11	15	23		3941
ENV	EVGKAMYAPPI	498	11	18	28		3942
ENV	RVGQAMYAPP	498	11	10	16		3943
ENV	QIRCSSNITGL	512	11	11	17		3944
ENV	DMRDNRSEL	552	11	37	58		3945
ENV	VVEREKRAVGI	588	11	11	17		3946
ENV	AVGIGAVELGF	595	11	11	17		3947
ENV	SITLTVQARQL	620	11	27	42		3948
ENV	ITLTVQARQL	621	11	27	42		3949
ENV	TVQARQLLSGI	624	11	36	56		3950
ENV	LLRAIEAQHLL	641	11	45	70		3951
ENV	AIEAQHLLKL	644	11	12	19		3952
ENV	AIEAQHLLQL	644	11	35	55		3953
ENV	AVERYLKDQ	668	11	23	36		3954
ENV	AVERYLRDQ	668	11	11	17		3955

Table X
HIV A24 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
ENV	RYLKDQQLGI	671	11	25	39		3956
ENV	RYLRDQQLGI	671	11	17	27		3957
ENV	YLRDQQLGI	672	11	27	42		3958
ENV	YLRDQQLGI	672	11	18	28		3959
ENV	LLGIWCGSGKL	678	11	46	72		3960
ENV	CTTNVPWNS	690	11	11	17		3961
ENV	NMTWMEWER	720	11	12	19		3962
ENV	WMEWEREIDN	723	11	10	16		3963
ENV	ELLEDKWAS	754	11	15	23		3964
ENV	ELLEDKWASL	755	11	11	17		3965
ENV	LLALDKWASL	757	11	18	28		3966
ENV	ALDKWASLW	757	11	10	16		3968
ENV	ELDKWASLWN	757	11	16	25		3969
ENV	KWASLWNWF	760	11	15	23		3970
ENV	WFDITNLW	767	11	10	16		3971
ENV	ITKWLWYIKIF	770	11	12	19		3972
ENV	ITNLWYIKIF	770	11	14	22		3973
ENV	KWLWYIKIFIM	772	11	15	23		3974
ENV	NWLWYIKIFIM	772	11	22	34		3975
ENV	WLWYIKIFIM	773	11	43	67		3976
ENV	KIFMIVGGI	778	11	31	48		3977
ENV	FIMVGGI	780	11	34	53		3978
ENV	MIVGGI	782	11	36	56		3979
ENV	IVGGI	783	11	12	19		3980
ENV	LIGLRI	787	11	15	23		3981
ENV	LIGLRI	787	11	20	31		3982
ENV	LIGLRI	789	11	14	22		3983
ENV	GLRIVAVLSI	789	11	19	30		3984
ENV	GLRIVAVLSI	802	11	47	73		3985
ENV	RVRQGYSPLSF	842	11	11	17		3986
ENV	SIRLVSGFLAL	844	11	16	25		3987
ENV	RLVSGFLALA	853	11	20	31		3988
ENV	AWDDLRSCL	861	11	18	28		3989
ENV	CLFSYIHLRDL	861	11	20	31		3990
ENV	CLFSYIHLRDL	862	11	13	20		3991
ENV	LFSYIHLRDL	862	11	10	16		3992
ENV	SYIHLRDL	864	11	10	16		3993
ENV	SYIHLRDL	878	11	22	34		3994
ENV	RIVELLGRRG	881	11	09	15		3995
ENV	ELLGRRGWEA	892	11	09	29		3996
ENV	GLRLGWGLK	894	11	12	23		3997
ENV	RLGWGLKYL	909	11	16	25		3998
ENV	YWGQELKNSA	926	11	16	25		3999
ENV	AIYAEGTDRI	953	11	33	52		4000
ENV	RIRQGLERALL	953	11	11	17		4001
GAG	SVLSGGEL	6	8	28	44		4002
GAG	SVLSGGEL	6	8	18	28		4003
GAG	KLDKWEKI	12	8	10	16		4004
GAG	IVWASREL	35	8	21	33		4005
GAG	LVWASREL	35	8	36	56		4005

Table X
HIV-1 A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
GAG	REALNPGL	45	8	20	31		4006
GAG	RFAVNPGL	45	8	16	25		4007
GAG	GTELRSL	73	8	12	19		4008
GAG	LPTNTATL	80	8	16	25		4009
GAG	LYNTVATL	80	8	22	34		4010
GAG	LYCVHQKI	87	8	13	20		4011
GAG	LYCVHQRI	87	8	18	28		4012
GAG	KVSNQYPI	148	8	15	27		4013
GAG	QVSNQYPI	148	8	27	48		4014
GAG	NYPIVQNL	152	8	31	48		4015
GAG	KVIEKAF	178	8	24	38		4016
GAG	KVVEEKAF	178	8	28	44		4017
GAG	VIPMFAL	189	8	46	72		4018
GAG	VIPMFAL	189	8	14	22		4019
GAG	ATPQDLNM	200	8	12	19		4020
GAG	DLNMLNI	204	8	12	19		4021
GAG	TLQEQIAW	263	8	12	19		4022
GAG	TLQEQIGW	263	8	27	42		4023
GAG	WMTNPPPI	270	8	20	31		4024
GAG	WMTSNPPPI	270	8	16	25		4025
GAG	PIPVGDY	279	8	11	17		4026
GAG	PIPVGEY	279	8	35	55		4027
GAG	DIYKRWII	284	8	17	27		4028
GAG	EYKRWII	284	8	39	61		4029
GAG	IYKRWII	285	8	54	84		4030
GAG	IILGLNKI	290	8	57	89		4031
GAG	GLNKIVRM	293	8	60	94		4032
GAG	RMYSPTSII	299	8	14	22		4033
GAG	RMYSPTSII	299	8	40	63		4034
GAG	MYSPVSII	300	8	14	22		4035
GAG	MYSPVSII	300	8	42	66		4036
GAG	ATQDVKNW	333	8	15	23		4037
GAG	ATQEVKNW	333	8	18	28		4038
GAG	NWMTDTLL	339	8	16	25		4039
GAG	NWMTETLL	339	8	36	56		4040
GAG	ALGPAATL	360	8	16	25		4041
GAG	ALGPGATL	360	8	18	28		4042
GAG	IMMQKSNF	408	8	11	17		4043
GAG	IMMQKSNF	408	8	27	42		4044
GAG	CTERQANF	459	8	55	87		4045
GAG	ETIDKDLY	537	8	01	25		4046
GAG	ELYPLASL	543	8	14	22		4047
GAG	ELYPLTSL	543	8	11	17		4048
GAG	PLASLKS	548	8	15	23		4049
GAG	PLTSLKSL	548	8	12	19		4050
GAG	PLTSLRSL	548	8	12	19		4051
GAG	LTSLKSLF	549	8	13	20		4052
GAG	LTSLRSLF	549	8	12	19		4053
GAG	SLFGNDPL	554	8	12	19		4054
GAG	SLFGSDPL	554	8	11	17		4055

Table X
HIV A24-Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
GAG	KYKLLHIVW	29	9	10	16		4056
GAG	KYRLKILVW	29	9	16	25		4057
GAG	HIVWASREL	34	9	21	33		4058
GAG	HLVWASREL	34	9	36	56		4059
GAG	RFALNPGLL	45	9	20	31		4060
GAG	RFVNPGLL	45	9	16	25	0.0100	4061
GAG	ETSEGRQI	54	9	16	25		4062
GAG	ILGQLQPSL	62	9	11	17		4063
GAG	SLOTGSEL	69	9	14	22		4064
GAG	SLFNTVATL	79	9	16	25		4065
GAG	SLYNTVATL	79	9	22	34		4066
GAG	LFTNVATLY	80	9	15	23		4067
GAG	LYNTVATLY	80	9	22	34		4068
GAG	TYLCVHQI	86	9	12	19		4069
GAG	TYLCVHQRI	86	9	15	23		4070
GAG	DVKDTKEAL	95	9	11	17		4071
GAG	EVKDTKEAL	95	9	20	31		4072
GAG	DTKEALDKI	98	9	32	50		4073
GAG	DTKEALEKI	98	9	10	16		4074
GAG	IVQNAQGQM	155	9	21	33		4075
GAG	IVQNLQGQM	155	9	29	45		4076
GAG	TLNAAVVKVI	172	9	30	47		4077
GAG	AFSPEVPM	184	9	50	78		4078
GAG	EVIPMFAL	188	9	46	72		4079
GAG	EVIPMFAL	188	9	14	22		4080
GAG	ATPDNLNMM	200	9	12	19		4081
GAG	ATPDNLNMM	200	9	42	66		4082
GAG	IVGGHQAAAM	211	9	12	19		4083
GAG	TVGGHQAAAM	211	9	47	73		4084
GAG	AMQMLKDTI	218	9	33	52		4085
GAG	AMQMLKETI	218	9	26	41		4086
GAG	TINEEAAEW	225	9	53	83		4087
GAG	DIAGTTSTL	256	9	48	75		4088
GAG	TTSTLQEQI	260	9	45	71		4089
GAG	STLQEQIAW	262	9	12	19		4090
GAG	STLQEQIGW	262	9	27	42		4091
GAG	TLQEQIAWM	263	9	12	19		4092
GAG	TLQEQIGWM	263	9	27	42		4093
GAG	GWMTNPPPI	269	9	18	28	0.0140	4094
GAG	GWMTSNPPI	269	9	10	16		4095
GAG	PVGDIYKRW	281	9	18	28		4096
GAG	PVGEIYKRW	281	9	40	63		4097
GAG	DIYKRWHIL	284	9	17	27		4098
GAG	EIYKRWHIL	284	9	37	58		4099
GAG	WILGLNKI	289	9	57	89		4100
GAG	GLNKIVRMY	293	9	60	94		4101
GAG	RMYSPTSIL	299	9	14	22		4102
GAG	RMYSPTSIL	299	9	40	63		4103
GAG	PRDYVDVDF	316	9	63	98		4104
GAG	YVDRFFKTL	320	9	27	42		4105

Table X
HIV A24 Super-YonH Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
GAG	YVDFYKTL	320	9	28	44		4106
GAG	ATQDVKNWM	333	9	15	23		4107
GAG	ATQEVKNWM	333	9	18	28		4108
GAG	NIMMORGNF	407	9	10	17		4109
GAG	TIMMORGNF	407	9	13	22		4110
GAG	CTEQANFL	459	9	55	87		4111
GAG	PTAPPAESF	495	9	20	31		4112
GAG	PTAPPAESF	495	9	15	23		4113
GAG	PTAPPAESF	507	9	02	67		4114
GAG	PTAPPAESF	507	9	01	33		4115
GAG	PIDKELYPL	534	9	12	19		4116
GAG	PIDKELYPL	538	9	01	25		4117
GAG	TIDKDLPL	538	9	01	25		4118
GAG	PLASLSLF	548	9	15	23		4119
GAG	PLTSLSLF	548	9	12	19		4120
GAG	PLTSLSLF	548	9	12	19		4121
GAG	VLSGGKLDW	7	10	15	23		4122
GAG	KLDAWEKIRL	12	10	16	25		4123
GAG	KLDKWEKIRL	12	10	10	16		4124
GAG	RLRPGKKKY	20	10	34	53		4125
GAG	VWASRELERF	36	10	45	70		4126
GAG	ETSEGCRQIL	54	10	14	22		4127
GAG	QILGLOPLSL	61	10	11	17		4128
GAG	QTGSEELRSL	71	10	12	19		4129
GAG	SLFNTVATLY	79	10	15	23		4130
GAG	SLYNTVATLY	79	10	22	34		4131
GAG	ATLYCVHQKI	85	10	12	19		4132
GAG	ATLYCVHQRI	85	10	15	23		4133
GAG	PIVQNAQQQM	154	10	21	33		4134
GAG	PIVQNLQGM	154	10	29	45		4135
GAG	ALSPRTLNAW	167	10	29	45		4136
GAG	ALSPRTLNAW	167	10	10	16		4137
GAG	RTLNAWVKVI	171	10	30	47		4138
GAG	WVKVIEEKAF	176	10	24	38		4139
GAG	WVKVVEEKAF	176	10	28	44		4140
GAG	AFSEVIPMF	184	10	50	78	0.0078	4141
GAG	ATPDNLNML	200	10	12	19		4142
GAG	ATPDNLNML	200	10	42	66		4143
GAG	NIVGGHQAAM	210	10	12	19		4144
GAG	NTVGGHQAAM	210	10	47	73		4145
GAG	DTINEAAEW	224	10	31	48		4146
GAG	ETINEAAEW	224	10	22	34		4147
GAG	RVHPVHAGPI	235	10	22	34		4148
GAG	RVHPVHAGPI	235	10	14	22		4149
GAG	QMRPRGSDI	248	10	44	69		4150
GAG	GTTSTLQEQI	259	10	45	70		4151
GAG	STLQEQIAWM	262	10	12	19		4152
GAG	STLQEQIWM	262	10	27	42		4153
GAG	PVGDIYKRWI	281	10	17	27		4154
GAG	PVGEIYKRWI	281	10	40	63		4155

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
GAG	IYKRWILGL	285	10	54	84	0.0140	4156
GAG	RWILGLNKI	288	10	56	88		4157
GAG	ILGLNKIVRM	291	10	57	89		4158
GAG	IVRMYSPISI	297	10	14	22		4159
GAG	IVRMYSPVSI	297	10	40	63		4160
GAG	MYSPISLDI	300	10	13	20		4161
GAG	MYSPVSLDI	300	10	40	63		4162
GAG	DIQGPKEPF	308	10	19	30		4163
GAG	DIRQGPKEPF	308	10	41	64		4164
GAG	PFRDYVDRFF	316	10	35	55		4165
GAG	PFRDYVDRFY	316	10	28	44		4166
GAG	DYVDRFFKTL	319	10	27	42		4167
GAG	DYVDRFYKTL	319	10	28	44		4168
GAG	DVKNWMTDT	336	10	12	19		4169
GAG	DVKNWMTET	336	10	11	17		4170
GAG	EVKNWMTETL	336	10	25	39		4171
GAG	ATIMMQRGNF	406	10	11	28		4172
GAG	CFNCGKEGHI	425	10	27	42		4173
GAG	CFNCGKEGHI	425	10	27	42		4174
GAG	TFPSOKQEP	522	10	09	45		4175
GAG	ETHDKDLYPL	537	10	01	25		4176
GAG	RTENSLYPPL	538	10	01	25		4177
GAG	LYPLASLSKL	544	10	09	17		4178
GAG	SVLSGGKLLDA	6	11	15	23		4179
GAG	IVWASRELERF	35	11	19	30		4180
GAG	IVWASRELER	35	11	25	39		4181
GAG	ELERFALNPGL	42	11	14	22		4182
GAG	ELERFAVNPGL	42	11	15	23		4183
GAG	LLETSEGRQI	52	11	16	25		4184
GAG	RIEVKDTKEAL	93	11	12	19		4185
GAG	NLQQQMVIQA	158	11	15	23		4186
GAG	MVHOAISPRTL	163	11	27	42		4187
GAG	AWVKVIEKA	175	11	24	38		4188
GAG	AWVKVVEKA	175	11	28	44		4189
GAG	ALSEGATPQDL	195	11	58	91		4190
GAG	IVGGHQAAMQ	211	11	11	17		4191
GAG	TVGGHQAAMQ	211	11	47	73		4192
GAG	TTSTLQEQIA	260	11	11	17		4193
GAG	TTSTLQEQIG	260	11	27	43		4194
GAG	QIGWMTNPPPI	267	11	18	29		4195
GAG	QIGWMTSNPPI	267	11	10	16		4196
GAG	PIPVGEIYKRW	279	11	34	53		4197
GAG	PVGDIYKRWII	281	11	17	27		4198
GAG	PVGDIYKRWII	281	11	39	61		4199
GAG	DIYKRWILGL	284	11	17	27		4200
GAG	EYKRWILGL	284	11	37	58		4201
GAG	IILGLNKIVRM	290	11	56	88		4202
GAG	ILGLNKIVRMY	291	11	57	89		4203
GAG	KIVRMYSPISI	296	11	14	22		4204
GAG	KIVRMYSPVSI	296	11	39	61		4205

Table X
HIV-A24 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
GAG	IVRMYSPVSIL	297	11	14	22		4206
GAG	IVRMYSPVSIL	297	11	40	63		4207
GAG	RMYSPTSILDI	299	11	13	20		4208
GAG	RMYSPTSILDI	299	11	38	59		4209
GAG	DVKNWMTDT	336	11	12	19		4210
GAG	DVKNWMTET	336	11	11	17		4211
GAG	EVKNWMTETL	336	11	25	39		4212
GAG	ILKALGPAATL	357	11	16	25		4213
GAG	ALGPAATLEE	360	11	16	25		4214
GAG	ALGPAATLEE	360	11	17	27		4215
GAG	ATAQQDLKGG	392	11	01	50		4216
GAG	CWKCKEGHIQ	446	11	46	72		4217
GAG	PTAPPAESFRF	495	11	10	16		4218
GAG	PTAPPAESFRF	495	11	14	22		4219
GAG	PTAPPAESFRF	507	11	02	67		4220
GAG	PTAPPAESFRF	507	11	01	33		4221
GAG	LYPLASLSLFL	544	11	09	17		4222
GAG	SLKSLFGNDPL	551	11	12	19		4223
NEF	DEKHGAI	57	8	14	22		4224
NEF	ATNADCAW	71	8	12	22		4225
NEF	PVRQVPL	95	8	48	75		4226
NEF	PMYKGF	105	8	12	19		4227
NEF	TYKGAIDL	107	8	12	19		4228
NEF	AFDLSFFL	111	8	18	28		4229
NEF	ALDLSHFL	111	8	11	17		4230
NEF	AVDLSHFL	111	8	15	23		4231
NEF	FLKEKGG	117	8	56	88		4232
NEF	DLDLVVY	185	8	20	31		4233
NEF	EILDWVY	185	8	33	52		4234
NEF	WVYHTQGF	191	8	13	20		4235
NEF	WVYHTQGY	191	8	21	33		4236
NEF	VYHTQGYF	192	8	13	20		4237
NEF	VYHTQGYF	192	8	21	33		4238
NEF	FFPDWQNY	199	8	17	27		4239
NEF	YFPDWQNY	199	8	36	56		4240
NEF	NYTPGPI	206	8	20	31		4241
NEF	GIRYPLTF	213	8	13	20		4242
NEF	GTRPLTF	213	8	13	20		4243
NEF	RPLTFGW	216	8	20	32		4244
NEF	RPLTFGW	216	8	27	43		4245
NEF	PLTFGWCF	219	8	43	67		4246
NEF	TFGWCFKL	222	8	40	63		4247
NEF	GVGAASQDL	45	-9	11	17		4248
NEF	GVGAVSQDL	45	9	21	33		4249
NEF	GVGAVSRDL	45	9	17	27		4250
NEF	ATNADCAWL	71	9	12	22		4251
NEF	QVPLRPMTF	100	9	10	16		4252
NEF	QVPLRPMTY	100	9	46	72		4253
NEF	MTYKGAFDL	106	9	12	19		4254
NEF	FFLUKEKGG	116	9	26	41		4255

Table X
HIV A24-Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
NEF	IIFLKEKGGL	116	9	29	45		4256
NEF	IYSKKRQEI	175	9	18	29		4257
NEF	LWVYHTQGF	190	9	13	20		4258
NEF	LWVYHTQGY	190	9	21	33		4259
NEF	WVYHTQGGF	191	9	13	20		4260
NEF	WVYHTQGYF	191	9	21	33		4261
NEF	HTQGFPPDW	194	9	14	22		4262
NEF	HTQGYFPDW	194	9	25	39		4263
NEF	NTQGYFPDW	194	9	12	19		4264
NEF	GFFPDWQNY	198	9	17	27		4265
NEF	GYFPDWQNY	198	9	36	56	0.0002	4266
NEF	YTPGPGIRY	207	9	17	27		4267
NEF	YTPGPGTRF	207	9	13	20		4268
NEF	LTFGWCFKL	221	9	39	61		4269
NEF	KWSKSSIVGW	4	10	20	31		4270
NEF	GFPVRPQVPL	93	10	48	75		4271
NEF	PMTYKGAFDL	105	10	22	34		4272
NEF	SFFLKEKGGL	115	10	18	28		4273
NEF	IYSKKRQEI	174	10	18	29		4274
NEF	IYSKKRQEI	175	10	13	20		4275
NEF	DLWVYHTQGF	188	10	21	33		4276
NEF	DLWVYHTQGY	188	10	13	20		4277
NEF	LWVYHTQGGF	190	10	13	20		4278
NEF	LWVYHTQGYF	190	10	21	33		4279
NEF	NYTPGPGIRY	206	10	17	27		4280
NEF	NYTPGPGTRF	206	10	13	20		4281
NEF	GIRYPLTFGW	213	10	13	20		4282
NEF	GTRPLTFGW	213	10	12	19		4283
NEF	RPLTFGWCF	216	10	17	27		4284
NEF	RYPLTFGWCF	216	10	21	33		4285
NEF	PLTFGWCFKL	219	10	39	61		4286
NEF	LLHPIQIHGM	257	10	10	16		4287
NEF	LLHPMSQHGM	257	10	12	19		4288
NEF	HMARELHPEY	320	10	10	16		4289
NEF	NTAATNADCA	68	11	12	19		4290
NEF	PVRPQVPLRP	95	11	47	73		4291
NEF	PLRPMTYKGA	102	11	12	19		4292
NEF	FLKEKGGLDGL	117	11	26	41		4293
NEF	FLKEKGGLLEGL	117	11	29	45		4294
NEF	GLIYSKKRQEI	173	11	18	28		4295
NEF	LIYSKKRQEI	174	11	18	28		4296
NEF	DLWVYHTQGF	188	11	13	20		4297
NEF	DLWVYHTQGY	188	11	21	33		4298
NEF	VYHTQGFPPD	192	11	13	20		4299
NEF	VYHTQGYFPD	192	11	21	33		4300
NEF	DWQNYTPGPG	203	11	18	28		4301
NEF	YTPGPGIRYPL	207	11	16	25		4302
NEF	YTPGPGTRFPL	207	11	13	20		4303
NEF	CLLHPMSQHGM	256	11	10	16		4304
NEF	HMARELHPEY	320	11	10	16		4305

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
POL	FFREDLAF	1	8	15	23		4306
POL	FFRENLAF	1	8	41	64		4307
POL	GTLCNCPQI	80	8	01	33		4308
POL	PTFNFPQI	80	8	01	33		4309
POL	NFPQITLW	86	8	22	34		4310
POL	SFPQITLW	86	8	23	36		4311
POL	ITLWQRPL	90	8	47	73		4312
POL	TIKIGGQL	99	8	17	27		4313
POL	TVKIGGQL	99	8	11	17		4314
POL	TVLEDINL	118	8	13	20		4315
POL	TVLEEINL	118	8	15	23		4316
POL	DINLPCKW	122	8	13	20		4317
POL	EINLPCKW	122	8	12	19		4318
POL	MIGGIGGF	133	8	62	97		4319
POL	GFIKVRQY	139	8	53	83		4320
POL	KVRQYDOI	142	8	41	64		4321
POL	EICGIKAI	152	8	19	30		4322
POL	EICGRKAI	152	8	24	38		4323
POL	NIHGRNLL	170	8	26	41		4324
POL	NIHGRNML	170	8	31	48		4325
POL	LTQIGCTL	177	8	42	66		4326
POL	LTQIGCTL	177	8	15	23		4327
POL	QIGCTLNF	179	8	41	64		4328
POL	QLGCTLNF	179	8	16	25		4329
POL	PVKLRPGM	195	8	56	88		4330
POL	KIKALTEI	217	8	28	44		4331
POL	KIKALVEI	217	8	15	23		4332
POL	LVEICTEM	221	8	15	24		4333
POL	EMEKEGKI	229	8	42	66		4334
POL	KIGPENPY	238	8	51	80		4335
POL	RIGPENPY	238	8	11	17		4336
POL	KWRKLVDF	259	8	59	92		4337
POL	KLVDREL	262	8	63	98		4338
POL	FWEVOLGI	276	8	57	89		4339
POL	GIPHPAGL	282	8	56	89		4340
POL	VLDVGDAY	297	8	60	94		4341
POL	SVPLDKDF	306	8	18	28		4342
POL	DFRKYTAF	312	8	42	66		4343
POL	GWKGSPI	341	8	59	92		4344
POL	MTKILEPF	353	8	44	69		4345
POL	DIVIQYM	366	8	18	28		4346
POL	EIVIQYM	366	8	24	38		4347
POL	IYQYMDL	369	8	61	95		4348
POL	DLYVGSDL	375	8	63	98		4349
POL	YVGSDEI	377	8	58	91		4350
POL	FLWMGYEL	416	8	64	100		4351
POL	WTVPQIQL	428	8	28	44		4352
POL	WTVPQIVL	428	8	13	20		4353
POL	QLPEKDSW	434	8	13	20		4354
POL	VLPEKDSW	434	8	13	20		4355

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
POL	TVNDIQKL	442	8	62	97		4356
POL	KLNVKLNW	448	8	62	97		4357
POL	KLNVASQI	452	8	61	95		4358
POL	KVKQLCKL	464	8	29	45		4359
POL	KVRQLCKL	464	8	19	30		4360
POL	LLRGAKAL	471	8	30	47		4361
POL	LLRGTKAL	471	8	24	38		4362
POL	ALTDIVPL	477	8	21	33		4363
POL	ALTEVIPL	477	8	16	25		4364
POL	PLTEEAEI	483	8	30	47		4365
POL	ELAEAREI	491	8	57	89		4366
POL	YYDPSKDL	510	8	43	67		4367
POL	KTGKYAKM	542	8	19	30		4368
POL	KTGKYARM	542	8	13	21		4369
POL	HTNDVKQL	553	8	49	77		4370
POL	LTEAVQKI	560	8	34	53		4371
POL	ATESIVIW	568	8	19	30		4372
POL	IWGIKPKF	574	8	11	17		4373
POL	IWGIKPKF	574	8	48	75		4374
POL	ETWWTDYW	591	8	10	16		4375
POL	DYWQATWI	596	8	20	31		4376
POL	EYWQATWI	596	8	37	58		4377
POL	TWIPEWEF	601	8	52	81		4378
POL	EFVNTPL	607	8	54	84		4379
POL	NTPPLVKL	610	8	57	89		4380
POL	LVKLWYQL	614	8	58	91		4381
POL	PIVGAETF	625	8	28	44		4382
POL	IVGAETFY	626	8	28	44		4383
POL	TTNOKTEL	664	8	55	86		4384
POL	KTELQAIY	668	8	12	19		4385
POL	NIVDSQY	686	8	62	97		4386
POL	VTDSQYAL	688	8	59	92		4387
POL	LIKKEKYY	717	8	35	55		4388
POL	WVPAHKGI	727	8	63	98		4389
POL	GIRKVLFL	747	8	51	80		4390
POL	KVLFLDGI	750	8	50	78		4391
POL	AMASDFNL	773	8	45	70		4392
POL	QVDCSPGI	805	8	57	89		4393
POL	CTHLEGKI	817	8	35	55		4394
POL	HLEKIL	819	8	31	48		4395
POL	HLEKIVIL	819	8	23	36		4396
POL	AVHVASGY	828	8	59	92		4397
POL	GYIEAEVI	834	8	54	84		4398
POL	ETGOETAY	844	8	59	92		4399
POL	ILKLAGRW	853	8	34	53		4400
POL	LLKLAGRW	853	8	25	39		4401
POL	HTDNGSNF	866	8	51	80		4402
POL	TTVKAACW	876	8	15	23		4403
POL	AVKAACWW	877	8	32	50		4404
POL	TVKAACWW	877	8	24	38		4405

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HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
POL	GIQEFGI	886	8	22	34		4406
POL	GIQEFGI	886	8	11	17		4407
POL	HLKTAQM	923	8	57	89		4408
POL	AVQMAVFI	927	8	60	94		4409
POL	NFKRGGI	936	8	60	94		4410
POL	GYSAGERI	945	8	57	89		4411
POL	QIKIQNF	968	8	12	19		4412
POL	QTKIQNF	968	8	35	55		4413
POL	KIQNFVY	971	8	52	81		4414
POL	IWKGPAPL	986	8	36	56		4415
POL	LWKGPAKL	986	8	19	30		4416
POL	VIQNSDI	1003	8	37	58		4417
POL	VIQDSEI	1003	8	12	19		4418
POL	PTRELQVW	30	9	13	20		4419
POL	GTTLNFPQI	79	9	01	17		4420
POL	AISLSLPQI	80	9	01	33		4421
POL	SFSFQITL	84	9	14	22		4422
POL	QITLWQPL	89	9	47	73		4423
POL	LWQRLVTI	92	9	21	33	0.0190	4424
POL	VTIKIGQL	98	9	17	27		4425
POL	VTVKIGQL	98	9	11	17		4426
POL	DTGADDTVL	112	9	61	95		4427
POL	DTVLEDINL	117	9	13	20		4428
POL	DTVLEENL	117	9	14	22		4429
POL	KMIGGIGF	132	9	62	97		4430
POL	MIGGIGFI	133	9	62	97	0.0011	4431
POL	KVRQYDQIL	142	9	21	33		4432
POL	QYDQILIEI	145	9	27	42		4433
POL	QYDQIPIEI	145	9	12	19		4434
POL	LVGTPVNI	163	9	54	84		4435
POL	PVNIIGRNL	168	9	26	41		4436
POL	PVNIIGRNM	168	9	24	38		4437
POL	LLTQIGCTL	176	9	21	33		4438
POL	MLTQIGCTL	176	9	18	28		4439
POL	MLTQLGCTL	176	9	10	16		4440
POL	TLNFPISPI	183	9	61	97		4441
POL	PIETVPVKL	190	9	53	83		4442
POL	QWPLTEEKI	210	9	56	88		4443
POL	LTEEKIKAL	213	9	56	88		4444
POL	ALVEICTEM	220	9	15	23		4445
POL	PYNTPIFAI	244	9	24	38	0.0310	4446
POL	PYNTPVFAI	244	9	37	57		4447
POL	ELNKRQDF	268	9	56	88		4448
POL	DFWEVQLGI	275	9	57	89		4449
POL	TVLDVGDAY	296	9	56	88		4450
POL	VLDVGDAYF	297	9	57	89		4451
POL	PLDKDFRKY	308	9	60	94		4452
POL	YTAFTPSI	316	9	19	30		4453
POL	SINNETPGI	323	9	37	58		4454
POL	SINNETPGI	323	9	32	50		4455
POL	SINNETPGI	323	9	11	17		4455

Table X
HIV A24-Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
POL	ETPGIRYQY	327	9	52	81		4456
POL	GIRYQYNVL	330	9	52	81		4457
POL	QYNVLPQGW	334	9	63	98	0.0036	4458
POL	GWKSPAF	341	9	59	92		4459
POL	IFQSSMTKI	348	9	38	59	0.0029	4460
POL	SMTKILEPF	352	9	43	67	0.0110	4461
POL	PERKQNPDI	359	9	16	25		4462
POL	VIYQMDL	368	9	51	80		4463
POL	IYQYMDL	369	9	61	95	0.0130	4464
POL	LYVGSLEI	376	9	58	91		4465
POL	EIQHIRAKI	383	9	26	41		4466
POL	EIGOIRTKI	383	9	21	33		4467
POL	KIEELREHL	390	9	19	30		4468
POL	ELREHLKW	393	9	17	27		4469
POL	ELRQHLLRW	393	9	15	23		4470
POL	PFLWMGYEL	415	9	64	100		4471
POL	GYELIIPDKW	420	9	60	94	0.0001	4472
POL	KWTVOPIQL	427	9	28	44		4473
POL	KWTVOPIVL	427	9	12	19		4474
POL	IVLPEKDSW	433	9	13	20		4475
POL	WTVNDIQKL	441	9	62	97		4476
POL	DIQKLVGKL	445	9	62	97		4477
POL	KLNVASQIY	452	9	60	94		4478
POL	KVKQLCKLL	464	9	28	44		4479
POL	KVRQLCKLL	464	9	19	30		4480
POL	KLRGAKAL	470	9	25	40		4481
POL	KLRGTAKAL	470	9	24	38		4482
POL	GTKALTEVI	474	9	11	17		4483
POL	LTEEALELE	484	9	37	58		4484
POL	ELAEAREIL	491	9	57	89		4485
POL	VYDPSKDL	509	9	39	61	0.0004	4486
POL	YDPSKDLI	510	9	35	55		4487
POL	TYQIQEPF	530	9	42	66	0.3000	4488
POL	IYQEPKLN	533	9	40	63	0.0520	4489
POL	QLTEAVQKI	559	9	34	53		4490
POL	KIATESIVI	566	9	14	22		4491
POL	VIWGTTPKF	573	9	47	73		4492
POL	KTPKFKLPI	577	9	17	27		4493
POL	KTPKFKLPI	577	9	29	45		4494
POL	KLPQKETW	582	9	20	31		4495
POL	RLPIQKETW	582	9	26	41		4496
POL	WTETWWTDY	589	9	10	16		4497
POL	WTETWWTDY	589	9	10	16		4498
POL	WTETWWTDY	589	9	10	16		4499
POL	WTETWWTDY	589	9	10	16		4500
POL	WTEYWQATW	594	9	24	38		4501
POL	ATWPEWEF	600	9	52	81		4502
POL	NTPLVKLW	610	9	57	89		4503
POL	PLVKLWYQL	613	9	54	84		4504
POL	WYQLEKDP	618	9	14	22		4505

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*2401	SEQ ID NO
POL	WYQLEKEPI	618	9	31	48		4506
POL	WYQLETEPI	618	9	11	17	0.0001	4507
POL	PIVGAETFY	625	9	28	44		4508
POL	ETKLGKAGY	641	9	35	55		4509
POL	DTTNQKTEL	663	9	26	41		4510
POL	ETTNQKTEL	663	9	29	45		4511
POL	KTELQAIHL	668	9	15	23		4512
POL	KTELQAIYL	668	9	12	19		4513
POL	ELQAIHLAL	670	9	16	25		4514
POL	ELQAIYLAL	670	9	12	19		4515
POL	HLALQDSGL	675	9	15	23		4516
POL	IVTDSQYAL	687	9	59	92		4517
POL	LVNQIEQL	709	9	19	30		4518
POL	LVSQIEQL	709	9	19	30		4519
POL	LIKKEKYYL	716	9	28	44		4520
POL	LIKKEKYYL	717	9	35	55		4521
POL	AWVPAHKGI	726	9	22	34		4522
POL	SWVPAHKGI	726	9	37	58		4523
POL	KYHSNWRAM	766	9	28	44		4524
POL	RYHSNWRAM	766	9	11	17		4525
POL	NWRAMASDF	770	9	43	67	0.0016	4526
POL	QVDCSPGIW	805	9	57	89		4527
POL	IWQLDCTHL	812	9	59	92	0.0095	4528
POL	CTHLEGGKII	817	9	35	55		4529
POL	CTHLEGGKVI	817	9	26	41		4530
POL	AVHVASGYI	828	9	53	83		4531
POL	ETQGETAYF	844	9	57	89		4532
POL	ETAYFILKL	848	9	31	48		4533
POL	ETAYFLLKL	848	9	27	42		4534
POL	FILKLAGRW	852	9	32	50		4535
POL	FLKLAGRW	852	9	25	39		4536
POL	STTVKAACW	875	9	15	23		4537
POL	TTVKAACWW	876	9	15	23		4538
POL	WWAGIKQEF	883	9	21	33	0.0120	4539
POL	WWAGIQQEF	883	9	11	17		4540
POL	VVESMNKEL	902	9	48	75		4541
POL	SMNKELKKI	905	9	53	83		4542
POL	QVRDQAEHL	916	9	48	75		4543
POL	QVREQAEHL	916	9	13	20		4544
POL	KTAVQMAVF	925	9	57	89		4545
POL	QMAVFIHNF	929	9	60	94	0.0190	4546
POL	GYSAGERII	945	9	41	64		4547
POL	IIDIIASDI	952	9	12	19		4548
POL	IIDIIATDI	952	9	29	45		4549
POL	IVDIIATDI	952	9	12	19		4550
POL	ATDIQTKEL	957	9	35	55		4551
POL	QTKELQKQI	961	9	46	72		4552
POL	ELQKQIKI	964	9	13	21		4553
POL	ELQKQITKI	964	9	34	54		4554
POL	KIQNFRVYY	971	9	52	81		4555

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
POL	YYRDSRDPI	978	9	34	53		4556
POL	YYRDSRDPI	978	9	14	22		4557
POL	PIWKGPAKL	985	9	36	56		4558
POL	PLWKGPAKL	985	9	19	30		4559
POL	IWKGPAPKL	986	9	35	55		4560
POL	LWKGPAKLL	986	9	18	28		4561
POL	VVIQNSDI	1002	9	37	58		4562
POL	VVIQNSDI	1002	9	12	19		4563
POL	VVPRRKAKI	1012	9	51	80		4564
POL	VVPRRKAKI	1012	9	11	17		4565
POL	IKDYGKOM	1020	9	11	17		4566
POL	IIRDYGKOM	1020	9	50	78		4567
POL	AFQGEAREF	7	10	10	16		4568
POL	STNSPTSREL	32	10	01	33		4569
POL	GTLCNPQITL	80	10	01	33		4570
POL	PTFNFPQITL	80	10	01	33		4571
POL	SFSFPQITLW	84	10	13	20		4572
POL	TLWQRPLVTI	91	10	21	33		4573
POL	LVTIKIGGQL	97	10	13	20		4574
POL	KIGGQLKEAL	101	10	23	36		4575
POL	NLPGKWKPKM	124	10	35	55		4576
POL	KWKPKMIGGI	128	10	42	66		4577
POL	RWKPKMIGGI	128	10	17	27		4578
POL	KMIGGIGGI	132	10	62	97	0.0001	4579
POL	FIKVRQYDQI	140	10	41	64		4580
POL	KVRQYDQILI	142	10	20	31		4581
POL	KVRQYDQIFI	142	10	13	20		4582
POL	LIEICGHKAI	150	10	10	16		4583
POL	LIEICGHKAI	150	10	13	20		4584
POL	VLGPTPVNI	162	10	53	83		4585
POL	LVGPTPVNII	163	10	52	81		4586
POL	PVNIIGRNLL	168	10	26	41		4587
POL	PVNIIGRNML	168	10	24	38		4588
POL	IIGRNLLTQI	171	10	21	33		4589
POL	IIGRNMLTQI	171	10	18	28		4590
POL	IIGRNMLTQL	171	10	11	17		4591
POL	NMLTQIGCTL	175	10	21	33		4592
POL	NMLTQIGCTL	175	10	18	28		4593
POL	NMLTQIGCTL	175	10	10	16		4594
POL	LTOIGCTLNF	177	10	41	64		4595
POL	LTOIGCTLNF	177	10	15	23		4596
POL	QIGCTLNFPI	179	10	41	64		4597
POL	QLGCTLNFPI	179	10	16	25		4598
POL	CTLNFPISPI	182	10	60	94		4599
POL	TVPVKLKPGM	193	10	54	84		4600
POL	GMDGPKVKQ	201	10	51	80		4601
POL	PLTEEKIKAL	212	10	54	84		4602
POL	CTEMEKEGKI	225	10	27	42		4603
POL	AIKKDSTKW	251	10	57	89		4604
POL	STKWRKLVDF	257	10	58	91		4605

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
POL	ELNKRQTDFW	268	10	57	89		4606
POL	RTQDFWEVQL	272	10	53	83		4607
POL	QLGPHIPAGL	280	10	56	89		4608
POL	VTVLVDVGDAY	295	10	56	88		4609
POL	TVLVDVGDAYF	296	10	57	89		4610
POL	YFSVPLDKDF	304	10	18	29		4611
POL	DERKYTAFTI	312	10	42	66		4612
POL	KYTAFTPSI	315	10	37	58		4613
POL	AIQSSMTKI	347	10	36	56		4614
POL	IFQSSMTKIL	348	10	38	59	0.0002	4615
POL	IVIYQYMDL	367	10	42	66		4616
POL	VIYQYMDL	368	10	51	80		4617
POL	DLYVGSLEI	375	10	58	91		4618
POL	KIEELREHL	390	10	19	30		4619
POL	KIEELROHLL	390	10	17	27		4620
POL	PIQLPEKDSW	432	10	13	20		4621
POL	PIVLPEKDSW	432	10	13	20		4622
POL	SWTVNDIQKL	440	10	54	84		4623
POL	NWASQIYAGI	454	10	27	42		4624
POL	NWASQIYPGI	454	10	29	45		4625
POL	IYAGIKVKQL	459	10	18	28		4626
POL	IYPGIKVKQL	459	10	11	17		4627
POL	IYPGIKVRQL	459	10	15	23		4628
POL	GIKVKQLCKL	462	10	28	44		4629
POL	GIKVRQLCKL	462	10	18	28		4630
POL	IVPLTEEAEL	481	10	13	20		4631
POL	VIPLTEEAEL	481	10	11	17		4632
POL	PLTEEAEL	483	10	30	47		4633
POL	ELELAENREI	489	10	53	83		4634
POL	ILKEPVHGVY	498	10	40	63		4635
POL	GVYYDPKDL	508	10	38	59		4636
POL	VYYDPKDL	509	10	31	48	0.0150	4637
POL	EIQKQGQDOW	520	10	13	20		4638
POL	EIQKQGQGW	520	10	15	23		4639
POL	WTYQIQEPF	529	10	42	66		4640
POL	QIQEPEKNL	532	10	40	63		4641
POL	PEKNLKTGKY	537	10	45	70		4642
POL	NLKTGKYAKM	540	10	18	29		4643
POL	NLKTGKYARM	540	10	13	21		4644
POL	AVQKIATESI	563	10	10	16		4645
POL	KIATESIVW	566	10	14	22		4646
POL	IVIWGKTPKF	572	10	47	73		4647
POL	IWGKTPKFL	574	10	17	27		4648
POL	IWGKTPKFL	574	10	30	47		4649
POL	PIQKETWEAW	584	10	15	23		4650
POL	PIQKETWETW	584	10	27	42		4651
POL	ETWETWWT	588	10	10	16		4652
POL	ETWETWWT	588	10	10	16		4653
POL	TWETWWT	589	10	10	16		4654
POL	WWTDYWQAT	593	10	14	22		4655

Table X
HIV A24 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
POL	WTEYWQAT	593	10	23	36		4656
POL	WTDYWQATW	594	10	14	22		4657
POL	WTEYWQATW	594	10	24	38		4658
POL	YWQATWIPE	597	10	52	81		4659
POL	EWEFVNTPL	605	10	50	78		4660
POL	FVNTPPLVKL	608	10	54	86	0.0660	4661
POL	NTPLVLKLY	610	10	57	89		4662
POL	LWYQLEKDP	617	10	14	22		4663
POL	LWYQLEKEPI	617	10	31	48		4664
POL	LWYQLETEPI	617	10	11	17		4665
POL	EVNIVTDSQY	684	10	59	92		4666
POL	NIVTDSQYAL	686	10	59	92		4667
POL	VTDQYALGI	688	10	58	91		4668
POL	ELVNQIEQL	708	10	18	28		4669
POL	ELVSQIEQL	708	10	19	30		4670
POL	LVNQEQLI	709	10	19	30		4671
POL	LVSQIEQLI	709	10	19	30		4672
POL	QLIKKEKVL	716	10	28	44		4673
POL	QVDKLVSAGI	739	10	15	23		4674
POL	QVDKLVSSGI	739	10	29	45		4675
POL	LVSAGIRKVL	743	10	15	23		4676
POL	LVSSGIRKVL	743	10	26	41		4677
POL	NLPPVAKEL	779	10	27	42		4678
POL	NLPPVAKEL	779	10	27	42		4679
POL	IVASCDKCOL	788	10	43	67		4680
POL	GIWQLDCTHL	811	10	59	92		4681
POL	CTHLEGRH	817	10	31	48		4682
POL	CTHLEGRVIL	817	10	23	36		4683
POL	LVAHVVASGY	826	10	53	83		4684
POL	ETGQETAYFI	844	10	31	48		4685
POL	ETGQETAYFL	844	10	26	41		4686
POL	YFLLKLAGRW	851	10	31	48		4687
POL	YFLLKLAGRW	851	10	25	39		4688
POL	TIHTDNGSNF	864	10	14	22		4689
POL	VHTDNGSNF	864	10	24	38		4690
POL	STTVKAACW	875	10	15	23		4691
POL	CWWAGIQQEF	882	10	21	33		4692
POL	CWWAGIQQEF	882	10	11	17		4693
POL	GIQEFEGIPY	886	10	22	34		4694
POL	GIQEFEGIPY	886	10	11	17		4695
POL	GVVSMNKL	901	10	48	75		4696
POL	SMNKLKKII	905	10	53	83		4697
POL	KTAVQMAVFI	925	10	56	88		4698
POL	RIIDIASDI	951	10	12	19		4699
POL	RIIDIASDI	951	10	29	45		4700
POL	RIVDIATDI	951	10	12	19		4701
POL	QTKELQKQII	961	10	10	16		4702
POL	IKIQNFRVY	969	10	12	19		4703
POL	ITKIQNFRVY	969	10	36	57		4704
POL	VYRDSRDPI	977	10	34	53		4705

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
POL	VYRDSRDPL	977	10	14	22		4706
POL	YYRDSRDPIW	978	10	34	53		4707
POL	YYRDSRDPLW	978	10	14	22		4708
POL	PIWKGPAKLL	985	10	35	55		4709
POL	PLWKGPAKLL	985	10	18	28		4710
POL	IWKGPAPKLLW	986	10	35	55		4711
POL	LWKGPAKLLW	986	10	18	28		4712
POL	LWKGGAIVI	994	10	59	92		4713
POL	AVVIQDSDI	1000	10	37	58		4714
POL	AVVIQDSEI	1000	10	12	19		4715
POL	KVPRRKAKI	1011	10	51	80		4716
POL	KVPRRKVKI	1011	10	11	17		4717
POL	VVPRRKAKII	1012	10	50	78		4718
POL	VVPRRKVKII	1012	10	11	17		4719
POL	KIKDYGKQM	1019	10	11	17		4720
POL	KIIRDYGKQM	1019	10	50	78		4721
POL	GTTLNFPQITF	79	11	01	17		4722
POL	AISLSPQITL	80	11	01	33		4723
POL	GTLNCPQITL	80	11	01	33		4724
POL	PTNFFQITLW	80	11	01	33		4725
POL	ITLWQRLVIT	90	11	19	30		4726
POL	LWQRLPLVTIKI	92	11	14	22		4727
POL	LWQRLPLVTIK	92	11	12	19		4728
POL	PLVTIKIGGQL	96	11	13	20		4729
POL	KIGGQLKEALL	101	11	23	36		4730
POL	LLDTGADDTV	110	11	61	95		4731
POL	VLEDINLPKW	119	11	13	20		4732
POL	VLEENLPKW	119	11	12	19		4733
POL	NLPKWPKKM	124	11	35	55		4734
POL	GIGGFIKVRQY	136	11	53	83		4735
POL	GFIKVRQYDQI	139	11	41	64		4736
POL	FIKVRQYDQIL	140	11	21	33		4737
POL	ILIEICGKKAI	149	11	13	20		4738
POL	TVLVGPTPVNI	161	11	53	83		4739
POL	VLVGPPTVNI	162	11	51	80		4740
POL	PTPVNIIGRNL	166	11	26	41		4741
POL	PTPVNIIGRNM	166	11	24	38		4742
POL	NIIGRNLLTQI	170	11	21	33		4743
POL	NIIGRNMLTQI	170	11	18	28		4744
POL	NIIGRNMLTQL	170	11	21	33		4745
POL	LLTQIGCTLNF	176	11	21	33		4746
POL	MLTQIGCTLNF	176	11	17	27		4747
POL	MLTQIGCTLN	176	11	10	16		4748
POL	ETVPVKLPG	192	11	51	80		4749
POL	EMEKEGKISKI	229	11	32	50		4750
POL	KISKIGPENPY	235	11	41	64		4751
POL	KISRIGPENPY	235	11	11	17		4752
POL	KWRKLVDFRE	259	11	59	92		4753
POL	GLKKKSVTV	288	11	49	77		4754
POL	SVTVLDVGDA	294	11	56	88		4755

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HIV A24 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*240I	SEQ ID NO
POL	VTVLVDGDAY	295	11	56	88		4756
POL	DVGDAYFSVP	299	11	54	84		4757
POL	AYFSVPLDKDF	303	11	18	28		4758
POL	SVPLDKDFRK	306	11	18	28		4759
POL	SINNETPGIRY	323	11	32	50		4760
POL	STNETPGIRY	323	11	11	17		4761
POL	RYQYNVLPQG	332	11	63	98		4762
POL	AIFQSSMTKIL	347	11	36	56		4763
POL	PFKQNPDIIV	359	11	14	22		4764
POL	DIVYQYMDL	366	11	18	28		4765
POL	EIVYQYMDL	366	11	24	38		4766
POL	IIVYQYMDL	367	11	42	66		4767
POL	YMDLTVVGS	372	11	61	95		4768
POL	DLEIGQIRAKI	381	11	26	41		4769
POL	DLEIGQIRTKI	381	11	20	31		4770
POL	RTKIELRQIIL	388	11	14	22		4771
POL	ELREHLKKG	393	11	14	22		4772
POL	ELROHLRWG	393	11	12	19		4773
POL	WNGYELIIPDK	418	11	60	94		4774
POL	DIQKLVGKLN	445	11	62	97		4775
POL	LVGKLNWASQ	449	11	60	94		4776
POL	QIYAGIKVKQL	458	11	18	29		4777
POL	QIYFGIKVKOL	458	11	11	17		4778
POL	QIYFGIKVRQL	458	11	14	22		4779
POL	GIKVKQLCKLL	462	11	27	42		4780
POL	GIKVRQLCKLL	462	11	18	28		4781
POL	LLRGAKALTDI	471	11	22	34		4782
POL	GTKALTEVIPL	474	11	11	17		4783
POL	DIVPLTEEAEL	480	11	13	20		4784
POL	EVIPLTEEAEL	480	11	11	17		4785
POL	ELELAENREIL	489	11	53	83		4786
POL	ILKEPVHGVY	497	11	40	63		4787
POL	ILKEPVHGVY	498	11	38	59		4788
POL	GVYYDFPSKDLI	508	11	31	48		4789
POL	QWTYQIYQEP	528	11	42	66		4790
POL	SIVWGKTPKF	571	11	41	64		4791
POL	VIWGKTPKF	573	11	17	27		4792
POL	VIWGKTPKFR	573	11	29	45		4793
POL	KFKLPIQKETW	580	11	20	31		4794
POL	KFKLPIQKETW	580	11	26	41		4795
POL	PIKETWEAW	584	11	15	23		4796
POL	PIKETWETW	584	11	27	42		4797
POL	ETWETWETD	588	11	10	16		4798
POL	TWWTDYWQA	592	11	10	16		4799
POL	TWWTDYWQA	592	11	12	19		4800
POL	WWTDYWQAT	593	11	14	22		4801
POL	WWTDYWQAT	593	11	23	36		4802
POL	DYWQATWIPE	596	11	19	30		4803
POL	EYWQATWIPE	596	11	33	52		4804
POL	EFVNTPLVKL	607	11	54	84		4805

Table X
HIV A24 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
POL	FVNTPLVLKL	608	11	54	86		4806
POL	KLWYQLEKDPH	616	11	14	22		4807
POL	KLWYQLEKEPI	616	11	31	48		4808
POL	KLWYQLETEPI	616	11	11	17		4809
POL	LTDTTNQKTE	661	11	19	30		4810
POL	LTETTNQKTE	661	11	25	39		4811
POL	TTNQKTELHAI	664	11	12	19		4812
POL	TTNQKTELQAI	664	11	42	66		4813
POL	KTELQAIHLAL	668	11	15	23		4814
POL	KTELQAIYLAL	668	11	12	19		4815
POL	AIHLALQDSGL	673	11	15	23		4816
POL	ALQDSGLEVNI	677	11	27	42		4817
POL	ALQDSGSEVNI	677	11	25	39		4818
POL	IVTDSQYALGI	687	11	58	91		4819
POL	VTDSQYALGII	688	11	58	91		4820
POL	ELVNQIEQLI	708	11	18	28		4821
POL	ELYSQIEQLI	708	11	19	30		4822
POL	LIKKEKVYLA	717	11	20	31		4823
POL	LIKKEKVYLSW	717	11	13	20		4824
POL	YLAWVPPIHKG	724	11	22	34		4825
POL	YLSWVPPIHKG	724	11	37	58		4826
POL	GIGGNEQVDKL	733	11	58	91		4827
POL	KLVSAGIRKVL	742	11	15	23		4828
POL	KLVSAGIRKVL	742	11	26	41		4829
POL	LVSSGIRKVL	743	11	15	23		4830
POL	LVSSGIRKVL	743	11	26	41		4831
POL	GIRKVLFLDGI	747	11	49	77		4832
POL	NWRAMASDF	770	11	41	64		4833
POL	AMASDFNLPI	773	11	18	28		4834
POL	EIVASCDKQCL	787	11	43	67		4835
POL	QVDCSPGIWQ	805	11	56	88		4836
POL	QLDCTHLEGI	814	11	33	52		4837
POL	ILVAHVHVASGY	825	11	53	83		4838
POL	LVAVHVASGYI	826	11	47	73		4839
POL	ETGQETAYFIL	844	11	31	48		4840
POL	ETGQETAYFLL	844	11	26	41		4841
POL	AYFILKLGR	850	11	31	48		4842
POL	AYFLKLGR	850	11	25	39		4843
POL	KLGRWPVKV	855	11	13	20		4844
POL	KLGRWPVKV	855	11	22	34		4845
POL	KVIHTDNGSNF	863	11	21	33		4846
POL	FTSAAVKAAC	873	11	27	42		4847
POL	FTSTTVKAAC	873	11	14	22		4848
POL	AVKAACWVA	877	11	10	16		4849
POL	TVKAACWVA	877	11	20	31		4850
POL	WWAGIKQEF	883	11	21	33		4851
POL	WWAGIQEF	883	11	57	89		4852
POL	HLKTAVQMAV	923	11	60	94		4853
POL	AVQMAVFIH	927	11	58	91		4854
POL	FIHFKRKG	933	11	58	91		4855

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HIV A24 Super-Motif Peptides With Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
POL	NFKRKGIGGY	936	11	59	92		4856
POL	GIGGSAGERI	942	11	57	89		4857
POL	GYSAGERIIDI	945	11	40	63		4858
POL	GYSAGERIIDI	945	11	14	22		4859
POL	IASDIOTKEL	955	11	14	22		4860
POL	IATIDIOTKEL	955	11	34	53		4861
POL	DIOTKELOKQI	959	11	44	69		4862
POL	QIKIQNFRVY	968	11	12	19		4863
POL	QITKIQNFRVY	968	11	35	55		4864
POL	IKIQNFRVY	969	11	12	19		4865
POL	ITKIQNFRVY	969	11	36	57		4866
POL	RVYRDSRDI	976	11	34	53		4867
POL	RVYRDSRDI	976	11	14	22		4868
POL	VYRDSRDI	977	11	34	53		4869
POL	VYRDSRDI	977	11	14	22		4870
POL	VYRDSRDI	977	11	35	55		4871
POL	PLWKGPAKLL	985	11	18	28		4872
POL	LLWKGPAKLL	985	11	59	92		4873
POL	LLWKGPAKLL	993	11	50	78		4874
POL	KVPRRKAKII	1011	11	11	17		4875
POL	KVPRRKAKII	1011	11	11	17		4876
REV	LLKTIVLJ	12	8	11	17		4877
REV	AVRIKIL	17	8	13	20		4878
REV	ILYQSNPY	23	8	27	42		4879
REV	QLPPIERL	78	8	14	22		4880
REV	QLPPIERL	78	8	37	58		4881
REV	LVEPAVL	114	8	11	17		4882
REV	AVRIKILY	17	9	13	20		4883
REV	KILYQSNPY	22	9	26	41		4884
REV	RWRARQOI	48	9	35	55		4885
REV	RWRARQOI	48	9	11	17		4886
REV	PVPLQLPPI	74	9	11	17		4887
REV	PVPLQLPPI	74	9	35	55		4888
REV	PLQLPIERL	76	10	11	17		4889
REV	PLQLPIERL	76	10	34	53		4890
REV	QLPPIERLTL	78	10	18	28		4891
REV	GTQGVGSPQI	97	10	11	18		4892
REV	IKILYQSNPY	20	11	18	28		4893
TAT	CYCKKCCF	28	8	11	17		4894
TAT	CYCKKCCY	28	8	11	17		4895
TAT	CFHCQVCF	34	8	11	17		4896
TAT	FLNKGLGI	41	8	14	22		4897
TAT	PVDPNLEPW	3	9	20	31		4898
TAT	PVDPNLEPW	3	9	14	22		4899
TAT	CFLNKGLGI	40	9	14	22		4900
TAT	FLNKGLGISY	41	10	14	22		4901
TAT	CFLNKGLGISY	40	11	14	22		4902
VIF	RWQVLIVW	4	8	10	16		4903
VIF	RWQVMIW	4	8	43	67		4904
VIF	IVWQVDRM	9	8	59	92		4905
VIF	KIRTWNSL	17	8	12	19		4905

Table X
HIV A24 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
VIF	RIRTWKSL	17	8	15	23		4906
VIF	RIRTWNSL	17	8	15	23		4907
VIF	SLVKHIMY	23	8	44	69		4908
VIF	LVKHHIMYI	24	8	19	30		4909
VIF	GWFYRHHY	37	8	20	31		4910
VIF	KISSEVHI	50	8	15	23		4911
VIF	KVSSEVHI	50	8	20	31		4912
VIF	RISSEVHI	50	8	15	23		4913
VIF	RLVITYW	65	8	12	19		4914
VIF	VIKTYWGL	67	8	10	16		4915
VIF	VITYWGL	67	8	22	34		4916
VIF	VVRTYWGL	67	8	10	16		4917
VIF	VVTYWGL	67	8	11	17		4918
VIF	HLGHGVS	83	8	25	39		4919
VIF	HLGGQVSI	83	8	26	41		4920
VIF	GVSEWRL	87	8	18	28		4921
VIF	STQIDPDL	100	8	12	19		4922
VIF	STQVDPL	100	8	11	17		4923
VIF	QLIHLYF	110	8	14	22		4924
VIF	QLHIMHYF	110	8	16	22		4925
VIF	HLYYFDCF	113	8	15	23		4926
VIF	HMIYFDCF	113	8	15	23		4927
VIF	IVSPRCEY	133	8	14	22		4928
VIF	KVGSLOYL	146	8	52	81		4929
VIF	QYLALAL	151	8	12	19		4930
VIF	QYLALKAL	151	8	11	17		4931
VIF	QYLALTAL	151	8	33	52		4932
VIF	YLALTALI	152	8	28	44		4933
VIF	ALIKPKKI	157	8	10	16		4934
VIF	PLPSVKKL	168	8	21	33		4935
VIF	PLPSVRKL	168	8	14	22		4936
VIF	MIVWQVDRM	8	9	46	72		4937
VIF	VWQVDRMKI	10	9	13	20		4938
VIF	VWQVDRMRI	10	9	48	75		4939
VIF	SLVKHHIMYI	23	9	19	30		4940
VIF	HIPLGDARL	56	9	13	20		4941
VIF	HIPLGEARL	56	9	20	31		4942
VIF	PLGEARLVI	58	9	10	16		4943
VIF	LVIKTYWGL	66	9	10	16		4944
VIF	LVITYWGL	66	9	22	34		4945
VIF	GLHTGERDW	73	9	22	34		4946
VIF	GLQTGERDW	73	9	12	19		4947
VIF	HTGERDWHL	75	9	21	33		4948
VIF	QTERDWHL	75	9	12	19		4949
VIF	SIEWRURY	89	9	11	17		4950
VIF	DLADQLJHL	106	9	18	28		4951
VIF	GLADQLIIM	106	9	15	23		4952
VIF	QYLALTALI	151	9	28	44		4953
VIF	VMIVWQVDR	7	10	44	69		4954
VIF	IVWQVDRMKI	9	10	12	19		4955

Table X
HIV A24-Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
VIF	IVWQVDRMRI	9	10	47	73		4956
VIF	QVDRMKIRTW	12	10	12	19		4957
VIF	QVDRMRINTW	12	10	10	16		4958
VIF	QVDRMRIRTW	12	10	31	48		4959
VIF	RMKIRTWNSL	15	10	12	19		4960
VIF	RMIRTWKSL	15	10	15	23		4961
VIF	RMIRTWNSL	15	10	15	23		4962
VIF	TKSLVKIHH	20	10	16	25		4963
VIF	TWNSLVKHH	20	10	25	39		4964
VIF	KISSEVHIPL	50	10	14	22		4965
VIF	KVSSEVHIPL	50	10	19	30		4966
VIF	RISSEVHIPL	50	10	13	20		4967
VIF	RLVITYTWGL	65	10	12	19		4968
VIF	DWHLGHGVS	81	10	21	33		4969
VIF	DWHLGQVSI	81	10	18	28		4970
VIF	ILGHGVSIEW	83	10	25	39		4971
VIF	ILGQGVSEW	83	10	26	41		4972
VIF	RYSTQVDPGL	98	10	10	16		4973
VIF	QIDPDLADQL	102	10	10	16		4974
VIF	QVDPGLADQL	102	10	14	22		4975
VIF	LHILYYFDCF	111	10	16	25		4976
VIF	LHIMHYFDCF	111	10	15	23		4977
VIF	YFDCFSNAI	116	10	28	44		4978
VIF	KVGSLOYLAL	146	10	51	80		4979
VIF	SLOYLALAL	149	10	12	19		4980
VIF	SLOYLALKAL	149	10	11	17		4981
VIF	SLOYLALTAL	149	10	31	48		4982
VIF	SVKKLTEDRW	174	10	13	20		4983
VIF	QVMIVWQVDR	6	11	43	67		4984
VIF	MIVWQVDRM	8	11	43	67		4985
VIF	RTWNSLVKHH	19	11	14	22		4986
VIF	RTWNSLVKHH	19	11	24	38		4987
VIF	RTWNSLVKHH	20	11	16	25		4988
VIF	TKSLVKHH	20	11	22	34		4989
VIF	EVHPLGDARL	54	11	13	20		4990
VIF	EVHPLGEARL	54	11	20	31		4991
VIF	HIPLGEARLVI	56	11	10	16		4992
VIF	YWGLHTGERD	71	11	22	34		4993
VIF	YWGLQTGERD	71	11	12	19		4994
VIF	GLHTGERDWH	73	11	21	33		4995
VIF	GLQTGERDWH	73	11	12	19		4996
VIF	GVSEWRLLR	87	11	10	16		4997
VIF	QIDPDLADQLI	102	11	10	16		4998
VIF	QVDPGLADQLI	102	11	14	22		4999
VIF	GLADQLIHHM	106	11	11	17		5000
VIF	QLIHLYYFDCF	110	11	13	20		5001
VIF	QLIHMYFDCF	110	11	14	22		5002
VIF	YYFDCFSNAI	115	11	20	31		5003
VIF	CFSDSAIRKAI	119	11	10	16		5004
VIF	CFSESARIRKAI	119	11	12	19		5005

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*240I	SEQ ID NO
VIF	CFSESAINAI	119	11	12	19		5006
VIF	SLQYLALTAI	149	11	27	42		5007
VIF	LIKPKKIPPL	158	11	10	16		5008
VIF	KTKGIRGSHIT	188	11	15	23		5009
VPR	ALELLEEL	19	8	10	16		5010
VPR	LELLEEL	19	8	44	69		5011
VPR	AVRHPRRI	30	8	14	22		5012
VPR	WLHGLGQY	38	8	11	17		5013
VPR	TWAGVEAI	53	8	16	25		5014
VPR	TWEGVEAI	53	8	20	31		5015
VPR	GVEAIRI	56	8	34	53		5016
VPR	IRILQQL	60	8	42	66		5017
VPR	IRILQQLLF	62	8	45	70		5018
VPR	ILOQLLF	63	8	37	58		5019
VPR	LLFVHFRI	67	8	44	69		5020
VPR	LLFVHFRI	67	8	12	19		5021
VPR	PYNEWTLLEL	14	9	30	47	0.1400	5022
VPR	WTLLELEL	18	9	42	69		5023
VPR	AVRHPRPW	30	9	14	22		5024
VPR	AVRHPRPW	30	9	34	53		5025
VPR	PWLIIGLQY	37	9	11	17		5026
VPR	WLHGLGQHI	38	9	20	31		5027
VPR	IYETYGDTW	46	9	31	48		5028
VPR	IYNTYGDTW	46	9	18	28		5029
VPR	DTWAGVEAI	52	9	16	25		5030
VPR	DTWEGVEAI	52	9	20	31		5031
VPR	TWAGVEAI	53	9	16	25		5032
VPR	TWEGVEAI	53	9	19	30		5033
VPR	GVEAIRIL	56	9	34	53		5034
VPR	AIRILQQL	59	9	39	61		5035
VPR	IRILQQL	60	9	42	66		5036
VPR	RILQQLFI	62	9	36	56		5037
VPR	QLLFHFRI	66	9	44	69		5038
VPR	QLLFVHFRI	66	9	10	16		5039
VPR	RIGCOHSRI	74	9	47	73		5040
VPR	RIGCRHSRI	74	9	12	19		5041
VPR	PYNEWTLLEL	14	10	30	47		5042
VPR	EWTLLELEL	17	10	40	63		5043
VPR	ELKNEAVRHF	25	10	17	27		5044
VPR	ELKSEAVRHF	25	10	15	23		5045
VPR	AVRHPRWL	30	10	14	22		5046
VPR	AVRHPRPW	30	10	34	53		5047
VPR	HFPRWLHSL	33	10	10	16		5048
VPR	HFPRWLHGL	33	10	24	38		5049
VPR	PWLHGLGQHI	37	10	12	19		5050
VPR	WLHGLGQHI	38	10	20	31		5051
VPR	HIYETYGDTW	45	10	17	27		5052
VPR	HIYNTYGDTW	45	10	14	22		5053
VPR	YIYETYGDTW	45	10	14	22		5054
VPR	DTWAGVEAI	52	10	16	25		5055

Table X
HIV A24 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO
VPR	DTWEGVEAH	52	10	19	30		5056
VPR	AIIRILQQLL	59	10	39	61		5057
VPR	IRILQQLLF	60	10	41	64		5058
VPR	ILQQLFIHF	63	10	35	55		5059
VPR	PWLHGLQHH	37	11	12	19		5060
VPR	QYVETYGDT	44	11	14	22		5061
VPR	TWAGVEAHRI	53	11	15	23		5062
VPR	TWEGVEAHRI	53	11	14	22		5063
VPR	AIIRILQQLL	59	11	38	59		5064
VPR	IRILQQLLF	60	11	33	52		5065
VPR	RILQQLFIHF	62	11	34	53		5066
VPR	HRIGCQHSRI	71	11	44	69		5067
VPR	HRIGCQHSRI	71	11	11	17		5068
VPR	RIGCQHSRIG	74	11	45	70		5069
VPR	RIGCRHSRIG	74	11	11	17		5070
VPU	KVDYRIVI	7	8	01	33		5071
VPU	LIIVVW	26	8	10	16		5072
VPU	IVVWTVF	30	8	15	23		5073
VPU	VVWTVFI	31	8	15	23		5074
VPU	WTVFIEY	34	8	12	19		5075
VPU	VFEYRKI	37	8	12	19		5076
VPU	KILRQKI	45	8	15	23		5077
VPU	EMGHIIAPW	89	8	11	17		5078
VPU	NYELAVGAL	5	9	01	25		5079
VPU	DYKLGVGAL	10	9	02	29		5080
VPU	DYRLGVGAL	10	9	03	43		5081
VPU	IIIVVWTI	27	9	23	36		5082
VPU	AIVVWTVF	29	9	14	22		5083
VPU	IVVWTVFI	30	9	15	23		5084
VPU	VWTVFIEY	33	9	12	19		5085
VPU	IVFEYRKI	36	9	12	19		5086
VPU	KIDRLIDRI	52	9	14	22		5087
VPU	VTLLSSSKL	94	9	01	25		5088
VPU	NYELAVGALI	5	10	01	25		5089
VPU	DYKLGVGALI	10	10	02	29		5090
VPU	DYRLGVGALI	10	10	03	43		5091
VPU	AIVVWTVFI	29	10	14	22		5092
VPU	VVWTVFIEY	31	10	12	19		5093
VPU	ILRQKIDRL	46	10	15	23		5094
VPU	GVEMGHIIAP	91	10	01	50		5095
VPU	LVTLSSSKL	91	10	01	33		5096
VPU	KVDYRIVIVAF	7	11	01	33		5097
VPU	KVDYRLGVGA	7	11	01	33		5098
VPU	RIDYRLGVGAL	7	11	01	33		5099
VPU	IVVWTVFIEY	30	11	12	19		5100
VPU	EYRKILRQKI	41	11	13	21		5101
VPU	KILRQKIDRL	45	11	15	23		5102
VPU	ILRQKIDRLI	46	11	13	20		5103
VPU	RIKEIRDDSDY	64	11	01	50		5104
VPU	RIREIRDDSDY	64	11	01	50		5105

Table XI
HIV B07 Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	B*0702	SEQ ID NO.
ENV	DNPQEVV	91	8	13	20		5106
ENV	APAGFAIL	265	8	29	45		5107
ENV	KPVVSTQL	299	8	34	53		5108
ENV	RPVVSTQL	299	8	26	41		5109
ENV	GPQTFYA	362	8	11	17		5110
ENV	LPCRKQI	485	8	31	48		5111
ENV	SPLSFQTL	808	8	30	47		5112
ENV	GPDRPEGI	822	8	15	23		5113
ENV	EPDRPERI	823	8	01	33		5114
ENV	PDPRPEGI	823	8	01	33		5115
ENV	DNPQEVVL	91	9	12	19	0.0002	5116
ENV	KPCVKLTPL	130	9	55	86	0.4100	5117
ENV	CPKVSFEPI	250	9	30	47	0.0550	5118
ENV	DPIPIHYCA	256	9	12	19		5119
ENV	EPIPIHYCA	256	9	26	41	0.0001	5120
ENV	IPHIYCTPA	259	9	36	56	0.0130	5121
ENV	IPHIYCTPA	259	9	18	28		5122
ENV	GPCKNVSTV	283	9	15	23		5123
ENV	GPCTNVSTV	283	9	11	17	0.0019	5124
ENV	KPVVSTQLL	299	9	34	53	0.0012	5125
ENV	RPVVSTQLL	299	9	26	41	0.0084	5126
ENV	DPEIVMHSF	428	9	14	22	0.0001	5127
ENV	LPCRKQII	485	9	20	31	0.0011	5128
ENV	LPCRKQIV	485	9	10	16		5129
ENV	APTKAKRRV	575	9	22	34	0.0082	5130
ENV	SPLSFQTL	808	9	10	16		5131
ENV	IPRRIRQGF	950	9	10	16		5132
ENV	IPRRIRQGL	950	9	24	38		5133
ENV	IPTRIRQGL	950	9	11	17		5134
ENV	VPTDNPQEI	88	10	25	39	0.0008	5135
ENV	VPTDNPQEV	88	10	21	33		5136
ENV	KPVVSTQLLL	299	10	34	53		5137
ENV	RPVVSTQLLL	299	10	26	41	0.0038	5138
ENV	RPNNTRKSI	347	10	17	27		5139
ENV	EPLGVAPTKA	570	10	21	33	0.0005	5140
ENV	APTKAKRRVV	575	10	22	34	0.1200	5141
ENV	VPVWKEATT	53	11	22	20	0.0022	5142
ENV	VPTDNPQEV	88	11	13	20		5143
ENV	KPCVKLTPLC	130	11	54	84	0.0004	5144
ENV	CPKVSFEPII	250	11	30	47		5145
ENV	DPIPIHYCAPA	256	11	10	16		5146
ENV	EPIPIHYCAPA	256	11	24	38		5147
ENV	EPIPIHYCTPA	256	11	10	16		5148
ENV	IPHIYCAPAGF	259	11	26	41		5149
ENV	IPHIYCTPAGF	259	11	10	16		5150
ENV	LPCRKQIINM	485	11	18	28		5151
ENV	RPGGDMRDN	547	11	38	55		5152
GAG	RPGGKKKY	22	8	35	55		5153
GAG	NPGLLETA	49	8	15	23		5154
GAG	SPRTLNAW	169	8	57	89	0.0036	5155

Table XI
HIV B07 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	B*0702	SEQ ID NO.
GAG	SPEVIPMF	186	8	55	86	0.0012	5156
GAG	TPQDLNMM	201	8	12	19		5157
GAG	TPQDLNTM	201	8	42	66	0.0001	5158
GAG	IPVHAGPI	237	8	38	59	0.0012	5159
GAG	GPIAPGQM	242	8	19	30	0.0005	5160
GAG	GPIPPGQM	242	8	17	27		5161
GAG	GPVAPGQM	242	8	10	16		5162
GAG	EPRGSDIA	251	8	56	88	0.0001	5163
GAG	PIPVGDI	278	8	10	16		5164
GAG	PIPVGEI	278	8	35	55	0.0001	5165
GAG	SPTSILDI	302	8	13	20		5166
GAG	SPVSILDI	302	8	40	63		5167
GAG	NPDKCKSL	351	8	11	17		5168
GAG	NPDKCKTIL	351	8	46	72	0.0003	5169
GAG	GPGHKARV	379	8	36	56	0.0002	5170
GAG	GPGHKARV	379	8	19	30		5171
GAG	APRKKGCW	440	8	55	86	0.0004	5172
GAG	PPAESFGF	498	8	10	16		5173
GAG	PPAESFRF	498	8	15	23		5174
GAG	PPAESFRF	510	8	02	67		5175
GAG	PPESFRF	510	8	01	33		5176
GAG	EPIDKELY	533	8	12	19		5177
GAG	EPIDKELY	537	8	01	25		5178
GAG	SPRTLNNAV	169	9	57	89	0.5500	5179
GAG	TPQDLNMMIL	201	9	12	19		5180
GAG	TPQDLNTML	201	9	42	66	0.0008	5181
GAG	HPVHAGPIA	237	9	19	30	0.0590	5182
GAG	NPPIPVGDI	277	9	10	16		5183
GAG	NPPIPVGEI	277	9	34	54	0.0002	5184
GAG	PIPVGDIY	278	9	10	16		5185
GAG	PIPVGEIY	278	9	35	55	0.0002	5186
GAG	GPKEFRDY	312	9	63	98	0.0002	5187
GAG	GPAATLEEM	362	9	16	25	0.0014	5188
GAG	GPGATLEEM	362	9	18	28		5189
GAG	GPGHKARVL	379	9	35	55	0.0290	5190
GAG	GPCHKARVL	379	9	19	30		5191
GAG	RPEPTAPPA	490	9	30	47	0.0014	5192
GAG	APPAESFGF	497	9	10	16		5193
GAG	APPEESFRF	497	9	15	23	0.0046	5194
GAG	RPEPTAPPA	504	9	01	50	0.0014	5195
GAG	APPAESFRF	509	9	02	67		5196
GAG	APPEESFRF	509	9	01	33		5197
GAG	TPSQKQEP	527	9	10	17		5198
GAG	YPLASLKS	545	9	08	17		5199
GAG	YPLASLRS	545	9	07	15	0.9900	5200
GAG	PPLASLKS	546	9	04	24		5201
GAG	EPLALRS	547	9	01	33		5202
GAG	PPLASLKS	547	9	01	33		5203
GAG	PPLSLKS	547	9	01	33		5204
GAG	RPGGKKKYKL	22	10	10	16		5205

Table XI
HIV B07 Supermot Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	B*0702	SEQ ID NO.
GAG	RPGGKKYRL	22	10	16	25		5206
GAG	SPEVPMFSA	186	10	41	64	0.0002	5207
GAG	SPEVPMFTA	186	10	13	20		5208
GAG	NPPVPVDIY	277	10	10	16		5209
GAG	NPPVGEIY	277	10	34	54	0.0002	5210
GAG	IPVGDYKRW	280	10	11	17		5211
GAG	IPVGEIYKRW	280	10	34	53	0.0002	5212
GAG	GPKEPRDYV	312	10	63	98	0.0002	5213
GAG	EPERDYVDRF	315	10	63	98	0.0002	5214
GAG	NPDCKTILKA	351	10	28	44	0.0002	5215
GAG	NPDCKTILRA	351	10	18	28		5216
GAG	GPAAATLEEMM	362	10	16	25	0.0020	5217
GAG	GPATLEEMM	362	10	18	28		5218
GAG	GPGHKARVLA	379	10	35	55	0.0002	5219
GAG	GPSHKARVLA	379	10	19	30		5220
GAG	PPAEPTAPPA	491	10	01	50		5221
GAG	EPTAPPAESF	494	10	20	31		5222
GAG	EPTAPPEESF	494	10	15	23	0.0002	5223
GAG	EPTAPPAESF	506	10	01	50		5224
GAG	EPTAPPEESF	506	10	01	50		5225
GAG	PPESFRFEEA	511	10	01	33		5226
GAG	EPIDKELYPL	533	10	12	19	0.0019	5227
GAG	EPIDKELYPL	537	10	01	25	0.0019	5228
GAG	YPLASLKSFL	545	10	08	17		5229
GAG	YPLASLKSFL	545	10	07	15	0.0140	5230
GAG	PPLASLKSFL	546	10	04	24		5231
GAG	EPLTALKSFL	547	10	01	33		5232
GAG	PPLASLKSFL	547	10	01	33		5233
GAG	PPLSLKSFL	547	10	01	33		5234
GAG	QPSLQTGSEEL	67	11	13	20		5235
GAG	YPIVQNAQGG	153	11	20	31		5236
GAG	YPIVQNLQGG	153	11	29	45		5237
GAG	SPRTLNAWVK	169	11	55	86	0.0076	5238
GAG	SPEVPMFSAL	186	11	41	64	0.0003	5239
GAG	SPEVPMFTAL	186	11	13	20		5240
GAG	IPMFALSLEGA	190	11	45	70	0.0004	5241
GAG	IPMFTALSLEGA	190	11	15	23		5242
GAG	TPQDLNMMMLN	201	11	11	17		5243
GAG	IPVGDYKRWI	280	11	10	16		5244
GAG	IPVGEIYKRWI	280	11	34	53	0.0001	5245
GAG	EPERDYVDRFF	315	11	35	55		5246
GAG	EPERDYVDRF	315	11	28	44	0.0001	5247
GAG	NPDCKTILKAL	351	11	28	44	0.0001	5248
GAG	NPDCKTILRAL	351	11	18	28		5249
GAG	WPSHKGKPGN	474	11	23	36		5250
GAG	WPSNKGKPGN	474	11	14	22		5251
GAG	PPESFRFEEA	510	11	11	17		5252
GAG	APTAAGKV	34	8	01	33		5253
NEF	VPLRPMTF	101	8	10	16		5254
							5255

Table XI
HIV B07-Superoxide Reagents with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	B*0702	SEQ ID NO.
NEF	VPLRPMY	101	8	46	73	0.0001	5256
NEF	RPMTYKAA	104	8	23	36		5257
NEF	RPMTYKGA	104	8	25	39		5258
NEF	TPGPGIRY	208	8	17	27		5259
NEF	TPGPGTRF	208	8	13	20		5260
NEF	GPGRYPL	210	8	17	27		5261
NEF	GPGRYPL	210	8	13	20		5262
NEF	VPVDPREV	230	8	11	17		5263
NEF	HPICQHGM	259	8	10	16		5264
NEF	HPMSQHGM	259	8	12	19		5265
NEF	EPAADGVGA	40	9	05	19	0.0001	5266
NEF	PPAAEGVGA	40	9	04	15		5267
NEF	FPVRPQVPL	94	9	48	75	0.7600	5268
NEF	RPQVPLRPM	98	9	47	73	1.7000	5269
NEF	RPMTYKGA	104	9	12	19		5270
NEF	FPLTFGWCF	217	9	17	27		5271
NEF	YPLTFGWCF	217	9	24	38		5272
NEF	APTAAGVGA	34	10	01	33		5273
NEF	EPAADGVGAV	40	10	04	15		5274
NEF	VPLRPMYKA	101	10	20	32	0.0001	5275
NEF	TPGPGIRYPL	208	10	16	25		5276
NEF	TPGPGTRFPL	210	10	13	20		5277
NEF	GPGRYPLTF	210	10	13	20		5278
NEF	GPGRYPLTF	210	10	13	20		5279
NEF	APTAAGVGA	34	11	01	33		5280
NEF	RPQVPLRPM	98	11	10	16		5281
NEF	RPQVPLRPM	98	11	36	56		5282
NEF	RPQVPLRPM	101	11	19	30		5283
NEF	VPLRPMYKA	101	11	23	37		5284
NEF	VPLRPMYKG	101	11	12	19		5285
NEF	RPMTYKGA	104	11	17	27		5286
NEF	FPLTFGWCFK	217	11	20	31		5287
NEF	YPLTFGWCFK	217	11	01	17		5288
POL	EPGEDREL	69	8	01	20		5289
POL	GPALSLV	70	8	01	22		5290
POL	RPLVTIKI	95	8	14	19		5291
POL	RPLVTIKI	95	8	12	19		5292
POL	KPKMIGGI	130	8	60	94	0.0023	5293
POL	GPVNVII	165	8	54	84	0.0001	5294
POL	SPIETVPV	189	8	56	88	0.0021	5295
POL	WPLTEEKI	211	8	56	88	0.0001	5296
POL	NPYNTPIF	243	8	24	38		5297
POL	NPYNTPVF	243	8	38	59	0.0008	5298
POL	TPGRYQY	328	8	52	81	0.0001	5299
POL	PPFLWMGY	414	8	64	100	0.0001	5300
POL	EPVHGYY	504	8	41	64		5301
POL	DPSKDLIA	512	8	34	53		5302
POL	TPKFKLPI	578	8	17	27		5303
POL	TPKFKLPI	578	8	30	47		5304
POL	LPIQKETW	583	8	47	73	0.0001	5305
POL	TPPLVKLW	611	8	57	89	0.0001	5306

Table XI
HIV B07 Super Motif peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	B*0702	SEQ ID NO.
POL	PPLVKLWY	612	8	57	89	0.0001	5306
POL	PPVAAKEI	781	8	27	42		5307
POL	PPVAAKEI	781	8	29	45	0.0001	5308
POL	NPOSQGVV	896	8	59	92	0.0001	5309
POL	DPIWKGPA	984	8	37	58		5310
POL	DPLWKGPA	984	8	15	23		5311
POL	VPRRKAKI	1013	8	51	80	0.0018	5312
POL	VPRRKVKI	1013	8	11	17		5313
POL	FPQGEAREF	8	9	10	16		5314
POL	SPTRRELQV	29	9	14	22	0.0210	5315
POL	SPTSRELQV	35	9	01	33		5316
POL	SPSSRELQV	38	9	01	50		5317
POL	VPTFNFPQI	79	9	01	17		5318
POL	LPGKWKPKM	125	9	39	61		5319
POL	LPGRWKPKM	125	9	16	25	0.0038	5320
POL	FPISPIETV	186	9	56	88	0.0016	5321
POL	VPVKLKPGM	194	9	56	88	0.0003	5322
POL	KPGMDGPKV	199	9	51	80	0.0002	5323
POL	GPKVKQWPL	205	9	51	80	0.0150	5324
POL	NPYNTPIFA	243	9	24	38		5325
POL	NPYNTPVFA	243	9	37	58	0.0002	5326
POL	SPAIFQSSM	345	9	42	66	0.4100	5327
POL	NPDIVIQY	364	9	17	27	0.0001	5328
POL	NPEIVIQY	364	9	23	36		5329
POL	EPPELWNGY	413	9	63	98	0.0001	5330
POL	LPEKDSWTV	435	9	40	63	0.0001	5331
POL	YFGIKVKQL	460	9	11	17		5332
POL	YFGIKVRQL	460	9	15	23		5333
POL	IPLTEEAEI	482	9	11	17		5334
POL	VPLTEEAEI	482	9	19	30	0.0001	5335
POL	TPPLVKLWY	611	9	57	89		5336
POL	EPVGAETF	624	9	21	33	0.0001	5337
POL	QPDKSESEL	701	9	37	58	0.0006	5338
POL	LPPVAAKEI	780	9	27	42		5339
POL	LPPVAAKEI	780	9	28	44	0.0006	5340
POL	PPVAAKEI	781	9	26	41		5341
POL	PPVAAKEI	781	9	28	78	0.0001	5342
POL	VPRRKAKII	1013	9	50	44	0.4800	5343
POL	VPRRKAKII	1013	9	11	17		5344
POL	SPTRRELQVW	29	10	13	20	0.0025	5345
POL	EPGEDRELSV	69	10	01	17		5346
POL	GPERSVCL	70	10	01	20		5347
POL	LPGKWKPKMI	125	10	39	61	0.0002	5348
POL	LPGRWKPKMI	125	10	15	23	0.0003	5349
POL	TPVNIIGNL	167	10	26	41		5350
POL	TPVNIIGNM	167	10	24	38		5351
POL	SPITVPVKL	189	10	53	83	0.0028	5352
POL	WPLTEEKIKA	211	10	54	84	0.0018	5353
POL	GPENPYNTPI	240	10	24	38		5354
POL	GPENPYNTPV	240	10	38	59	0.0002	5355

Table XI
HIV B07 Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	B*0702	SEQ ID NO.
POL	NPYNTPIFAI	243	10	24	38		5356
POL	NPYNTPVFAL	243	10	37	58	0.0034	5357
POL	VPLDKDFRKY	307	10	18	28	0.0002	5358
POL	TPGIRYQYNV	328	10	51	80	0.0004	5359
POL	LPQGWKGSFA	338	10	58	92	0.0120	5360
POL	EPERKQNPDI	358	10	16	25	0.0002	5361
POL	NPDIVYQYM	364	10	17	27	0.0005	5362
POL	NPEIVYQYM	364	10	23	36		5363
POL	PPFLWMGYEL	414	10	64	100	0.0002	5364
POL	HPDKWTVPQI	424	10	53	83	0.0012	5365
POL	DPSKDLIAEI	512	10	26	41	0.0002	5366
POL	LPIQKETWEA	583	10	15	23		5367
POL	PPLVKLWYQL	612	10	53	83	0.0002	5368
POL	EPVGAETFY	624	10	21	33	0.0002	5369
POL	QPDKSESELV	701	10	37	58	0.0002	5370
POL	LPPIVAKIIV	780	10	26	41		5371
POL	LPVVAKEIV	780	10	27	42	0.0002	5372
POL	PPVVAKEIVA	781	10	25	39		5373
POL	PPVVAKEIVA	781	10	28	44	0.0066	5374
POL	IPVETGQETA	841	10	58	91	0.0002	5375
POL	IPYNPQSQV	893	10	63	98	0.0023	5376
POL	DPIWKGPALK	984	10	35	55		5377
POL	DPLWKGPAKL	984	10	15	23	0.0001	5378
POL	VPTNFQITL	79	11	01	17		5379
POL	FPQITLWQRPL	87	11	40	63		5380
POL	KPKMIGGIGF	130	11	60	94	0.0004	5381
POL	TPVNIIGRNLL	167	11	26	41	0.0002	5382
POL	TPVNIIGRNML	167	11	24	38		5383
POL	FPSPITVPV	186	11	55	86	0.0067	5384
POL	WPLTEEKIKAL	211	11	54	84	0.0001	5385
POL	GPENPNTPIF	240	11	24	38		5386
POL	GPENPNTVPF	240	11	38	59	0.0001	5387
POL	HPAGLKKKKS	285	11	50	78	0.0001	5388
POL	IPSNNETPGI	321	11	31	48		5389
POL	IPSTNNETPGI	321	11	11	17		5390
POL	TPGIRYQYNVL	328	11	51	80	0.0015	5391
POL	LPQGWKGSFAI	338	11	58	92	0.0002	5392
POL	EPFRKQNPDI	358	11	14	22		5393
POL	EPFLWMGYE	413	11	63	98	0.0001	5394
POL	HPDKWTVPQI	424	11	12	19		5395
POL	QPIQLPEKDSW	431	11	13	20		5396
POL	QPIVLPEKDSW	431	11	13	20		5397
POL	IPLTEEAELEL	482	11	11	17		5398
POL	VPLTEEAELEL	482	11	19	30		5399
POL	EPFKNLTKG	536	11	45	70	0.0001	5400
POL	LPIQKETWEA	583	11	15	23		5401
POL	LPIQKETWET	583	11	27	42		5402
POL	TPPLVKLWYQ	611	11	53	83		5403
POL	EPVGAETFYV	624	11	21	33	0.0001	5404
POL	LPPIVAKIIVA	780	11	25	39		5405

Table XI
HIV B07-Super Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	B*0702	SEQ ID NO.
POL	LPPVVAKEIVA	780	11	27	42	0.0001	5406
POL	IPAETGQETAY	841	11	58	91	0.0001	5407
POL	IPYNPQSQGVV	893	11	59	92	0.0120	5408
POL	NPQSQGVVES	896	11	53	83	0.0001	5409
POL	DPIWKGPAKLL	984	11	34	53		5410
POL	DPLWKGPAKL	984	11	14	22		5411
REV	SPEGTRQA	33	8	13	20		5412
REV	RPAETPVPL	70	8	20	31		5413
REV	VPLQLPPI	75	8	11	17		5414
REV	VPLQLPPL	75	8	36	56	0.0490	5415
REV	PPLERLTL	80	8	19	30	0.0001	5416
REV	LPPLERLTL	79	9	19	30	0.3100	5417
REV	QPQGTETGV	100	9	05	18		5418
REV	PPSPEGTRQA	30	10	12	19		5419
REV	RPAEPVPLQL	70	10	20	31		5420
REV	EPVPLQLPPI	73	10	11	17	0.0023	5421
REV	PPPSPEGTRQA	29	11	12	19		5422
REV	VPLQLPPIERL	75	11	34	53		5423
REV	VPLQLPPIERL	75	11	26	41	0.0001	5424
TAT	HPGSQPKTA	16	9	10	16	0.0007	5425
TAT	HPGSQPKTA	16	9	10	16		5426
TAT	HPGSQPKTA	16	9	10	16		5427
TAT	EPVDPNLEPW	2	10	13	20		5428
TAT	EPVDPNLEPW	2	10	13	20		5429
TAT	EPVDPNLEPW	2	10	13	20	0.0001	5430
VIF	HPKISSEV	48	8	13	20		5431
VIF	HPKISSEV	48	8	13	20		5432
VIF	HPKISSEV	48	8	13	20		5433
VIF	HPKISSEV	48	8	13	20		5434
VIF	IPLDARL	57	8	20	31		5435
VIF	IPLDARL	57	8	20	31		5436
VIF	DPGLADQL	104	8	19	30		5437
VIF	DPGLADQL	104	8	19	30		5438
VIF	SPRCEYQA	135	8	21	33	0.0008	5439
VIF	IPLDARLV	57	9	11	17		5440
VIF	IPLDARLV	57	9	19	30		5441
VIF	IPLDARLV	57	9	19	30	0.0002	5442
VIF	DPGLADQLI	104	9	19	30		5443
VIF	DPGLADQLI	104	9	10	16		5444
VIF	KPKKIKPPL	160	9	21	33		5445
VIF	PPLPVSKKL	167	9	14	22		5446
VIF	PPLPVSKKL	167	9	13	20		5447
VIF	PPLPVSKKL	167	10	13	20		5448
VIF	HPKISSEVHI	48	10	19	30	0.0330	5449
VIF	HPKISSEVHI	48	10	13	20		5450
VIF	HPKISSEVHI	48	10	13	20		5451
VIF	IPLDARLV	57	10	20	31		5452
VIF	KPLPSVKKL	166	10	18	28		5453
VIF	DPGLADQLIHL	104	11	30	47		5454
VPR	EPYNEWTL	13	8	10	16		5455
VPR	FPRIWLHSL	34	9	10	16		5456
VPR	FPRIWLHSL	34	9	24	38		5457
VPR	GPQREPYNEW	9	10	37	58	0.0001	5458

Table XI
HIV B07-Super-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	B*0702	SEQ ID NO.
VPR	EPYNEWTLLEL	13	10	29	45	0.0054	5456
VPR	RPWLHGLGQY	36	10	10	16		5457
VPR	EPYNEWTLLEL	13	11	29	45		5458
VPR	RPWLHGLGQH	36	11	12	19		5459
VPU	APWDVDDL	99	8	12	19		5460

Table XII
HIV B27 Super-Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
ENV	KKLWTLYL	9	8	01	50	5461
ENV	RKSWSLYI	9	8	01	50	5462
ENV	WRWGTFLF	15	8	01	50	5463
ENV	WRWGTMLL	15	8	01	50	5464
ENV	EKLWTVVY	43	8	09	15	5465
ENV	WKEATTTL	56	8	23	36	5466
ENV	MHEDIISL	117	8	29	45	5467
ENV	IKNCSFNI	182	8	13	20	5468
ENV	PKVSFEPI	251	8	30	47	5469
ENV	LKCNDKKF	272	8	13	20	5470
ENV	AKTIIVQL	330	8	14	22	5471
ENV	ORGPGRAF	360	8	01	33	5472
ENV	KKKKTGYI	374	8	01	50	5473
ENV	IRQAHCNI	381	8	17	27	5474
ENV	IKQINMW	489	8	33	52	5475
ENV	IKQIVNMW	489	8	13	21	5476
ENV	QRVGOAMY	497	8	11	17	5477
ENV	PRPGGDM	546	8	43	67	5478
ENV	WRSELYKY	557	8	54	84	5479
ENV	YKYKVVEI	562	8	13	20	5480
ENV	YKYKVVKI	562	8	29	45	5481
ENV	ARQLLSGI	627	8	38	59	5482
ENV	VRQLLSGI	627	8	10	16	5483
ENV	LKLTWVGI	652	8	13	20	5484
ENV	EKNEQDLL	749	8	17	27	5485
ENV	EKNEQELL	749	8	18	28	5486
ENV	LRIFAVL	790	8	17	27	5487
ENV	LRIVFAVL	790	8	28	44	5488
ENV	VRQGYSPF	803	8	56	88	5489
ENV	IRLVNGFL	843	8	11	17	5490
ENV	IRLVSGFL	843	8	13	20	5491
ENV	YHRLRDFI	865	8	13	20	5492
ENV	YHRLRDLI	865	8	15	23	5493
ENV	HRLRDFIL	866	8	13	20	5494
ENV	HRLRDLII	866	8	13	20	5495
ENV	GRKGWEAL	884	8	09	15	5496
ENV	LKGLRLGW	890	8	12	40	5497
ENV	LRGLQRGW	890	8	17	40	5498
ENV	LRGLGWEG	893	8	05	17	5499
ENV	LKYLWNLL	900	8	10	32	5500
ENV	LKYWVNLL	900	8	14	22	5501
ENV	LKNSAINL	914	8	14	22	5502
ENV	LKNSAISL	914	8	10	16	5503
ENV	LKNSAVSL	914	8	10	16	5504
ENV	PRRIRQGF	951	8	13	20	5505
ENV	PRRIRQGL	951	8	11	17	5506
ENV	GKDLWTVVY	42	9	26	41	5507
ENV	EKLWTVVY	43	9	01	33	5508
ENV	WKEATTTLF	56	9	09	15	5509
ENV	WKNNMVEQM	109	9	23	36	5510
				35	55	

Table XII
 HIV B2.7 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
ENV	MHEDIISLW	117	9	29	45	5511
ENV	GKNEINDTY	218	9	01	20	5512
ENV	IIYYCAPAGF	261	9	27	42	5513
ENV	IIYYCTPAGF	261	9	10	16	5514
ENV	IKPVVSTQL	298	9	33	52	5515
ENV	IRPVVSTQL	298	9	26	41	5516
ENV	CRKIQINM	487	9	30	47	5517
ENV	CRKIQVNM	487	9	12	19	5518
ENV	GKAMYAPPI	501	9	23	36	5519
ENV	GRAMYAPPI	501	9	12	19	5520
ENV	MRDNWRSEL	553	9	40	63	5521
ENV	YKVVKIEPL	564	9	25	39	5522
ENV	EREKRAVGI	590	9	11	17	5523
ENV	QHLLKLTW	649	9	13	20	5524
ENV	QHLLQLTW	649	9	34	53	5525
ENV	QHMLQLTW	649	9	10	16	5526
ENV	IKQLQARVL	659	9	40	63	5527
ENV	ARVLAVERY	664	9	33	52	5528
ENV	ERYLKDQQL	670	9	30	47	5529
ENV	ERYLRDQQL	670	9	18	28	5530
ENV	LKDQQLGI	673	9	27	42	5531
ENV	LRDQQLGI	673	9	19	30	5532
ENV	DKWASLWNW	759	9	26	41	5533
ENV	TKWLWYIKI	771	9	15	23	5534
ENV	LRNLCLFSY	857	9	16	25	5535
ENV	LRSLCLFSY	857	9	35	55	5536
ENV	YHRLRDFIL	865	9	13	20	5537
ENV	YHRLRDLIL	865	9	13	20	5538
ENV	HRLRDLILI	866	9	11	17	5539
ENV	LKNSAVSLI	914	9	11	17	5540
ENV	IRQGLERAL	954	9	34	53	5541
ENV	KKLWTLYLAM	9	10	01	50	5542
ENV	RKWSLYLIAM	9	10	01	50	5543
ENV	WRWGTLFLGM	15	10	01	50	5544
ENV	WRWGTMLLGM	15	10	01	50	5545
ENV	GKDLWVTYY	42	10	01	33	5546
ENV	LKPCVKLTPL	129	10	55	86	5547
ENV	VKLTPLCVTL	133	10	52	81	5548
ENV	PKVSFEPIPI	251	10	30	47	5549
ENV	IKPVVSTQLL	298	10	33	52	5550
ENV	IRPVVSTQLL	298	10	26	41	5551
ENV	MHSFNCGGEF	433	10	13	20	5552
ENV	THSFNCGGEF	433	10	22	34	5553
ENV	THSFNCRGEF	433	10	13	20	5554
ENV	CRKIQINMW	487	10	30	47	5555
ENV	CRKIQVNMW	487	10	30	47	5556
ENV	IRCSSNITGL	513	10	12	19	5557
ENV	MRDNWRSELY	553	10	40	63	5558
ENV	KRAVGIGAVF	593	10	11	17	5559
ENV	LRAIEAQQHL	642	10	45	70	5560

Table XII
 HIV B27 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
ENV	ARVLAVERYL	664	10	33	52	5561
ENV	ERYLKDQQL	670	10	29	45	5562
ENV	ERYLRDQQL	670	10	17	27	5563
ENV	LKDQQLGIW	673	10	27	42	5564
ENV	LRDQQLGIW	673	10	19	30	5565
ENV	EKNEQDLAL	749	10	17	27	5566
ENV	EKNEQELLE	749	10	13	20	5567
ENV	DKWASLWNWF	759	10	26	41	5568
ENV	TKWLWYKIF	771	10	12	19	5569
ENV	LRIFAVLSI	790	10	14	22	5570
ENV	LRIFAVLSI	790	10	19	30	5571
ENV	NRVRQGYSP	801	10	52	81	5572
ENV	VRQGYSPSF	803	10	48	75	5573
ENV	PRGPRPEGI	820	10	12	19	5574
ENV	IRLVSGFLAL	843	10	11	17	5575
ENV	YIIRLDLLI	865	10	11	17	5576
ENV	IRLGWEGLY	893	10	09	29	5577
ENV	LKYWWNLQY	900	10	14	22	5578
ENV	IRQGLERALL	954	10	33	52	5579
ENV	WRWGTFLGML	15	11	01	50	5580
ENV	WRWGTMLGML	15	11	01	50	5581
ENV	YRLNCNTSAI	235	11	15	24	5582
ENV	HYCAPAGEAI	261	11	27	42	5583
ENV	IKPVVSTQLL	298	11	33	52	5584
ENV	IRPVVSTQLL	298	11	26	41	5585
ENV	TRPNNTRKSI	346	11	12	19	5586
ENV	QRGPGRAFTI	360	11	01	33	5587
ENV	MHSFNCGGEFF	433	11	13	20	5588
ENV	THSFNCGGEFF	433	11	21	33	5589
ENV	THSFNCRGEFF	433	11	13	20	5590
ENV	IRCSNITGLL	513	11	10	16	5591
ENV	YKYKVVKIEPL	562	11	25	39	5592
ENV	EKRAVGIGAVF	592	11	10	16	5593
ENV	KRAVGIGAVFL	593	11	11	17	5594
ENV	LRAIEAQHLL	642	11	44	69	5595
ENV	QHLLKLTWGI	649	11	13	20	5596
ENV	QHLLQLTVWGI	649	11	34	53	5597
ENV	LKLTWVGKQL	652	11	13	20	5598
ENV	GKLICTTAVPW	686	11	19	30	5599
ENV	GKLICTTNVPW	686	11	17	27	5600
ENV	GKLICTTTPW	686	11	12	19	5601
ENV	TKWLWYKIFI	771	11	12	19	5602
ENV	IKIFMIVGGL	777	11	38	59	5603
ENV	LKGLRLGWEG	890	11	08	27	5604
ENV	IRLGWEGLYL	893	11	09	29	5605
ENV	LKYWWNLQYW	900	11	14	22	5606
ENV	LHPRRIRQGL	948	11	12	19	5607
ENV	RRIRQGLERAL	952	11	16	25	5608
ENV	TRIRQGLERAL	952	11	11	17	5609
GAG	DKWEKIRL	14	8	18	28	5610

Table XII
 HIV-B27 Super-Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
GAG	KKYRLKHH	28	8	10	16	5611
GAG	KKYRLKHL	28	8	16	25	5612
GAG	YKLKHIVW	30	8	13	20	5613
GAG	YRLKHLVW	30	8	17	27	5614
GAG	CRQLGQL	59	8	15	23	5615
GAG	IKDTKEAL	96	8	10	16	5616
GAG	VKDTKEAL	96	8	33	52	5617
GAG	VRDTKEAL	96	8	10	16	5618
GAG	TKEALDKI	99	8	33	52	5619
GAG	TKEALEKI	99	8	10	16	5620
GAG	GHQAAMQM	214	8	61	95	5621
GAG	KRWILGL	287	8	55	86	5622
GAG	PKEPRDY	313	8	63	98	5623
GAG	FRDYVDRF	317	8	64	100	5624
GAG	CKTILKAL	354	8	28	44	5625
GAG	CKTILRAL	354	8	18	28	5626
GAG	ARVLAEM	384	8	57	89	5627
GAG	HKGRPGNF	477	8	23	37	5628
GAG	SKGRPGNF	477	8	14	23	5629
GAG	LKDKEPPL	535	8	11	18	5630
GAG	ERTENSLY	537	8	01	25	5631
GAG	EKEEKGLY	538	8	01	25	5632
GAG	GKLDAREKI	11	9	17	27	5633
GAG	LRPGGKKY	21	9	35	55	5634
GAG	KKYRLKHL	27	9	13	20	5635
GAG	SRELRFAL	39	9	22	34	5636
GAG	ERFALNPL	44	9	15	23	5637
GAG	ERFVNPL	44	9	15	23	5638
GAG	VKVEEKAF	177	9	24	38	5639
GAG	VKVVEEKAF	177	9	28	44	5640
GAG	EKAFSPEVI	182	9	48	75	5641
GAG	GHQAAMQML	214	9	61	95	5642
GAG	LHPVHAGPI	236	9	22	34	5643
GAG	VHPVHAGPI	236	9	14	22	5644
GAG	MREPRGSDI	249	9	44	69	5645
GAG	YKRWIILGL	286	9	55	86	5646
GAG	VRMYSPTS	298	9	14	22	5647
GAG	VRMYSPTS	298	9	40	63	5648
GAG	IKQGPKEPF	309	9	20	31	5649
GAG	IRQGPKEPF	309	9	42	66	5650
GAG	FRDYVDRFY	317	9	35	55	5651
GAG	FRDYVDRFY	317	9	29	45	5652
GAG	VKNWMTDIL	337	9	16	25	5653
GAG	VKNWMTETL	337	9	36	56	5654
GAG	SHKGRPGNF	476	9	23	37	5655
GAG	HKGRPGNFI	477	9	23	37	5656
GAG	NKGRPGNFI	477	9	09	15	5657
GAG	RKEPTAPPL	492	9	01	50	5658
GAG	DKDKELYPL	536	9	01	25	5659

Table XII


Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
GAG	GKKYRLKHL	25	10	12	19	5661
GAG	KKYRLKHIVW	28	10	10	16	5662
GAG	KKYRLKHLVW	28	10	16	25	5663
GAG	KHIVWASREL	33	10	21	33	5664
GAG	KHLVWASREL	33	10	36	56	5665
GAG	ERFALNPGLL	44	10	15	23	5666
GAG	ERFALNPGLL	44	10	15	23	5667
GAG	ERFALNPGLL	44	10	27	42	5668
GAG	VHQALSPRTL	164	10	11	17	5669
GAG	VHQALSPRTL	164	10	14	22	5670
GAG	VRMYSPTSIL	298	10	40	63	5671
GAG	VRMYSPTSIL	337	10	16	25	5672
GAG	VKNWMTDTLL	337	10	36	56	5673
GAG	VKNWMTDTLL	337	10	16	25	5674
GAG	LKALGPAATL	358	10	57	89	5675
GAG	HKARVLAEAM	382	10	53	83	5676
GAG	CRAPRKGCW	438	10	46	72	5677
GAG	WRCQKEGHIQM	447	10	54	84	5678
GAG	ERQANFLGKI	464	10	23	37	5679
GAG	SIKGRPGNHL	476	10	01	50	5680
GAG	TRKEPTAPPL	491	10	12	19	5681
GAG	QKQEPIDKEL	530	10	01	25	5682
GAG	EKEEGLYPL	538	10	13	21	5683
GAG	DKELYPLASL	541	10	10	16	5684
GAG	DKELYPLTSL	541	10	12	19	5685
GAG	LKSLFGNDPL	552	11	11	17	5686
GAG	ARASVLSGGEL	3	11	28	44	5687
GAG	ARASVLSGGKL	3	11	16	25	5688
GAG	GKLDAAWEKIRL	11	11	33	52	5689
GAG	IRLRPGGKKKY	19	11	10	16	5690
GAG	LRPGGKKKYKL	21	11	16	25	5691
GAG	LRPGGKKKYRL	21	11	13	20	5692
GAG	KKKYRLKHLVW	27	11	21	33	5693
GAG	LKHIVWASREL	32	11	22	34	5694
GAG	LKHLVWASREL	32	11	13	20	5695
GAG	LRSLYNTVATL	77	11	16	25	5696
GAG	VKDTKEALDKI	96	11	30	48	5697
GAG	PRTLNAWVKVI	170	11	48	75	5698
GAG	EKAPEVPIPM	182	11	22	34	5699
GAG	DRLHPVHAGPI	234	11	14	22	5700
GAG	DRVHPVHAGPI	234	11	17	27	5701
GAG	VHAGPIAPGQM	239	11	17	27	5702
GAG	VHAGPIPPGQM	239	11	55	86	5703
GAG	KRWHLGLNKI	287	11	35	55	5704
GAG	GIHKARVLAEAM	381	11	30	48	5705
GAG	SHIKARVLAEAM	381	11	50	78	5706
GAG	MXDCTERQANF	456	11	54	84	5707
GAG	ERQANFLGKIW	464	11	12	19	5708
GAG	QKQEPIDKELY	530	11	01	25	5709
GAG	LKDKEPPLASL	535	11	01	25	5710
GAG	ERTENSLYPPL	537	11	01	25	5710

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
NEF	GKWSKSSI	3	8	18	28	5711
NEF	SKSSIVGW	6	8	20	31	5712
NEF	EKGGLDGL	121	8	26	41	5713
NEF	EKGGLEGL	121	8	34	53	5714
NEF	SKKRQEIL	177	8	25	39	5715
NEF	KRQDILD	181	8	18	28	5716
NEF	KRQEILD	181	8	32	50	5717
NEF	ARELHPEF	322	8	11	17	5718
NEF	ARELHPEY	322	8	24	38	5719
NEF	EKGGLDGLI	121	9	23	36	5720
NEF	EKGGLEGLI	121	9	27	42	5721
NEF	KKRQEIDL	179	9	25	39	5722
NEF	OKRQDILD	179	9	12	19	5723
NEF	KRQDILDW	181	9	18	28	5724
NEF	KRQEILDW	181	9	32	50	5725
NEF	IRYPLTFGW	214	9	13	20	5726
NEF	TRPPLTFGW	214	9	12	19	5727
NEF	LHPICQHGM	258	9	10	16	5728
NEF	LHPMSQHGM	258	9	12	19	5729
NEF	ARELHPEFY	322	9	11	17	5730
NEF	ARELHPEY	322	9	21	33	5731
NEF	SRDLEKHGAI	50	10	14	22	5732
NEF	VRPQVPLRIM	97	10	47	73	5733
NEF	LRPMYTKGAF	103	10	12	19	5734
NEF	SHFLKEKGG	115	10	29	45	5735
NEF	LKEKGGDGL	118	10	26	42	5736
NEF	LKEKGGLEGL	118	10	29	47	5737
NEF	EKGGLDGLIY	121	10	21	33	5738
NEF	EKGGLEGLIY	121	10	19	30	5739
NEF	SKKRQEILD	177	10	25	39	5740
NEF	KKRQEILDW	179	10	25	39	5741
NEF	OKRQDILDW	179	10	12	19	5742
NEF	YHTOGFFPDW	193	10	14	22	5743
NEF	YHTQGYFPDW	193	10	25	39	5744
NEF	GKWSKSSIVGW	3	11	18	28	5745
NEF	LKEKGGDGLI	118	11	23	37	5746
NEF	LKEKGGLEGLI	118	11	24	39	5747
NEF	SKKRQEILDW	177	11	25	39	5748
NEF	KRQDILDWVY	181	11	16	25	5749
NEF	KRQEILDWVY	181	11	29	45	5750
NEF	TRPPLTFGWCF	214	11	10	16	5751
POL	TRRELQVW	43	8	13	20	5752
POL	GKWKPKMI	127	8	41	64	5753
POL	GRWKPKMI	127	8	16	25	5754
POL	VRQYDQIL	143	8	21	33	5755
POL	HKAIGTVL	156	8	20	31	5756
POL	KKAIGTVL	156	8	29	45	5757
POL	GRNLLTQI	173	8	21	33	5758
POL	GRNMLTQI	173	8	19	30	5759
POL	GRNMLTQL	173	8	11	17	5760

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	PKVKQWPL	206	8	51	80	5761
POL	KKKDSTKW	253	8	57	89	5762
POL	NKRTQDFW	270	8	57	89	5763
POL	KKKSVTVL	291	8	50	78	5764
POL	RKYTAFTI	314	8	62	97	5765
POL	IRYOYNVL	331	8	53	83	5766
POL	WKGSPAIF	342	8	59	92	5767
POL	FRKQNPDI	360	8	16	25	5768
POL	HRKIEEL	387	8	26	41	5769
POL	HRTKIEEL	387	8	22	34	5770
POL	LREHLKWL	394	8	17	27	5771
POL	LRQHLLRW	394	8	15	23	5772
POL	EHLLK WGF	396	8	14	22	5773
POL	QHLLRWGF	396	8	12	19	5774
POL	KHOKEPPF	409	8	62	97	5775
POL	KKEPFLW	411	8	63	98	5776
POL	DKWTVPQI	426	8	54	84	5777
POL	VKQLCKLL	465	8	28	44	5778
POL	VRQLCKLL	465	8	19	30	5779
POL	TKALTEVI	475	8	11	17	5780
POL	SKDLIAEL	514	8	27	42	5781
POL	QKQGQDQW	522	8	16	25	5782
POL	QKQGQGW	522	8	24	38	5783
POL	QKIATESI	565	8	14	22	5784
POL	GKTPKFKL	576	8	17	27	5785
POL	GKTPKFKL	576	8	30	47	5786
POL	QKETWEAW	586	8	15	23	5787
POL	QKETWETW	586	8	27	42	5788
POL	TKLGKAGY	642	8	10	16	5789
POL	GKQKVSVL	654	8	36	56	5790
POL	OKTELHAI	667	8	24	38	5791
POL	QKTELQAI	667	8	12	19	5792
POL	IKKEKVYL	718	8	42	66	5793
POL	DKLVSAGI	741	8	35	55	5794
POL	DKLVSSGI	741	8	16	25	5795
POL	YHNNWRAM	767	8	29	45	5796
POL	YHSNWRAM	767	8	10	16	5797
POL	WRAMASDF	771	8	39	61	5798
POL	THLEGGKI	818	8	43	67	5799
POL	THLEGGKI	818	8	35	55	5800
POL	VHVASGYI	829	8	26	41	5801
POL	GRWPKVI	858	8	53	83	5802
POL	GRWPKVI	858	8	13	21	5803
POL	NKELKKII	907	8	22	35	5804
POL	VRDQAEHL	917	8	57	89	5805
POL	VREQAEHL	917	8	48	75	5806
POL	RKGIGGY	939	8	13	20	5807
POL	TKELQKQI	962	8	59	92	5808
POL	YRDSRDPI	979	8	47	75	5809
				35	55	5810

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	YRDSRDPL	979	8	14	22	5811
POL	WKGPAKLL	987	8	59	92	5812
POL	PRRKAKII	1014	8	50	78	5813
POL	PRRKVKII	1014	8	11	17	5814
POL	IKDYGKQM	1021	8	11	17	5815
POL	IRDYGKQM	1021	8	50	78	5816
POL	QRPLVTIKI	94	9	14	22	5817
POL	QRPLVTVKI	94	9	12	19	5818
POL	WKPKMIGGI	129	9	60	94	5819
POL	IKVRQYDQI	141	9	41	64	5820
POL	VRQYDQILI	143	9	20	31	5821
POL	VRQYDQIPI	143	9	13	20	5822
POL	GIIKAIGTVL	155	9	20	31	5823
POL	GIIKAIGTVL	155	9	29	45	5824
POL	EKIKALTEI	216	9	28	44	5825
POL	EKIKALVEI	216	9	15	23	5826
POL	EKEGKISKI	231	9	36	56	5827
POL	SKIGPENPY	237	9	42	66	5828
POL	SRIGPENPY	237	9	11	17	5829
POL	IKKKDSTKW	252	9	57	89	5830
POL	TKWRKLVDF	258	9	59	92	5831
POL	RKLVDFREL	261	9	63	98	5832
POL	KKKSXTVL	290	9	50	78	5833
POL	FRKYTAFTI	313	9	61	97	5834
POL	RKQNPDI	361	9	14	22	5835
POL	QIRAKIEEL	386	9	26	41	5836
POL	QIRTKIEEL	386	9	22	34	5837
POL	KKHQKEPPF	408	9	60	94	5838
POL	KHOKEPFL	409	9	62	97	5839
POL	QKEPPFLWM	411	9	63	98	5840
POL	QKLVGKLNW	447	9	62	97	5841
POL	GKLNWASQI	451	9	61	95	5842
POL	IKVKQLCKL	463	9	29	45	5843
POL	IKVRQLCKL	463	9	18	28	5844
POL	LKEPVHGVY	502	9	41	64	5845
POL	FKNLKTGKY	538	9	45	70	5846
POL	YKNLKTGKY	538	9	10	16	5847
POL	LKTGKYAKM	541	9	19	30	5848
POL	LKTGKYARM	541	9	13	20	5849
POL	AHTNDVKQL	552	9	46	72	5850
POL	QKETWEAWW	586	9	15	23	5851
POL	QKETWETWW	586	9	27	42	5852
POL	QKTELQAIY	667	9	12	19	5853
POL	KKEKYVLAW	719	9	20	32	5854
POL	KKEKYVLSW	719	9	13	21	5855
POL	RKVFLDGI	749	9	50	78	5856
POL	DHEKYHSNW	763	9	10	16	5857
POL	EHEKYHSNW	763	9	20	31	5858
POL	EHERYHSNW	763	9	13	20	5859
POL	THLEGKIIL	818	9	31	48	5860

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	THLECKVIL	818	9	23	36	5861
POL	IHTDNGSNF	865	9	42	66	5862
POL	IKQEFIPY	887	9	26	41	5863
POL	EHUKTAVQM	922	9	57	89	5864
POL	KRKGIGGY	938	9	59	92	5865
POL	TKELQKQII	962	9	10	16	5866
POL	IKIQNFRVY	970	9	12	19	5867
POL	TKIQNERVY	970	9	37	58	5868
POL	YRDSRDPW	979	9	35	55	5869
POL	YRDSRDPW	979	9	14	22	5870
POL	WKGPAKLLW	987	9	59	92	5871
POL	WKGPAKLLW	995	9	61	95	5872
POL	WKAGAVVI	1016	9	41	64	5873
POL	RKAKIIRDY	131	10	62	97	5874
POL	PKMIGGIGGF	141	10	21	33	5875
POL	IKVRQYDOIL	254	10	58	91	5876
POL	KKDSTKWRKL	260	10	63	98	5877
POL	WRKLVDFREL	289	10	49	78	5878
POL	LKKKKSIVL	310	10	18	28	5879
POL	DKDFRKYTAF	360	10	14	22	5880
POL	FRKQNPDI	361	10	14	22	5881
POL	RKQNPDI	389	10	13	20	5882
POL	AKIEELREHL	389	10	14	22	5883
POL	TKIEELRQIIL	394	10	14	22	5884
POL	LREHLLKWWGF	394	10	12	19	5885
POL	LRQHLLRWGF	407	10	60	94	5886
POL	DKKHQKEPFF	408	10	62	97	5887
POL	KKHOKEPFLL	409	10	44	94	5888
POL	KHOKEPFLL	426	10	28	44	5889
POL	DKWTVPQIQL	426	10	12	19	5890
POL	DKWTVPQIQL	437	10	41	64	5891
POL	EKDSWTVNDI	451	10	60	94	5892
POL	GKLNWASQIY	463	10	28	44	5893
POL	IKVKQLCKLL	463	10	18	28	5894
POL	IKVRQLCKLL	469	10	25	39	5895
POL	CKLLRGAKAL	469	10	24	38	5896
POL	CKLLRGAKAL	472	10	22	34	5897
POL	LRGAKALTDI	475	10	17	27	5898
POL	AKALTDIVPL	475	10	11	17	5899
POL	TKALTEVIPL	475	10	39	61	5900
POL	LKEPVHGVVY	502	10	15	23	5901
POL	QKQGQDQWTY	522	10	24	38	5902
POL	QKQGQDQWTY	522	10	14	22	5903
POL	QKQGQDQWTY	565	10	17	27	5904
POL	QKATESIVI	576	10	29	45	5905
POL	GKTPKFKLPI	576	10	20	32	5906
POL	GKTPKFKLPI	581	10	26	41	5907
POL	FKLPQKETW	581	10	18	28	5908
POL	FRLPQKETW	652	10	15	23	5909
POL	DRGRQKVVSL	667	10	12	19	5910
POL	QKTELQAIHL	667	10			
POL	QKTELQAIYL	667	10			

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HLV-B27-Super-Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	IHLALQDSGL	674	10	15	23	5911
POL	IKKEKVYLAW	718	10	20	31	5912
POL	IRKLVFLDSW	718	10	13	20	5913
POL	IRKLVFLDGI	748	10	49	77	5914
POL	DKAQEEHEKY	758	10	25	39	5915
POL	DKAQEEHERY	758	10	15	23	5916
POL	EKYHSNWRAM	765	10	28	44	5917
POL	ERYHSNWRAM	765	10	10	16	5918
POL	WRAMASDFNL	771	10	41	64	5919
POL	DKCQLKGEAM	793	10	44	69	5920
POL	VKAACWWAGI	878	10	31	48	5921
POL	LKTAVQMAVF	924	10	57	89	5922
POL	IIIFKRKGGI	934	10	58	91	5923
POL	FKRKGIGGY	937	10	59	92	5924
POL	QKQIKIQNF	966	10	12	19	5925
POL	QKQIKIQNF	966	10	34	53	5926
POL	IKIQNFRVYY	970	10	12	19	5927
POL	TKIQNFRVYY	970	10	37	58	5928
POL	RRKAKIIRDY	1015	10	41	64	5929
POL	TRANSPTREL	22	11	11	17	5930
POL	ERAIISPATREL	25	11	01	50	5931
POL	SRANSPSTRDL	25	11	01	50	5932
POL	TRANSPTREL	34	11	01	33	5933
POL	TRANSPTREL	36	11	01	33	5934
POL	IKIGQLKEAL	100	11	19	30	5935
POL	GWKPKMIGGI	127	11	41	64	5936
POL	GRWPKMIGGI	127	11	16	25	5937
POL	PKMIGGIGGI	131	11	62	97	5938
POL	IKVRQYDQILI	141	11	20	31	5939
POL	IKVRQYDQILI	141	11	13	20	5940
POL	VRQYDQIPIEI	143	11	20	31	5941
POL	VRQYDQIPIEI	143	11	12	19	5942
POL	VKQWPLTEKI	208	11	52	81	5943
POL	IKALVEICTEM	218	11	15	23	5944
POL	KKKDKTKWRKL	253	11	57	89	5945
POL	FRELNRKRTQDF	266	11	57	89	5946
POL	KRTQDFWEVQL	271	11	52	81	5947
POL	RKYTAFTPSI	314	11	37	58	5948
POL	FRKQNPDIIVY	360	11	14	22	5949
POL	AKIEELREHLL	389	11	13	20	5950
POL	TKIEELRQHLL	389	11	14	22	5951
POL	DKKHQKEPPLW	407	11	60	94	5952
POL	KKHQKEPPLW	408	11	60	94	5953
POL	KHQKEPPLWM	409	11	62	97	5954
POL	QKEPPLWMGY	411	11	63	98	5955
POL	LHPDKWTVPQI	423	11	53	83	5956
POL	LRGTRKALTEVI	472	11	30	47	5957
POL	VKQLTEAVQKI	557	11	14	22	5958
POL	OKIATESIVIV	565	11	16	25	5959
POL	EKEPIVGAETF	622	11	16	25	5960

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	NREIKLGKAGY	639	11	28	44	5961
POL	DKSESELYNQI	703	11	18		5962
POL	DKSESELYNQI	703	11	19	30	5963
POL	MHGQVDCSPGI	802	11	52	81	5964
POL	LKTAVQMAVFI	924	11	56	88	5965
POL	ERIIDIASDI	950	11	12	19	5966
POL	ERIIDIATDI	950	11	29	45	5967
POL	ERIVDIATDI	950	11	11	17	5968
POL	TKELQKQIKI	962	11	10	16	5969
POL	TKELQKQITKI	962	11	31	49	5970
POL	IKVVPRRKAKI	1010	11	51	80	5971
POL	IKVVPRRKVKI	1010	11	11	17	5972
POL	PRKAKIIRDY	1014	11	41	64	5973
POL	AKIIRDYKQM	1018	11	42	66	5974
REV	VRIIKILY	18	8	18	28	5975
REV	RKNRRRRW	42	8	21	33	5976
REV	RKNRRRRW	42	8	40	63	5977
REV	WRARQROI	49	8	36	56	5978
REV	WRERQROI	49	8	11	17	5979
REV	ERLSTCL	61	8	11	17	5980
REV	ARKNRRRRW	41	9	18	28	5981
REV	ARKNRRRRW	41	9	39	61	5982
REV	ARQRQHSI	51	9	10	16	5983
REV	GRPAEPVPL	69	9	20	31	5984
REV	GRSAEPVPL	69	9	12	19	5985
REV	GRSGDSDEEL	3	10	17	27	5986
REV	IKILYQSNPY	21	10	25	39	5987
REV	RRWRARQROI	47	10	34	53	5988
REV	RRWRERQROI	47	10	11	17	5989
REV	GRSGDSDEEL	3	11	16	25	5990
REV	RRWRARQROI	46	11	34	53	5991
REV	RRWRERQROI	46	11	11	17	5992
REV	WRARQHSI	49	11	10	16	5993
REV	GRPAEPVPLQI	69	11	20	31	5994
REV	GRSAEPVPLQI	69	11	12	19	5995
TAT	KKGLGISY	43	8	15	23	5996
TAT	NKGLGISY	43	8	14	22	5997
TAT	TKGLGISY	43	8	19	30	5998
VIF	DRMKIRTW	14	8	12	19	5999
VIF	DRMRINTW	14	8	10	16	6000
VIF	DRMRITW	14	8	32	50	6001
VIF	ARLVITTY	64	8	11	17	6002
VIF	LHTGERDW	74	8	22	34	6003
VIF	GHGVSVIEW	85	8	31	48	6004
VIF	GHNVGSL	143	8	47	73	6005
VIF	NKVGSLQY	145	8	47	75	6006
VIF	PKIKIPPL	161	8	19	30	6007
VIF	KKLTEDRW	176	8	13	21	6008
VIF	GHRGSHTM	191	8	25	39	6009
VIF	NRWQVLIVW	3	9	10	16	6010

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Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
VIF	NRQVMIVW	3	9	42	66	6011
VIF	MKIRTWNSL	16	9	12	19	6012
VIF	MRIRTWKS	16	9	15	23	6013
VIF	MRIRTWNSL	16	9	15	23	6014
VIF	WKSIVKHIM	21	9	18	28	6015
VIF	WKSIVKYIM	21	9	10	16	6016
VIF	PKISSEVHI	49	9	15	23	6017
VIF	PKISSEVHI	49	9	20	31	6018
VIF	PRISSEVHI	49	9	15	23	6019
VIF	ARLVITYW	64	9	11	17	6020
VIF	WHLGHGVS	82	9	23	36	6021
VIF	WHLGHGVS	82	9	26	41	6022
VIF	IHLVYDFC	112	9	16	25	6023
VIF	IIMVYDFC	112	9	15	23	6024
VIF	NKVGSLQYL	145	9	47	75	6025
VIF	VKKLTEDRW	175	9	13	20	6026
VIF	WKSIVKHIMY	21	10	18	28	6027
VIF	AKGWFYRIHY	35	10	10	16	6028
VIF	VHPLGDARL	55	10	13	20	6029
VIF	VHPLGEARL	55	10	20	31	6030
VIF	LITGERDWHL	74	10	21	33	6031
VIF	GHVGSIEWRL	85	10	15	23	6032
VIF	GHVGSLOQY	143	10	47	73	6033
VIF	IKPKKIKPPL	159	10	10	16	6034
VIF	TKGHRGSHTM	189	10	18	29	6035
VIF	DRMKIRTWNSL	14	11	12	19	6036
VIF	DRMRITWKS	14	11	15	23	6037
VIF	DRMRITWNSL	14	11	15	23	6038
VIF	WKSIVKHIMYI	21	11	11	17	6039
VIF	RHPKVSSEVHI	47	11	16	25	6040
VIF	PKISSEVHIPL	49	11	14	22	6041
VIF	PKISSEVHIPL	49	11	19	30	6042
VIF	PRISSEVHIPL	49	11	13	20	6043
VIF	ARLVITYWGL	64	11	11	17	6044
VIF	WHLGHGVSIEW	82	11	23	36	6045
VIF	WHLGHGVSIEW	82	11	26	41	6046
VIF	GHVGSLOQYL	143	11	47	73	6047
VIF	NKVGSLQYLAL	145	11	46	73	6048
VPR	QREPYNEW	11	8	38	59	6049
VPR	VRHFPRIW	31	8	14	22	6050
VPR	VRHFPRIW	31	8	34	53	6051
VPR	RUFPRWL	32	8	14	22	6052
VPR	RHFPRWL	32	8	34	53	6053
VPR	PRWLHSL	35	8	10	16	6054
VPR	PRWLHGL	35	8	24	38	6055
VPR	LHGLGQHI	39	8	20	31	6056
VPR	IRILQQLL	61	8	45	70	6057
VPR	CRHSRIGI	77	8	11	17	6058
VPR	QHSRIGI	78	8	16	25	6059
VPR	LKNEAVRHF	26	9	18	28	6060

Table XII
 HIV B27 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
VPR	LKQEA VRHF	26	9	11	17	6061
VPR	LKSEAVRIHF	26	9	15	23	6062
VPR	VRHFPRWL	31	9	14	22	6063
VPR	VRHFPRWL	31	9	34	53	6064
VPR	LHGLGQHY	39	9	20	31	6065
VPR	IRILQQLF	61	9	44	69	6066
VPR	QREPYNEWTL	11	10	30	47	6067
VPR	IRILQQLFI	61	10	36	56	6068
VPR	FRIGCQHSRI	73	10	44	69	6069
VPR	FRIGCRHSRI	73	10	12	19	6070
VPR	RIHFPRWLHSL	32	11	10	16	6071
VPR	RIHFPRWLHGL	32	11	24	38	6072
VPR	PRPWLHGLGQY	35	11	10	16	6073
VPR	QHYYETYGDW	44	11	17	27	6074
VPR	QHYYNTYGDW	44	11	13	20	6075
VPU	QRKIDRLI	49	8	21	33	6076
VPU	AKVDYRIVI	6	9	01	33	6077
VPU	RKILRQRKI	44	9	13	21	6078
VPU	LRQRKIDRL	47	9	17	27	6079
VPU	YRKILRQRKI	42	10	13	21	6080
VPU	#KKLLKQKKI	43	10	01	50	6081
VPU	LRQRKIDRLI	47	10	15	24	6082
VPU	RKIDRLIDRI	51	10	12	19	6083
VPU	QRKIDRLIDRI	49	11	12	19	6084

Table XIII
HIV B58 Super-Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
ENV	NTSPRSRV	376	8	01	33	6085
ENV	NTSPRSRVAY	376	10	01	33	6086
ENV	TAGNSSRAAY	376	10	01	33	6087
ENV	TSNSSSTPI	160	11	01	33	6088
ENV	GTAGNSSRAAY	375	11	01	33	6089
ENV	HTEGNITL	478	8	01	50	6090
ENV	NANITPCRI	478	10	01	50	6091
ENV	STRTHREKRAV	586	11	01	50	6092
ENV	DSSNSTGNY	218	9	01	20	6093
ENV	STNGTETF	537	8	01	17	6094
ENV	NTEINKTETF	537	10	01	17	6095
ENV	NTTGNITETF	537	10	01	17	6096
ENV	GSENGTETF	538	9	02	18	6097
ENV	NTKRSIRI	351	8	10	16	6098
ENV	SSLKGLRL	886	8	10	16	6099
ENV	SSLKGLRLGW	886	10	10	16	6100
ENV	CTPAGFAI	264	8	10	16	6101
ENV	QSSGGDPEI	423	9	10	16	6102
ENV	QSSGGDPEIV	423	10	10	16	6103
ENV	WSQELKNSAV	910	10	10	16	6104
ENV	FAIKCNDKKF	269	11	10	16	6105
ENV	RAVGIGAVF	594	9	11	17	6106
ENV	RAVGIGAVFL	594	10	11	17	6107
ENV	AARTVELL	876	8	11	17	6108
ENV	GTDRIEV	932	8	11	17	6109
ENV	LALDKWASL	756	9	11	17	6110
ENV	IAARTVELL	874	9	11	17	6111
ENV	VSLLNATAI	919	9	11	17	6112
ENV	YATGDIIGDI	368	10	11	17	6113
ENV	TTNVPWNSSW	691	10	11	17	6114
ENV	LALDKWASLW	756	10	11	17	6115
ENV	ISNWLWYIKI	770	10	11	17	6116
ENV	RSIRLVNGFL	841	10	11	17	6117
ENV	CTTNVPWNSSW	690	11	11	17	6118
ENV	ISNWLWYIKIF	770	11	11	17	6119
ENV	SAVSLNATAI	919	11	11	17	6120
ENV	VSLLNATAIIV	919	11	11	17	6121
ENV	RAVGIGAV	594	8	12	19	6122
ENV	EAQHLLKLTIV	646	9	12	19	6123
ENV	EAQHLLKL	646	11	12	19	6124
ENV	RAMYAPPI	502	8	12	19	6125
ENV	GALFLGFL	601	8	12	19	6126
ENV	IAARTVEL	874	8	12	19	6127
ENV	PTRIROGL	951	8	12	19	6128
ENV	ATGDIIGDI	369	9	12	19	6129
ENV	RSIRLVNGF	841	9	12	19	6130
ENV	MTWMEWEREI	721	10	12	19	6131
ENV	RAIHIPRRI	945	10	12	19	6132
ENV	PTDPNPQEVVL	89	11	12	19	6133
ENV	TSVITQACPKV	242	11	12	19	6134

Table XIII
HIV-B58 Super-Variant Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
ENV	GTGPKKNVSTV	281	11	12	19	6135
ENV	TTTSHFNCRGEF	432	11	12	19	6136
ENV	CSGKLICTTV	684	11	12	19	6137
ENV	ITKWLWYIKIF	770	11	12	19	6138
ENV	FSYHRLRDL	863	11	12	19	6139
ENV	LAEEVVI	312	8	13	20	6140
ENV	GAMFLGFL	601	8	13	20	6141
ENV	RSIRLVSGF	841	9	13	20	6142
ENV	PTDIPNQEVV	89	10	13	20	6143
ENV	SAITQACPKV	243	10	13	20	6144
ENV	GSLAEVVI	310	10	13	20	6145
ENV	SSGGDPEIVM	424	10	13	20	6146
ENV	RSIRLVSGFL	841	10	13	20	6147
ENV	FSYHRLRDFI	863	10	13	20	6148
ENV	TSAITQACPKV	242	11	13	20	6149
ENV	FSYHRLRDFIL	863	11	13	20	6150
ENV	NAKTHIVQL	329	9	14	22	6151
ENV	QAMYAPPI	502	8	14	22	6152
ENV	ISNWLWYI	770	8	14	22	6153
ENV	GSLAEVVI	310	9	14	22	6154
ENV	ITNWLWYIKI	770	10	14	22	6155
ENV	FSYHRLRDL	863	10	14	22	6156
ENV	IAVAEGTDRV	927	10	14	22	6157
ENV	ITNWLWYIKIF	770	11	14	22	6158
ENV	IAVAEGTDRVI	927	11	14	22	6159
ENV	ITKWLWYIKI	770	10	15	23	6160
ENV	ITLPCRKHQII	483	11	15	23	6161
ENV	IAVAEGTDRII	927	11	15	23	6162
ENV	GSLAEVVI	310	8	16	25	6163
ENV	SSGGDLEI	424	8	16	25	6164
ENV	ITKWLWYI	770	8	16	25	6165
ENV	VAEGTDRV	929	8	16	25	6166
ENV	HSFNCRGEF	434	9	16	25	6167
ENV	VSGFLALAW	846	9	16	25	6168
ENV	VAEGTDRVI	929	9	16	25	6169
ENV	HSFNCRGEFF	434	10	16	25	6170
ENV	IAVAEGTDRI	927	10	16	25	6171
ENV	TTTSHFNCGGEF	432	11	16	25	6172
ENV	HSFNCRGEFFY	434	11	16	25	6173
ENV	GTGPKKNV	281	8	17	27	6174
ENV	DAKAYDTEV	70	9	17	27	6175
ENV	ASLWNWFDI	762	9	17	27	6176
ENV	KAYDTEVINV	72	10	17	27	6177
ENV	VAPTKAKRRV	574	10	17	27	6178
ENV	WASLWNWFDI	761	10	17	27	6179
ENV	ASDAKAYDTEV	68	11	17	27	6180
ENV	KAYDTEVINW	72	11	17	27	6181
ENV	VAPTKAKRRV	574	11	17	27	6182
ENV	CSGKLICTTV	684	11	17	27	6183
ENV	SSGGDPEIV	424	9	18	28	6184

Table XIII

HIV-B58 Super-Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
ENV	FSYHRLRDF	863	9	18	28	6185
ENV	VAEGTDRII	929	9	18	28	6186
ENV	DTEVIINWV	75	8	19	30	6187
ENV	SSNITGLL	516	8	19	30	6188
ENV	ITNWLWYI	770	8	19	30	6189
ENV	VAEGTDRI	929	8	19	30	6190
ENV	CSSNITGLL	515	9	19	30	6191
ENV	SSNITGLL	516	9	19	30	6192
ENV	CSSNITGLL	515	10	19	30	6193
ENV	CSGKLICTTAV	684	11	19	30	6194
ENV	LALAWDDLRLSL	850	11	19	30	6195
ENV	LAWDDLRLSL	852	9	20	31	6196
ENV	CSSNITGL	852	11	20	31	6197
ENV	PTDPNPFQEV	515	8	21	33	6198
ENV	ETRPFGGDM	89	9	21	33	6199
ENV	PTKAKRRV	544	10	21	33	6200
ENV	GAVFLGFL	576	8	22	34	6201
ENV	PTKAKRRV	601	8	22	34	6202
ENV	KAMYAPPI	576	9	22	34	6203
ENV	FSYHRLRDL	502	8	23	36	6204
ENV	SSGGDPEI	863	9	23	36	6205
ENV	LALAWDDL	424	8	24	38	6206
ENV	PTDPNPFQEI	850	8	25	39	6207
ENV	ITLPCRKQI	89	9	25	39	6208
ENV	LSGIVQQNNL	483	10	25	39	6209
ENV	CTHGIRPV	631	11	25	39	6210
ENV	QSNLLRAI	294	8	26	41	6211
ENV	CTHGIRPV	638	8	26	41	6212
ENV	ITLTVQARQL	294	9	26	41	6213
ENV	ITLTVQARQL	621	10	27	42	6214
ENV	VSFEPIHY	621	11	27	42	6215
ENV	YSPLSFQTL	253	10	28	44	6216
ENV	CAPAGFAI	807	9	29	46	6217
ENV	CAPAGFAI	264	8	29	45	6218
ENV	ITQACPKVSF	264	9	29	45	6219
ENV	VSFEPIPI	245	10	29	45	6220
ENV	WASLWNWF	253	8	30	47	6221
ENV	QACTPKVSPEPI	761	8	30	47	6222
ENV	FVLSIVNRV	248	11	30	47	6223
ENV	RSCLFSYHRL	794	10	31	48	6224
ENV	CTHGIRPV	858	11	31	48	6225
ENV	LSGIVQQQSNL	294	9	32	50	6226
ENV	CTHGIRPV	631	11	32	50	6227
ENV	QARVLAVERY	294	8	33	52	6228
ENV	QARVLAVERYL	663	10	33	52	6229
ENV	EAQQLLLQLTV	663	11	33	52	6230
ENV	VTENFNMW	646	11	34	54	6231
ENV	AAGSTMGAASI	102	8	34	53	6232
ENV	LSIVNRVRQGY	611	11	34	53	6233
ENV		797	11	34	53	6234

Table XIII
 HIV B58 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
ENV	EAQQLLQL	646	9	35	56	6235
ENV	RSCLFSY	858	8	35	55	6236
ENV	HSFNCGGEFF	434	10	35	55	6237
ENV	HSFNCGGEFF	434	11	35	55	6238
ENV	AASITLV	618	8	36	56	6239
ENV	HSFNCGGEF	434	9	36	56	6240
ENV	GAASITLV	617	9	36	56	6241
ENV	LTVQARQL	623	9	36	56	6242
ENV	ITQACPKV	245	8	37	58	6243
ENV	LTVQARQL	623	8	38	59	6244
ENV	QARQLLSGI	626	9	38	59	6245
ENV	QARQLLSGIV	626	10	38	59	6246
ENV	STMGAASI	614	8	39	61	6247
ENV	GSTMGAASI	613	9	39	61	6248
ENV	STMGAASITL	614	10	39	61	6249
ENV	GSTMGAASITL	613	11	39	61	6250
ENV	QACPKVSF	248	8	40	63	6251
ENV	CASDAKAY	67	8	42	66	6252
ENV	RAIEAQQHLL	643	10	44	69	6253
ENV	RAIEAQQHLL	643	9	45	70	6254
ENV	ISLWDQSL	122	8	48	75	6255
ENV	QSLKPCVKL	127	9	48	75	6256
ENV	RSELYKYKVV	558	10	49	77	6257
ENV	RSELYKYKVV	558	9	50	78	6258
ENV	STVQCTHGI	289	9	51	80	6259
ENV	STVQCTHGI	288	10	51	80	6260
ENV	LTPLCVTL	135	8	54	84	6261
ENV	VTVYGVVPV	47	9	55	86	6262
ENV	VTVYGVVPVV	47	10	55	86	6263
ENV	STQLLLNGSL	303	10	57	89	6264
ENV	VSTQLLLNGSL	302	11	57	89	6265
ENV	LTVWGIKQL	654	9	59	92	6266
GAG	TAPPESF	508	8	01	33	6267
GAG	ETIDKDLY	537	8	01	25	6268
GAG	PTAPPESF	507	9	01	33	6269
GAG	PTAPPESF	508	10	01	33	6270
GAG	ETIDKDLYPL	537	10	01	25	6271
GAG	RTENSLYPPL	538	10	01	25	6272
GAG	AAAIMMQKSNF	405	11	01	25	6273
GAG	SATIMMQKGNF	405	11	01	25	6274
GAG	PTAPPESFRF	507	11	01	33	6275
GAG	GAATAATDSNI	123	10	01	50	6276
GAG	AADKGVSONY	130	10	01	50	6277
GAG	AAGTGNSSQV	130	10	01	50	6278
GAG	GANSIPVGD	276	10	01	50	6279
GAG	SAQQDLKGGY	393	10	01	50	6280
GAG	TAQQDLKGGY	393	10	01	50	6281
GAG	GANSIPVGDY	276	11	01	50	6282
GAG	ASAQDLKGGY	392	11	01	50	6283
GAG	ATAQDLKGGY	392	11	01	50	6284

Table XIII
HIV B58 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
GAG	PAEPTAPPAEI	492	11	01	50	6285
GAG	TAPPAESF	508	8	02	67	6286
GAG	PTAPPAESF	507	9	02	67	6287
GAG	TAPPAESFRF	508	10	02	67	6288
GAG	PTAPPAESFRF	507	11	02	67	6289
GAG	GTRPGNYV	480	8	02	100	6290
GAG	AADKGVSONY	129	11	02	18	6291
GAG	EADGKVSQNY	129	10	04	36	6292
GAG	AAIMMOKSNF	406	10	06	15	6293
GAG	TTPSQKQEPH	522	10	09	45	6294
GAG	GASLEEMM	364	8	10	16	6295
GAG	DTKEALEKI	98	9	10	16	6296
GAG	TAPPAESFGF	496	10	10	16	6297
GAG	QALSPRTLNAW	166	11	10	16	6298
GAG	PTAPPAESFGF	495	11	10	16	6299
GAG	ATIMMORGNE	406	10	11	28	6300
GAG	PSQKQEPH	528	8	11	18	6301
GAG	SSKGRPGNF	476	9	11	18	6302
GAG	TTSTLQEQIAW	260	11	11	17	6303
GAG	QALSPRTL	166	8	11	17	6304
GAG	ASQEVKNW	333	8	11	17	6305
GAG	ASVLSGGEL	5	9	11	17	6306
GAG	QASQEVKNW	332	9	11	17	6307
GAG	ASQEVKNWM	333	9	11	17	6308
GAG	NANPDCKSI	349	9	11	17	6309
GAG	RASVLSGGEL	4	10	11	17	6310
GAG	QASQEVKNWM	332	10	11	17	6311
GAG	NANPDCKSIL	349	10	11	17	6312
GAG	PSSKGRPGNF	475	10	11	17	6313
GAG	QTGSEELRSL	71	10	12	19	6314
GAG	GSEELKSL	73	8	12	19	6315
GAG	GTEELRSL	73	8	12	19	6316
GAG	ATPQDLNM	200	8	12	19	6317
GAG	LTSLSLF	549	8	12	19	6318
GAG	GSEELRSLY	73	9	12	19	6319
GAG	GATPQDLNM	199	9	12	19	6320
GAG	ATPQDLNMM	200	9	12	19	6321
GAG	STLQEQIAW	262	9	12	19	6322
GAG	RAEQASQEV	329	9	12	19	6323
GAG	KSLFGNDPL	553	9	12	19	6324
GAG	ATLYCVHQKI	85	10	12	19	6325
GAG	GATPQDLNMM	199	10	12	19	6326
GAG	ATPQDLNMMML	200	10	12	19	6327
GAG	TSTLQEQIAW	261	10	12	19	6328
GAG	STLQEQIAWM	262	10	12	19	6329
GAG	VATLYCVHQKI	84	11	12	19	6330
GAG	GATPQDLNMMML	199	11	12	19	6331
GAG	TSTLQEQIAWM	261	11	12	19	6332
GAG	TSNPPVPGEI	272	11	12	19	6333
GAG	LTSLSLSLF	549	8	13	20	6334

Table XIII
HIV-B58 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
GAG	YSPITSILDI	301	9	13	20	6335
GAG	PSLQTGSEEL	68	10	13	20	6336
GAG	NSSQVSONY	144	9	14	31	6337
GAG	NSSQVSONYPI	144	11	14	31	6338
GAG	TSEGCROIL	55	9	14	22	6339
GAG	ETSEGCROIL	54	10	14	22	6340
GAG	AAEWDVRVHPV	230	10	14	22	6341
GAG	PSNKGRRGNF	475	10	14	22	6342
GAG	TAPPEESFRF	496	10	14	22	6343
GAG	EAAEWDVRVHPV	229	11	14	22	6344
GAG	PTAPPEESFRF	495	11	14	22	6345
GAG	SSQVSONY	145	8	15	31	6346
GAG	SSQVSONYPI	145	10	15	31	6347
GAG	SSQVSONYPIV	145	11	15	31	6348
GAG	RSLYNTIVATL	78	10	15	24	6349
GAG	RSLYNTIVATLY	78	11	15	24	6350
GAG	EAAEWDVRV	229	8	15	23	6351
GAG	ATQDVKNW	333	8	15	23	6352
GAG	TAPPEESF	496	8	15	23	6353
GAG	LASLSLF	549	8	15	23	6354
GAG	RAEQATQDV	329	9	15	23	6355
GAG	QATQDVKNW	332	9	15	23	6356
GAG	ATQDVKNWM	333	9	15	23	6357
GAG	PTAPPEESF	495	9	15	23	6358
GAG	ATLYCVIHQRI	85	10	15	23	6359
GAG	QATQDVKNWM	332	10	15	23	6360
GAG	VATLYCVIHQRI	84	11	15	23	6361
GAG	FAVNPGLL	46	8	16	25	6362
GAG	TSEGCROQI	55	8	16	25	6363
GAG	GSEELRSL	73	8	16	25	6364
GAG	TSNPPIPV	272	8	16	25	6365
GAG	PAATLEEM	363	8	16	25	6366
GAG	AATLEEMM	364	8	16	25	6367
GAG	LSGGKLDAA	8	9	16	25	6368
GAG	ETSEGCROQI	54	9	16	25	6369
GAG	MTSNPPIPV	271	9	16	25	6370
GAG	KALGPAATL	359	9	16	25	6371
GAG	PAATLEEMM	363	9	16	25	6372
GAG	DAWEKIRL	14	8	17	27	6373
GAG	LSPTLNAAW	168	9	17	27	6374
GAG	ASRELERFAV	38	10	17	27	6375
GAG	LSPTLNAAWV	168	10	17	27	6376
GAG	HAGPIPPQM	240	10	17	27	6377
GAG	WASRELERFAV	37	11	17	27	6378
GAG	ATQEVKNW	333	8	18	28	6379
GAG	QATQEVKNW	332	9	18	28	6380
GAG	ATQEVKNWM	333	9	18	28	6381
GAG	HAGPIAPQM	240	10	18	28	6382
GAG	QATQEVKNWM	332	10	18	28	6383
GAG	PSHKARVL	380	8	19	30	6384

Table XIII
HIV B58 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
GAG	TAPPAESF	496	8	20	31	6385
GAG	MTNNPIPV	271	9	20	31	6386
GAG	PTAPPAESF	495	9	20	31	6387
GAG	FALNPGLL	46	8	22	34	6388
GAG	ASRELERFAL	38	10	22	34	6389
GAG	ETINEEAAEW	224	10	22	34	6390
GAG	WASRELERFAL	37	11	22	34	6391
GAG	PSHKORPGNF	475	10	23	36	6392
GAG	PSHKGRPGNFI	475	11	23	36	6393
GAG	AAMQMLKETI	217	10	26	41	6394
GAG	QAAQMMLKETI	216	11	26	41	6395
GAG	TTSTLQEQIGW	260	11	27	43	6396
GAG	STLQEQIGW	262	9	27	42	6397
GAG	RAEQATQEV	329	9	27	42	6398
GAG	TSTLQEQIGW	261	10	27	42	6399
GAG	TSTLQEQIGWM	262	10	27	42	6400
GAG	TSTLQEQIGWM	261	11	27	42	6401
GAG	VSQNYPIVQNL	149	11	28	48	6402
GAG	ASVLSGGKL	5	9	28	44	6403
GAG	RASVLSGGKL	4	10	28	44	6404
GAG	QAISPRTL	166	8	29	45	6405
GAG	GATLEEMM	364	8	29	45	6406
GAG	QAISPRTLNAW	166	11	29	45	6407
GAG	RTLNAWVKVI	171	10	30	47	6408
GAG	RTLNAWVKVV	171	10	31	48	6409
GAG	DTINEEAAEW	224	10	31	48	6410
GAG	DTKEALDKI	98	9	32	50	6411
GAG	AAMQMLKDTI	217	10	33	52	6412
GAG	QAAQMMLKDTI	216	11	33	52	6413
GAG	AAEWDRLHPV	230	10	34	53	6414
GAG	EAIEWDRLHPV	229	11	34	53	6415
GAG	LAEMSQV	387	8	36	57	6416
GAG	ISPRTLNAW	168	9	36	56	6417
GAG	ISPRTLNAW	168	10	36	56	6418
GAG	EAAEWDRL	229	8	39	61	6419
GAG	YSPVSILDI	301	9	40	63	6420
GAG	NTVATLYCV	82	9	41	64	6421
GAG	ATPQDLNTM	200	9	42	66	6422
GAG	GATPQDLNTM	199	10	42	66	6423
GAG	ATPQDLNTML	200	10	42	66	6424
GAG	GATPQDLNTML	199	11	42	66	6425
GAG	TTSTLQEQI	260	9	45	71	6426
GAG	NANPDCKTI	349	9	45	70	6427
GAG	GTTSTLQEQI	259	10	45	70	6428
GAG	NANPDCKTIL	349	10	45	70	6429
GAG	ASRELERF	38	8	46	72	6430
GAG	WASRELERF	37	9	46	72	6431
GAG	TSTLQEQI	261	8	47	73	6432
GAG	NTVGGHQAAM	210	10	47	73	6433
GAG	GSDIAGTTSTL	254	11	47	73	6434

Table XIII
HIV-B58 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
GAG	VSONYPIV	149	8	48	83	6435
GAG	IAGTTSTL	257	8	48	75	6436
GAG	KAFSPEVI	183	8	50	78	6437
GAG	KAFSPEVIM	183	10	50	78	6438
GAG	KAFSPEVIMF	183	11	50	78	6439
GAG	RAPRKKGCW	439	9	53	83	6440
GAG	FSPEVIM	185	8	54	84	6441
GAG	FSPEVIMF	185	9	54	84	6442
GAG	CTERQANF	459	8	55	87	6443
GAG	CTERQANFL	459	9	55	87	6444
GAG	QANFLGKI	466	8	57	89	6445
GAG	KARVLAEM	383	9	57	89	6446
GAG	QANFLGKIW	466	9	57	89	6447
GAG	LSEGATPQDL	196	10	58	91	6448
GAG	RTLNAWVKV	171	9	61	95	6449
NEF	QAEPAAAGV	34	9	01	33	6450
NEF	QTEPAAAGV	32	9	01	17	6451
NEF	RAEPAAAGV	32	9	01	17	6452
NEF	RTEPAAAGV	32	9	01	17	6453
NEF	QAEPAAEGV	33	9	01	17	6454
NEF	QAPTAAGV	33	9	01	17	6455
NEF	RAQEPAAAGV	32	11	01	17	6456
NEF	GAFDLSFF	110	8	10	16	6457
NEF	GAFDLSFFL	110	9	10	16	6458
NEF	MARELHPEY	321	9	10	16	6459
NEF	MARELHPEYY	321	10	10	16	6460
NEF	AADGVGV	42	8	11	18	6461
NEF	PAADGVGV	41	9	11	17	6462
NEF	VSRDLEKHGAI	49	11	11	17	6463
NEF	ATNADCAW	71	8	12	22	6464
NEF	AATNADCAW	70	9	12	22	6465
NEF	ATNADCAWL	71	9	12	22	6466
NEF	AATNADCAWL	70	10	12	22	6467
NEF	PAAEVGV	41	9	12	19	6468
NEF	MTYKGAFDL	106	9	12	19	6469
NEF	NTQGYFPDW	194	9	12	19	6470
NEF	TAATNADCAW	69	10	12	19	6471
NEF	GTRPLTFGW	213	10	12	19	6472
NEF	NTAATNADCAW	68	11	12	19	6473
NEF	TAATNADCAWL	69	11	12	19	6474
NEF	GTRPLTF	213	8	13	20	6475
NEF	YTPGPGTRF	207	9	13	20	6476
NEF	YTPGPGTRFPL	207	11	13	20	6477
NEF	HTQGFDPW	194	9	14	22	6478
NEF	EAQEEEEV	82	8	16	25	6479
NEF	EAQEEEEVGF	82	10	16	25	6480
NEF	YTPGPGIRYPL	207	11	16	25	6481
NEF	AAEGVGAV	42	8	17	28	6482
NEF	YTPGPGIRY	207	9	17	27	6483
NEF	WSKSSIVGW	5	9	20	31	6484

Table XIII
HLV B58 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
NEF	YSKKRQEI	176	8	22	34	6485
NEF	YSKKRQEI	176	9	22	34	6486
NEF	LSFLKEKGG	114	11	22	34	6487
NEF	YSKKRQEI	176	11	22	34	6488
NEF	HTQGYFPDW	194	9	25	39	6489
NEF	LSHFLKEKGG	114	11	27	42	6490
NEF	LTFGWCFKL	221	10	35	55	6491
NEF	LTFGWCFKL	221	9	39	61	6492
POL	NSPTSREL	34	8	01	33	6493
POL	PTSRELQV	36	8	01	33	6494
POL	GTLNCPQI	80	8	01	33	6495
POL	PTNFPPQI	80	8	01	33	6496
POL	STNSPTSREL	32	10	01	33	6497
POL	NSPTSRELQV	34	10	01	33	6498
POL	RANSPSSREL	35	10	01	33	6499
POL	GTLNCPQIHL	80	10	01	33	6500
POL	PTNFPPQIHL	80	10	01	33	6501
POL	NSNSPTSREL	31	11	01	33	6502
POL	GTLNCPQIHLW	80	11	01	33	6503
POL	PTNFPPQIHLW	80	11	01	33	6504
POL	NSPSSREL	37	8	01	50	6505
POL	NSPTTREL	39	8	01	50	6506
POL	PSSRELQV	39	8	01	50	6507
POL	NSPSSRELQV	37	10	01	50	6508
POL	RANSPTTREL	37	10	01	50	6509
POL	NSPTTRELQV	39	10	01	50	6510
POL	GADRQGV	70	8	01	20	6511
POL	GSGRAVPI	70	8	01	20	6512
POL	GADRQGVSF	70	10	01	20	6513
POL	GSGRAVPICL	70	10	01	20	6514
POL	GTLNFPQI	79	9	01	17	6515
POL	GAISLSLPQI	79	10	01	17	6516
POL	GTLNFPQIF	79	11	01	17	6517
POL	PSLSFPQI	79	8	02	33	6518
POL	PSLSFPQITL	79	10	02	33	6519
POL	SSFSFPQI	82	11	02	33	6520
POL	SSFSFPQITL	82	8	03	30	6521
POL	SSFSFPQITLW	82	10	03	30	6522
POL	VSFSFPQITLW	78	11	03	30	6523
POL	VSFSFPQI	78	11	07	15	6524
POL	VSFSFPQITL	78	8	08	17	6525
POL	ETWWTDYW	591	10	08	17	6526
POL	RANSPTSREL	26	8	10	16	6527
POL	ETWETWTDY	588	10	10	16	6528
POL	ETWETWWTEY	588	10	10	16	6529
POL	QTKELQKQI	961	10	10	16	6530
POL	LAFPPQGEAREF	6	10	10	16	6531
POL	RSATINDVKQL	550	11	10	16	6532
POL	EAVQKIATESI	562	11	10	16	6533
						6534

Table XIII
HIV D58 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	ETWETWWTDYW	588	11	10	16	6535
POL	RTAHTNDV	550	8	11	17	6536
POL	WAGIQQEF	884	8	11	17	6537
POL	VTVKIGGQL	98	9	11	17	6538
POL	STNNETPGI	323	9	11	17	6539
POL	GTKALTEVI	474	9	11	17	6540
POL	GSNFTSTV	870	9	11	17	6541
POL	GADDTVLEEM	114	10	11	17	6542
POL	ISRIGPENPY	236	10	11	17	6543
POL	PSTNNETPGI	322	10	11	17	6544
POL	TAHTNDVKQL	551	10	11	17	6545
POL	WAGIQQEFGI	884	10	11	17	6546
POL	STNNETPGIRY	323	11	11	17	6547
POL	ESWTYNDIQKL	439	11	11	17	6548
POL	GTKALTEVIPL	474	11	11	17	6549
POL	ESWTVNDI	439	8	11	17	6550
POL	KTELQAIY	668	8	12	19	6551
POL	KTELQAIYL	668	9	12	19	6552
POL	NSPTRRELQVW	28	11	12	19	6553
POL	TTNOKTELHAI	664	11	12	19	6554
POL	KTELQAIYLAL	668	11	12	19	6555
POL	GAVVIQDNSEI	999	11	12	19	6556
POL	KTCKYARM	542	8	13	21	6557
POL	WTVQPIVL	428	8	13	20	6558
POL	PTRELOVW	30	9	13	20	6559
POL	DTVLEDINL	117	9	13	20	6560
POL	NSPTRRELQV	28	10	13	20	6561
POL	LAGRWVPVKTI	856	10	13	20	6562
POL	RAKIEELREHL	388	11	13	20	6563
POL	IATESIVI	567	8	14	22	6564
POL	IATESIVW	567	9	14	22	6565
POL	NSPTSREL	28	8	14	22	6566
POL	PTRELOV	30	8	14	22	6567
POL	FSFPQITLW	85	9	14	22	6568
POL	DTVLEEINL	117	9	14	22	6569
POL	WTDYWQATW	594	9	14	22	6570
POL	SAGERIVDI	947	9	14	22	6571
POL	ASDIQTKEL	957	9	14	22	6572
POL	WTDYWQATWI	594	10	14	22	6573
POL	TSTTVKAAACW	874	10	14	22	6574
POL	YSAGERIVDI	946	10	14	22	6575
POL	SAGERIVDIH	947	10	14	22	6576
POL	IASDIQTKEL	956	10	14	22	6577
POL	RTKIEELRQHL	388	11	14	22	6578
POL	FTSTTVKAAACW	873	11	14	22	6579
POL	TSTTVKAAACW	874	11	14	22	6580
POL	YSAGERIVDII	946	11	14	22	6581
POL	KALVEICTEM	219	10	14	24	6582
POL	FSFPQITL	85	8	15	23	6583
POL	LTQLGCTL	177	8	15	23	6584

Table XIII
HIV B58 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	RSAHTNDV	550	8	15	23	6585
POL	VSAGIRKV	744	8	15	23	6586
POL	SAGIRKVL	745	8	15	23	6587
POL	TTVKAACW	876	8	15	23	6588
POL	KTELQAIHL	668	9	15	23	6589
POL	VSAGIRKVL	744	9	15	23	6590
POL	SAGIRKVLV	745	9	15	23	6591
POL	STTVKAACW	875	9	15	23	6592
POL	TTVKAACW	876	9	15	23	6593
POL	GADDTVLEDI	114	10	15	23	6594
POL	LTQLGCTLNF	177	10	15	23	6595
POL	LTEEKIKALV	213	10	15	23	6596
POL	VSAGIRKVLV	744	10	15	23	6597
POL	SAGIRKVLFL	745	10	15	23	6598
POL	STTVKAACW	875	10	15	23	6599
POL	KTELOAHILAL	668	11	15	23	6600
POL	VSAGIRKVLFL	744	11	15	23	6601
POL	KAQEEIERY	759	9	16	25	6602
POL	YSAGERIV	946	8	16	25	6603
POL	KALTEVPL	476	9	16	25	6604
POL	RANSPTRREL	26	10	16	25	6605
POL	SAITNDVKQL	551	10	16	25	6606
POL	NSPTRREL	28	8	17	27	6607
POL	VTIKGGQL	98	9	17	27	6608
POL	KTPKFKLPI	577	9	17	27	6609
POL	GAKALTDIVPL	474	11	17	27	6610
POL	FSVPLDKDF	305	9	18	28	6611
POL	YAGIKVKQL	460	9	18	28	6612
POL	GADDTVLEEI	114	10	18	28	6613
POL	ITLWQRPLVT	90	11	18	28	6614
POL	KTGKYAKM	542	8	19	30	6615
POL	GTKALTEV	474	8	19	30	6616
POL	ATESIVW	568	8	19	30	6617
POL	GAHTNDVKQL	551	10	19	30	6618
POL	KSESELVNOI	704	10	19	30	6619
POL	KSESELVSQI	704	10	19	30	6620
POL	ITLWQRPLVTI	90	11	19	30	6621
POL	LTDTTNOKTEL	661	11	19	30	6622
POL	KSESELVNOII	704	11	19	30	6623
POL	KSESELVSQII	704	11	19	30	6624
POL	VSQHEQL	710	8	20	31	6625
POL	VSQHEQLI	710	9	20	31	6626
POL	MASDFNLPIV	774	11	20	31	6627
POL	ESELVSQI	706	8	21	33	6628
POL	WAGIKQEF	884	8	21	33	6629
POL	KALTDIVPL	476	9	21	33	6630
POL	ESELVSQII	706	9	21	33	6631
POL	ASDFNLPIV	775	10	21	33	6632
POL	WAGIKQEFGI	884	10	21	33	6633
POL	LAWVPAHKG	725	10	22	34	6634

Table XIII
 CHY/B58 Super-Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	MASDFNLPI	774	10	22	34	6635
POL	LAGRWPKVI	856	10	22	34	6636
POL	ASDFNLPI	775	9	23	36	6637
POL	CTHLEKGVIL	817	10	23	36	6638
POL	CTHLEKGVILV	817	11	23	36	6639
POL	GAKALTDIV	474	9	24	38	6640
POL	WTEYWQATW	594	9	24	38	6641
POL	WTEYWQATWI	594	10	24	38	6642
POL	PTPVNIIGRNM	166	11	24	38	6643
POL	GAKALTDI	474	8	25	39	6644
POL	DSGSEVNI	680	8	25	39	6645
POL	DSGSEVNIV	680	9	25	39	6646
POL	ASDFNLPPV	775	9	25	39	6647
POL	LALQDSGSEV	676	10	25	39	6648
POL	SSGIRKVLFL	745	10	25	39	6649
POL	MASDFNLPPV	774	10	25	39	6650
POL	ASDFNLPPV	775	10	25	39	6651
POL	LTETTNQKTEL	661	11	25	39	6652
POL	VSSGIRKVLFL	744	11	25	39	6653
POL	MASDFNLPPV	774	11	25	39	6654
POL	ASQIYAGIKV	456	10	26	41	6655
POL	VSSGIRKV	744	8	26	41	6656
POL	SSGIRKVL	745	8	26	41	6657
POL	CTHLEKGV	817	8	26	41	6658
POL	PSKDLIAEI	513	9	26	41	6659
POL	DTTNQKTEL	663	9	26	41	6660
POL	VSSGIRKVL	744	9	26	41	6661
POL	SSGIRKVLV	745	9	26	41	6662
POL	CTHLEKVI	817	9	26	41	6663
POL	GSNFTSAAV	870	9	26	41	6664
POL	VSSGIRKVLV	744	10	26	41	6665
POL	ETGQETAYFL	844	10	26	41	6666
POL	PTPVNIIGRNL	166	11	26	41	6667
POL	WASQIYAGIKV	455	11	26	41	6668
POL	ETGQETAYFLL	844	11	26	41	6669
POL	ASQIYAGI	456	8	27	43	6670
POL	KAQEEIEKY	759	9	27	43	6671
POL	ASQIYPGIKV	456	10	27	43	6672
POL	LALQDSGL	676	8	27	42	6673
POL	ESELVNQI	706	8	27	42	6674
POL	TAYFLLKL	849	8	27	42	6675
POL	WASQIYAGI	455	9	27	42	6676
POL	ESELVNQII	706	9	27	42	6677
POL	ETAYFLLKL	848	9	27	42	6678
POL	CTEMEKEGI	225	10	27	42	6679
POL	LALQDSGLEV	676	10	27	42	6680
POL	TSAAVKAAACW	874	10	27	42	6681
POL	WASQIYPGIKV	455	11	27	42	6682
POL	FTSAAVKAAACW	873	11	27	42	6683
POL	TSAAVKAAACWW	874	11	27	42	6684

Table XIII
 HIV-1 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	WTQPIQL	428	8	28	44	6685
POL	DSGLEVNI	680	8	28	44	6686
POL	AAVKAACW	876	8	28	44	6687
POL	DSGLEVNIV	680	9	28	44	6688
POL	SAAYKAACW	875	9	28	44	6689
POL	AAVKAACWW	876	9	28	44	6690
POL	VTDRGRQKVV	650	10	28	44	6691
POL	SAAVKAACWW	875	10	28	44	6692
POL	ASQIYPGI	456	8	29	46	6693
POL	WASQIYPGI	455	9	29	45	6694
POL	KTPKRLPI	577	9	29	45	6695
POL	ETTNQKTEL	663	9	29	45	6696
POL	AANRETKL	637	8	30	47	6697
POL	GAANRETKL	636	9	30	47	6698
POL	VTDRGRQKV	650	9	30	47	6699
POL	LAGRWPKV	856	9	30	47	6700
POL	KAACWWAGI	879	9	31	49	6701
POL	ETAYFILKL	848	9	31	48	6702
POL	PSINNETPGI	322	10	31	48	6703
POL	CTHLEFKIL	817	10	31	48	6704
POL	ETQGETAYFI	844	10	31	48	6705
POL	CTHLEGKIILV	817	11	31	48	6706
POL	ETQGETAYFIL	844	11	31	48	6707
POL	TAYFILKL	849	8	32	50	6708
POL	AACWWAGI	880	8	32	50	6709
POL	HSNWRAMASDF	768	11	32	50	6710
POL	SSMTKILEPF	351	10	33	52	6711
POL	QSSMTKILEPF	350	11	33	52	6712
POL	LTEAVQKI	560	8	34	53	6713
POL	CTHLEGKI	817	8	35	55	6714
POL	ETKLGKAGY	641	9	35	55	6715
POL	CTHLEGKII	817	9	35	55	6716
POL	ATDIQTKEL	957	9	35	55	6717
POL	ETKLGKAGYV	641	10	35	55	6718
POL	IATDIQTKEL	956	10	35	55	6719
POL	ITKIQNFRV	969	9	36	57	6720
POL	ITKIQNFRVY	969	10	36	57	6721
POL	PAFOSSMTKI	346	11	36	57	6722
POL	QAQPDKSESEL	699	11	36	56	6723
POL	TAFTIPSI	317	8	37	56	6724
POL	YTAFTIPSI	316	9	37	58	6725
POL	LTEAELEL	484	9	37	58	6726
POL	LSWVPAHKGI	725	10	37	58	6727
POL	GAVVIQDINSDI	999	11	37	58	6728
POL	QSSMTKIL	350	8	38	59	6729
POL	KAKIIRDY	1017	8	41	64	6730
POL	RAMASDFNL	772	9	41	64	6731
POL	SAGERIIDI	947	9	41	64	6732
POL	LTQIGCTLNF	177	10	41	64	6733
						6734

Table XIII
 HIV B58 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	YSAGERIIDI	946	10	41	64	6735
POL	SAGERIIDI	947	10	41	64	6736
POL	YSAGERIIDI	946	11	41	64	6737
POL	LTQIGCTL	177	8	42	66	6738
POL	PAIFQSSM	346	8	42	66	6739
POL	YSAGERII	946	8	42	66	6740
POL	ISKIGPENPY	236	10	42	66	6741
POL	GSPAIFQSSM	344	10	42	66	6742
POL	WTYQIQEPF	529	10	42	66	6743
POL	TTNQKTELQAI	664	11	42	66	6744
POL	DSWTVNDI	439	8	43	67	6745
POL	ASCDKCOL	790	8	43	67	6746
POL	VASCDKCOL	789	9	43	67	6747
POL	DSWTVNDIOKL	439	11	43	67	6748
POL	MTKILEPF	353	8	44	69	6749
POL	QTKELQKQI	961	9	46	72	6750
POL	ITLWQRPL	90	8	47	73	6751
POL	ITLWQRPLV	90	9	47	73	6752
POL	KAIGTVLV	157	8	48	75	6753
POL	ITNDVKQL	553	8	49	77	6754
POL	PAGLKKKKS	286	10	50	78	6755
POL	QATWIPEWFEV	599	11	51	81	6756
POL	KSVTVLDV	293	8	51	80	6757
POL	HTDNGSNF	866	8	51	80	6758
POL	ATWIPEWFEV	600	10	51	80	6759
POL	ETVPVKLPGM	192	11	51	80	6760
POL	ETPGIRYQYNV	327	11	51	80	6761
POL	QATWIPEWFE	599	10	52	83	6762
POL	ETPGIRYQY	327	9	52	81	6763
POL	ATWIPEWFE	600	9	52	81	6764
POL	VASGYIEAEV	831	10	52	81	6765
POL	VASGYIEAEVI	831	11	52	81	6766
POL	ASGYIEAEV	832	9	53	83	6767
POL	QSQGVVESM	898	9	53	83	6768
POL	GTVLVGPTPV	160	10	53	83	6769
POL	RTQDFWEVQL	272	10	53	83	6770
POL	VAVHVASGYI	827	10	53	83	6771
POL	ASGYIEAEVI	832	10	53	83	6772
POL	ESMKNELKKI	904	10	53	83	6773
POL	ISPIETVPVKL	188	11	53	83	6774
POL	ESMKNELKKII	904	11	53	83	6775
POL	QATWIPEW	599	8	54	86	6776
POL	RTQDFWEV	272	8	55	86	6777
POL	DAYFSVPL	302	8	55	86	6778
POL	TTNQKTEL	664	8	55	86	6779
POL	ISPIETVPV	188	9	56	88	6780
POL	LTEEKIKAL	213	9	56	88	6781
POL	VTVLDVGDAY	295	10	56	88	6782
POL	KTAVQMAVFI	925	10	56	88	6783
POL	VTVLDVGDAYF	295	11	56	88	6784

Table XIII
 HIV B58 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	PAETGOETAYF	842	11	56	88	6785
POL	LAENREIL	492	8	57	89	6786
POL	NTPLVLKL	610	8	57	89	6787
POL	CSPGIWQL	808	8	57	89	6788
POL	KTAVQMAV	925	8	57	89	6789
POL	NTPLVLKLW	610	9	57	89	6790
POL	ETGOETAYF	844	9	57	89	6791
POL	KTAVQMAVF	925	9	57	89	6792
POL	NTPLVLKLWY	610	10	57	89	6793
POL	FAIKKKSTKW	250	11	57	89	6794
POL	QAEHLKTAVQM	920	11	57	89	6795
POL	STKWRKLVDF	257	10	58	91	6796
POL	VTDQYALGI	688	10	58	91	6797
POL	PAETGOETAY	842	10	58	91	6798
POL	STKWRKLVDF	256	11	58	91	6799
POL	VTDQYALGII	688	11	58	91	6800
POL	DSTKWRKL	256	8	59	92	6801
POL	STKWRKLV	257	8	59	92	6802
POL	VTDQYAL	688	8	59	92	6803
POL	DSQYALGI	690	8	59	92	6804
POL	ETGOETAY	844	8	59	92	6805
POL	DSTKWRKLV	256	9	59	92	6806
POL	DSQYALGII	690	9	59	92	6807
POL	VAVHVASGY	827	9	59	92	6808
POL	QAEHLKTAV	920	9	59	92	6809
POL	TAVQMAVFI	926	9	59	92	6810
POL	MAVFIINF	930	8	60	94	6811
POL	CTLNFIPI	182	10	60	94	6812
POL	TAVQMAVF	926	8	61	95	6813
POL	DTGADDTVL	112	9	61	95	6814
POL	WTVNDIQKL	441	10	61	95	6815
POL	WTVNDIQKL	441	9	62	97	6816
POL	DTGADDTV	112	8	63	98	6817
REV	RARQRQHSI	50	10	10	16	6818
REV	GTQGVGSPQI	97	10	11	18	6819
REV	RSAPVPL	70	8	12	19	6820
REV	SAEPVPLQL	71	9	12	19	6821
REV	RSAPVPLQL	70	10	12	19	6822
REV	RSQDSDELL	4	10	16	25	6823
REV	QARKNRNRW	40	10	16	25	6824
REV	RSQDSDEEL	4	9	17	27	6825
REV	GTSGTQGV	94	8	21	33	6826
REV	PAEPVPLQL	71	9	21	33	6827
REV	QARRNRNRW	40	10	38	59	6828
TAT	PTGPKESKKV	88	11	12	19	6829
VIF	KSLVKYHM	22	8	10	16	6830
VIF	FSDSAIRKAI	120	10	10	16	6831
VIF	YSTQIDPDL	99	9	11	17	6832
VIF	YSTQVDPGL	99	9	11	17	6833
VIF	STQVDPGL	100	8	11	17	6834

Table XIII
HIV B58 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
VIF	KSLVKHHIMYI	22	10	11	17	6835
VIF	VSEWRLLRRY	88	10	11	17	6836
VIF	FSEAIRKAIL	120	11	11	17	6837
VIF	GSLOYLALKAL	148	11	11	17	6838
VIF	STQIDPDL	100	8	12	19	6839
VIF	ESAIRNAI	122	8	12	19	6840
VIF	SAIRNAIL	123	8	12	19	6841
VIF	QITGERDWHL	75	9	12	19	6842
VIF	ESAIRNAIL	122	9	12	19	6843
VIF	KTKPLPSV	164	9	12	19	6844
VIF	FSEAIRKAI	120	10	12	19	6845
VIF	FSEAIRNAI	120	10	12	19	6846
VIF	FSEAIRNAIL	120	11	12	19	6847
VIF	GSLOYLALAL	148	11	12	19	6848
VIF	LADQLIHIMY	107	10	13	20	6849
VIF	ESRIIPKVSSEV	45	11	13	20	6850
VIF	LADQLIHIMYF	107	11	13	20	6851
VIF	PSVKKLTEDRW	173	11	13	20	6852
VIF	NSLVKHHIMYV	22	10	14	22	6853
VIF	LADQLIHILYY	107	10	14	22	6854
VIF	RTWKSLSVKHHIM	19	11	14	22	6855
VIF	LADQLIHILYYF	107	11	14	22	6856
VIF	LADQLIHLY	107	9	15	23	6857
VIF	KTKGHRGSHTM	188	11	15	23	6858
VIF	ESAIRKAIL	122	9	16	25	6859
VIF	LADQLHIM	107	8	17	27	6860
VIF	ESAIRKAI	122	8	17	27	6861
VIF	KSLVKHHIM	22	8	18	28	6862
VIF	KSLVKHHIMY	22	9	18	28	6863
VIF	DSAIRKAIL	122	9	19	30	6864
VIF	DSAIRKAI	122	8	20	31	6865
VIF	HTGERDWHIL	75	9	21	33	6866
VIF	NSLVKHHIMY	22	9	24	38	6867
VIF	RTWNSLSVKHHIM	19	11	24	38	6868
VIF	LADQLHIL	107	8	25	39	6869
VIF	NSLVKHHIM	22	8	27	42	6870
VIF	ISSEVHIPL	51	9	27	42	6871
VIF	VSEVHIPL	51	9	27	42	6872
VIF	GSLOYLALTAL	148	11	31	48	6873
VIF	SAIRKAIL	123	8	35	55	6874
VIF	QAGHNKVGSL	141	10	38	59	6875
VIF	SSEVHIPL	52	8	55	86	6876
VIF	GSLOYLAL	148	8	58	91	6877
VPR	WALELLEL	18	9	59	15	6878
VPR	ETYGDTWTGV	48	10	11	17	6879
VPR	EAVRHFPRI	29	9	14	22	6880
VPR	EAVRHFPRIW	29	10	14	22	6881
VPR	EAVRHFPRIWL	29	11	14	22	6882
VPR	KSEAVRHIF	27	8	15	23	6883
VPR	WAGVEAIRI	54	10	15	23	6884

Table XIII
 HIV-B58 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
VPR	WAGVEAIRIL	54	11	15	23	6885
VPR	WAGVEAII	54	8	16	25	6886
VPR	DTWAGVEAI	52	9	16	25	6887
VPR	ETYGDTWAGV	48	10	16	25	6888
VPR	NTYGDTWEGV	48	10	16	25	6889
VPR	DTWAGVEAII	52	10	16	25	6890
VPR	DTWEGVEAII	52	10	19	30	6891
VPR	DTWEGVEAI	52	9	20	31	6892
VPR	EAIRILQQL	58	10	33	52	6893
VPR	EAIRILQQLL	58	11	33	52	6894
VPR	EAVRIHFPRW	29	10	34	53	6895
VPR	EAVRIHFPRWL	29	11	34	53	6896
VPR	WTLLELLEL	18	9	42	69	6897
VPU	LAKVDYRI	5	8	01	25	6898
VPU	LAKVDYRL	5	8	01	25	6899
VPU	LAKVDYRIV	5	9	01	25	6900
VPU	LAKVDYRIVI	5	10	01	25	6901
VPU	LAKVDYRLGV	5	10	01	25	6902
VPU	LAKVDYRIVIV	5	11	01	25	6903
VPU	VTLLSSSKL	94	9	01	50	6904
VPU	LAIVVALVV	13	8	12	20	6905
VPU	WTIVFIEY	34	8	12	19	6906
VPU	ESEGDAQEEL	75	9	13	20	6907
VPU	ESEGDTTEL	75	9	13	20	6908
VPU	IAIVVWTIV	28	9	20	31	6909
VPU	IAIVVWTI	28	8	23	36	6910

Table XIV

HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
ENV	GIGPGQTF	360	8	01	33	6911
ENV	SIGSGQAF	360	8	01	33	6912
ENV	KLREIRQF	405	8	01	25	6913
ENV	EPDRTERI	823	8	01	33	6914
ENV	PPDRPEGI	823	8	01	33	6915
ENV	GIGPGQTFY	360	9	01	33	6916
ENV	SIGSGQAFY	360	9	01	33	6917
ENV	SIGSGQAFYV	360	10	01	33	6918
ENV	KQLYATVY	34	8	01	50	6919
ENV	QLYATVYAGV	34	10	01	50	6920
ENV	KQLYATVYSGV	34	11	01	50	6921
ENV	TIGAMFLGF	599	9	03	27	6922
ENV	MLGAMFLGF	599	9	04	36	6923
ENV	SLRGLQRGW	889	9	05	18	6924
ENV	RLGWEGLYLW	894	11	07	23	6925
ENV	RLGWEGLYKY	894	9	09	29	6926
ENV	GLRLGWEGLYKY	892	11	09	29	6927
ENV	LILGLVII	21	8	09	15	6928
ENV	IPRRIRQGF	950	8	10	16	6929
ENV	ALFYKLDV	202	8	10	16	6930
ENV	HMLQLTVW	650	8	10	16	6931
ENV	DITNLWLY	769	8	10	16	6932
ENV	DIRQAHICNV	380	9	10	16	6933
ENV	LPCRKQIV	485	9	10	16	6934
ENV	MLQLTVWGI	651	9	10	16	6935
ENV	DITNLWLYI	769	9	10	16	6936
ENV	SOELKNSAV	911	9	10	16	6937
ENV	PIHYCTPAGF	260	10	10	16	6938
ENV	TLPCRKQIV	484	10	10	16	6939
ENV	IPHYCTPAGF	259	11	10	16	6940
ENV	RVGOAMYAPPI	498	11	10	16	6941
ENV	WMEWERIDNY	723	11	10	16	6942
ENV	ALDKWASLWNW	757	11	10	16	6943
ENV	SLKGLRLGW	889	9	11	39	6944
ENV	GIGAVFLGF	598	9	11	18	6945
ENV	KLWVTVYY	44	8	11	17	6946
ENV	AVGIGAVF	595	8	11	17	6947
ENV	KLWVTVYYGV	44	10	11	17	6948
ENV	AVGIGAVFLGF	595	11	11	17	6949
ENV	RIGPGQTF	357	8	11	17	6950
ENV	NITLPCR	482	8	11	17	6951
ENV	WQRYGQAM	496	8	11	17	6952
ENV	QIRCSSNI	512	8	11	17	6953
ENV	ALFYRLDVV	202	9	11	17	6954
ENV	GPCTNVSTV	283	9	11	17	6955
ENV	RIGPGQTFY	357	9	11	17	6956
ENV	WQRYGQAMY	496	9	11	17	6957
ENV	GQIRCSSNI	511	9	11	17	6958
ENV	ALDKWASLW	757	9	11	17	6959
ENV	AVSLLNATAI	918	10	11	17	6960

Table XIV
HIV B62 Super-Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
ENV	NITLPCRIKQI	482	11	11	17	6961
ENV	VVEREKRAVGI	588	11	11	17	6962
ENV	LLALDKWASLW	755	11	11	17	6963
ENV	NMWKNDMMV	107	8	12	19	6964
ENV	ALFYRLDV	202	8	12	19	6965
ENV	RIKQIVNM	488	8	12	19	6966
ENV	KLICITTV	687	8	12	19	6967
ENV	WMEWEREI	723	8	12	19	6968
ENV	ILKCNDKKF	271	9	12	19	6969
ENV	RIKQIVNMW	488	9	12	19	6970
ENV	LICTTTVPW	688	9	12	19	6971
ENV	GOELKNSAI	911	9	12	19	6972
ENV	ALHIPRRI	946	9	12	19	6973
ENV	AILKCNDKKF	270	10	12	19	6974
ENV	KLICITTVPW	687	10	12	19	6975
ENV	NMTWMEWEREI	720	11	12	19	6976
ENV	IVGGLIGLRRI	783	11	12	19	6977
ENV	ELYKYKVVEI	560	10	13	21	6978
ENV	DPNPQEVV	91	8	13	20	6979
ENV	HLKLTW	650	8	13	20	6980
ENV	NVPWNSSW	693	8	13	20	6981
ENV	EIWDNMTW	716	8	13	20	6982
ENV	SIRLVNGF	842	8	13	20	6983
ENV	SIRLVSGF	842	8	13	20	6984
ENV	RLRDLLI	867	8	13	20	6985
ENV	ILHIPRRI	947	8	13	20	6986
ENV	EIKNCSFI	181	9	13	20	6987
ENV	AITQACPKV	244	9	13	20	6988
ENV	SLAEDEVV	311	9	13	20	6989
ENV	QOHLKLTV	648	9	13	20	6990
ENV	LLKLTWGI	651	9	13	20	6991
ENV	AOQHLLKLTV	647	10	13	20	6992
ENV	QQHLLKLTW	648	10	13	20	6993
ENV	HLKLTWGI	650	10	13	20	6994
ENV	EQELLELDKW	752	10	13	20	6995
ENV	VPTDPNPQEVV	88	11	13	20	6996
ENV	VMHSFNCGGEF	432	11	13	20	6997
ENV	TITLPCRIKQI	482	11	13	20	6998
ENV	AOQHLLKLTW	647	11	13	20	6999
ENV	SLAEDEVV	311	8	14	22	7000
ENV	TITLPCRI	482	8	14	22	7001
ENV	SLLNATAI	920	8	14	22	7002
ENV	DPEIVMHSF	428	9	14	22	7003
ENV	GOAMYAPPI	501	9	14	22	7004
ENV	RIIFAVLSI	791	9	14	22	7005
ENV	AVAEGTDRV	928	9	14	22	7006
ENV	EQDLLALDKW	752	10	14	22	7007
ENV	RIFAVLSIV	791	10	14	22	7008
ENV	SLLNATAIIV	920	10	14	22	7009
ENV	AVAEGTDRVI	928	10	14	22	7010

Table XIV
 HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
ENV	VITQACPKVSF	244	11	14	22	7011
ENV	GLRIIFVLSI	789	11	14	22	7012
ENV	AIATAEGTDRV	926	11	14	22	7013
ENV	RLNCNTSAI	236	10	15	24	7014
ENV	GLIGLRII	786	8	15	23	7015
ENV	IIFAVLSI	792	8	15	23	7016
ENV	GPDRPEGI	822	8	15	23	7017
ENV	LINCNTSAI	237	9	15	23	7018
ENV	VITQACPKV	244	9	15	23	7019
ENV	GPCKNVSTV	283	9	15	23	7020
ENV	DIRQAHONI	380	9	15	23	7021
ENV	GLIGLRIIF	786	9	15	23	7022
ENV	IIFAVLSIV	792	9	15	23	7023
ENV	LLNATAIIV	921	9	15	23	7024
ENV	SVITQACPKV	243	10	15	23	7025
ENV	TLPCRIKQII	484	10	15	23	7026
ENV	NMWQEVGKAM	494	10	15	23	7027
ENV	AVAEGTDRII	928	10	15	23	7028
ENV	NMWQEVGKAMY	494	11	15	23	7029
ENV	GLIGLRIIFAV	786	11	15	23	7030
ENV	LIGLRIIF	787	8	16	25	7031
ENV	VVQREKRAV	588	9	16	25	7032
ENV	AVAEGTDRI	928	9	16	25	7033
ENV	RVVQREKRAV	587	10	16	25	7034
ENV	LIGLRIIFAV	787	10	16	25	7035
ENV	LVSGLALAW	845	10	16	25	7036
ENV	DLRNLCFSY	856	10	16	25	7037
ENV	LLNSLAEEV	307	11	16	25	7038
ENV	ELDKWASLWNW	757	11	16	25	7039
ENV	RLVSGFLALAW	844	11	16	25	7040
ENV	AIATAEGTDRI	926	11	16	25	7041
ENV	VQREKRAV	589	8	17	27	7042
ENV	IINMWQEV	492	8	17	27	7043
ENV	KLICTTNV	687	8	17	27	7044
ENV	SLWNWFDI	763	8	17	27	7045
ENV	DLRNLCF	836	8	17	27	7046
ENV	QIINMWQEV	491	9	17	27	7047
ENV	LICTTNVPW	688	9	17	27	7048
ENV	RPNNNTRKSI	347	10	17	27	7049
ENV	KQIINMWQEV	490	10	17	27	7050
ENV	EIFRPGGDM	544	10	17	27	7051
ENV	KLICTTNVPW	687	10	17	27	7052
ENV	RIVFAVLSIV	791	10	17	27	7053
ENV	GVAPTKAKRRV	573	11	17	27	7054
ENV	WQEVGKAM	496	8	18	28	7055
ENV	GLRIIFAV	789	8	18	28	7056
ENV	WQEVGKAMY	496	9	18	28	7057
ENV	ELDKWASLW	757	9	18	28	7058
ENV	IIFAVLSIV	792	9	18	28	7059
ENV	YLDDQQLGI	672	10	18	28	7060

Table XIV
HIV B62 Super-Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
ENV	LPCRKQIINM	485	11	18	28	7061
ENV	EVGKAMYATPI	498	11	18	28	7062
ENV	YLRDQQLGIW	672	11	18	28	7063
ENV	LLELDKWASLW	755	11	18	28	7064
ENV	CLFSYHRLRDF	861	11	18	28	7065
ENV	KLICTTAV	687	8	19	30	7066
ENV	LICTTAVPW	688	9	19	30	7067
ENV	RIVFAVLSI	791	9	19	30	7068
ENV	KLICTTAVPW	687	10	19	30	7069
ENV	GLRIVFAVLSI	789	11	19	30	7070
ENV	ELLELDKW	754	8	20	31	7071
ENV	IVFAVLSI	792	8	20	31	7072
ENV	LPCRKQII	485	9	20	31	7073
ENV	NMVEQMIHEDI	112	10	20	31	7074
ENV	NMVEQMIHEDII	112	11	20	31	7075
ENV	DLLALDKW	754	8	21	33	7076
ENV	DLITTHSF	428	9	21	33	7077
ENV	VPTDPNPQEV	88	10	21	33	7078
ENV	LIGLRIVFAV	787	10	21	33	7079
ENV	CVPTDPNPQEV	87	11	21	33	7080
ENV	GLIGLRIVFAV	786	11	21	33	7081
ENV	APTAKARRV	575	9	22	34	7082
ENV	IVELLGRGW	575	10	22	34	7083
ENV	PWVKEATTLF	879	10	22	34	7084
ENV	EQMIHEDISLW	54	11	22	34	7085
ENV	TVQCTHGIRPV	115	11	22	34	7086
ENV	RIVELLGRGW	290	11	22	34	7087
ENV	ELGRRGW	878	11	22	34	7088
ENV	MVEQMIHEDI	881	8	23	37	7089
ENV	VVKIEPLGV	113	9	23	36	7090
ENV	MVEQMIHEDII	566	9	23	36	7091
ENV	KVKIEPLGV	113	10	23	36	7092
ENV	EQMHEDI	565	8	24	38	7093
ENV	VVEREKRAV	115	9	25	39	7094
ENV	VPTDPNPQEI	588	10	25	39	7095
ENV	VQCTHGIRPV	88	10	25	39	7096
ENV	RVVEREKRAV	292	10	25	39	7097
ENV	QQQNLLRAI	587	10	25	39	7098
ENV	CVPTDPNPQEI	636	11	25	39	7099
ENV	VQCTHGIRPV	87	11	25	39	7100
ENV	VQQQNLLRAI	292	11	25	39	7101
ENV	TLPCRKQI	635	9	26	41	7102
ENV	QQNLLRAI	484	9	26	41	7103
ENV	QQSLLRAI	637	9	26	41	7104
ENV	QQSLLRAI	637	9	26	41	7105
ENV	IPHYCAPAGF	636	10	26	41	7106
ENV	VQQSLLRAI	259	11	26	41	7107
ENV	VQQSLLRAI	635	11	26	41	7108
ENV	PIIHYCAPAGF	635	10	27	42	7109
ENV	YLKDDQQLLGI	260	10	27	42	7110
ENV		672		27		

Table XIV
HAY-B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
ENV	YKDDQQLGIW	672	11	27	42	7111
ENV	KVSFEPIHY	252	11	28	44	7112
ENV	TVQCTHIGKPV	290	11	28	44	7113
ENV	ELYKYKVKI	560	10	29	46	7114
ENV	LIGLRIVF	787	8	29	45	7115
ENV	GLRIVFAV	789	8	29	45	7116
ENV	GLIGLRIVF	786	9	29	45	7117
ENV	QMHEDIISLW	116	10	29	45	7118
ENV	RIKQIINM	488	8	30	47	7119
ENV	TQACPKVSF	247	9	30	47	7120
ENV	CPKVSFEPI	250	9	30	47	7121
ENV	KVSFEPIPI	252	9	30	47	7122
ENV	RIKQIINMW	488	9	30	47	7123
ENV	NMWKNMVEQM	107	11	30	47	7124
ENV	CPKVSFEPIPI	250	11	30	47	7125
ENV	IVGGLIGLRIV	783	11	30	47	7126
ENV	LPCRKIQI	485	8	31	47	7127
ENV	AVLSIVNRV	795	9	31	48	7128
ENV	VQCTHIGKPV	292	11	31	48	7129
ENV	KIFIMVGGI	778	11	31	48	7130
ENV	GLIGLRIV	786	8	32	50	7131
ENV	VQCTHIGKPV	292	10	32	50	7132
ENV	LQARVLAV	662	8	33	52	7133
ENV	RVLAVERY	665	8	33	52	7134
ENV	QLQARVLAV	661	9	33	52	7135
ENV	KOLQARVLAV	660	10	33	52	7136
ENV	LQARVLAVERY	662	11	33	52	7137
ENV	NLWVTVYGV	44	10	34	54	7138
ENV	NVTENFNM	101	8	34	53	7139
ENV	NMWKNNMV	107	8	34	53	7140
ENV	HLLQLTVW	650	8	34	53	7141
ENV	NVTENFNMW	101	9	34	53	7142
ENV	QQHLLQLTV	648	9	34	53	7143
ENV	LLQLTVWGI	651	9	34	53	7144
ENV	AQHLQLTV	647	10	34	53	7145
ENV	QQHLLQLTVW	648	10	34	53	7146
ENV	HLLQLTVWGI	650	10	34	53	7147
ENV	AQHLQLTVW	647	11	34	53	7148
ENV	NLWVTVY	44	8	35	56	7149
ENV	IMIVGGI	781	8	35	56	7150
ENV	FIMIVGGI	780	9	35	55	7151
ENV	DLRSLCLFSY	856	10	35	55	7152
ENV	VQARQLLSGI	625	10	36	56	7153
ENV	SIVNRVQGY	798	10	36	56	7154
ENV	TMGAASTLTV	615	11	36	56	7155
ENV	TVQARQLLSGI	624	11	36	56	7156
ENV	VQARQLLSGIV	625	11	36	56	7157
ENV	MIVGGIIGLRI	782	11	36	56	7158
ENV	DMRDNWRSELY	552	11	37	58	7159
ENV	VLSIVNRV	796	8	38	59	7160

Table XIV
 HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
ENV	DLSLCLF	856	8	38	59	7161
ENV	IVNRVROGY	799	9	38	59	7162
ENV	RPGGDMRDNW	547	11	38	59	7163
ENV	YIKIFIMV	776	9	39	61	7164
ENV	GIKQLQARV	658	9	40	63	7165
ENV	TLFCASDAKAY	64	11	40	63	7166
ENV	IVGGLJGLRI	783	10	42	66	7167
ENV	YIKIFIMI	776	8	43	67	7168
ENV	WLWYIKIFIM	773	10	43	67	7169
ENV	WLWYIKIFIMI	773	11	43	67	7170
ENV	LQLTVWGI	652	8	44	69	7171
ENV	SLWDOSLKPCV	123	11	47	75	7172
ENV	RVRQGYSPLSF	802	11	47	73	7173
ENV	ROGYSPLSF	804	9	48	75	7174
ENV	GIWGCOKLI	680	10	48	75	7175
ENV	ROLLSGIV	628	8	49	77	7176
ENV	NVWATIIACV	80	9	49	77	7177
ENV	WLWYIKIFI	773	9	49	77	7178
ENV	DQSLKPCV	126	8	50	78	7179
ENV	WLWYIKIF	773	8	50	78	7180
ENV	TVQCTHGI	290	8	51	80	7181
ENV	DQQLGIW	675	8	51	80	7182
ENV	NVSTVQCTHGI	287	11	51	80	7183
ENV	KPCVKLTPLCV	130	11	54	84	7184
ENV	TVYYGVVP	48	8	55	86	7185
ENV	TVYYGVVPW	48	9	55	86	7186
ENV	CVKLTPLCV	132	9	55	86	7187
ENV	FLGAAGSTM	608	9	55	86	7188
ENV	WVTVYGVVP	46	10	55	86	7189
ENV	WVTVYGVVPV	46	11	55	86	7190
ENV	ELYKYKV	560	8	56	89	7191
ENV	WVTVYGV	46	8	58	91	7192
GAG	PPESFRF	510	8	01	33	7193
GAG	EPIDKELY	537	8	01	25	7194
GAG	APPESFRF	509	9	01	33	7195
GAG	KQEPIDKELY	535	10	01	25	7196
GAG	KQETHDKDLY	535	10	01	25	7197
GAG	EPLTALRSIF	547	10	01	33	7198
GAG	PPLASLSLF	547	10	01	33	7199
GAG	PPLISLSLF	547	10	01	33	7200
GAG	EPTAPAESF	506	10	01	50	7201
GAG	EPTAPPESF	506	10	01	50	7202
GAG	PPAESFRF	510	8	02	67	7203
GAG	APPAESFRF	509	9	02	67	7204
GAG	PPLASLSLF	546	10	04	24	7205
GAG	YPLASLSLF	545	10	07	15	7206
GAG	YPLASLSLF	545	10	08	17	7207
GAG	NIMMQRGNF	407	9	10	17	7208
GAG	TPSQKQEP	527	9	10	17	7209
GAG	NPPIPVGDI	277	9	10	16	7210

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
GAG	NPPIPVGDIY	277	10	10	16	7211
GAG	QIGWMTSNPPI	267	11	10	16	7212
GAG	KLDKWEKI	12	8	10	16	7213
GAG	GPVAPGQM	242	8	10	16	7214
GAG	PIIPVGGDI	278	8	10	16	7215
GAG	PIAESFGF	498	8	10	16	7216
GAG	PIIPVGGDIY	278	9	10	16	7217
GAG	APPAESFGF	497	9	10	16	7218
GAG	ALSPRTLNAW	167	10	10	16	7219
GAG	ALSPRTLNAWV	167	11	10	16	7220
GAG	IPVGGDIYKRWI	280	11	10	16	7221
GAG	VQNANPDKSI	347	11	10	16	7222
GAG	PIPVGGDIY	279	8	11	17	7223
GAG	SQEVKNWM	334	8	11	17	7224
GAG	IMMOKSNF	408	8	11	17	7225
GAG	PQDLNMLNI	202	10	11	17	7226
GAG	IPVGGDIYKRW	280	10	11	17	7227
GAG	EQASQEVKNW	331	10	11	17	7228
GAG	TPQDLNMLNI	201	11	11	17	7229
GAG	PODLNMLNIV	202	11	11	17	7230
GAG	IVGGIIQAAMQM	211	11	11	17	7231
GAG	TLRAEQATQDV	327	11	11	17	7232
GAG	EQASQEVKNWM	331	11	11	17	7233
GAG	WPSSKGRPGNF	474	11	11	17	7234
GAG	EPIDKELY	533	8	12	19	7235
GAG	KQEPIDKELY	531	10	12	19	7236
GAG	TPQDLNMM	201	8	12	19	7237
GAG	DLNMLNI	204	8	12	19	7238
GAG	TLQEQIAW	263	8	12	19	7239
GAG	TLYCVHQKI	86	9	12	19	7240
GAG	DLNMLNIV	204	9	12	19	7241
GAG	IVGGHQAAAM	211	9	12	19	7242
GAG	TLQEQIAWM	263	9	12	19	7243
GAG	PLTSLKSLF	548	9	12	19	7244
GAG	PLTSLRSLF	548	9	12	19	7245
GAG	NIVGGHQAAAM	210	10	12	19	7246
GAG	TLRAEQASQEV	327	11	12	19	7247
GAG	TIMMQRGNF	407	9	13	22	7248
GAG	SPTSILDI	302	8	13	20	7249
GAG	RMYSPTSILDI	299	11	13	20	7250
GAG	LQEQIAWM	264	8	14	22	7251
GAG	RMYSPTSI	299	8	14	22	7252
GAG	VQNAQGQMV	156	9	14	22	7253
GAG	IVQNAQGQMV	155	10	14	22	7254
GAG	RVHPVHAGPI	235	10	14	22	7255
GAG	IVRMYSPTSI	297	10	14	22	7256
GAG	PIVQNAQGQMV	154	11	14	22	7257
GAG	KIVRMYSPTSI	296	11	14	22	7258
GAG	WPSNKGRI'GNF	474	11	14	22	7259
GAG	KVSQNYPI	148	8	15	27	7260

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
GAG	KVSNYPV	148	9	15	27	7261
GAG	TQDVKNWM	334	8	15	23	7262
GAG	PPEESRF	498	8	15	23	7263
GAG	ELRSLYNTV	76	9	15	23	7264
GAG	TYLCVHQRI	86	9	15	23	7265
GAG	APPEESRF	497	9	15	23	7266
GAG	PLSLKSLF	548	9	15	23	7267
GAG	VLSGGKLDW	7	10	15	23	7268
GAG	SLFNTVATLY	79	10	15	23	7269
GAG	LQGMVHQAI	159	10	15	23	7270
GAG	EQATQDVKNW	331	10	15	23	7271
GAG	EPTAPPEESF	494	10	15	23	7272
GAG	SVLSGGKLDW	6	11	15	23	7273
GAG	NLQGMVHQAI	158	11	15	23	7274
GAG	EQATQDVKNWM	331	11	15	23	7275
GAG	WMTSNPPI	270	8	16	25	7276
GAG	GPAATLEEM	362	9	16	25	7277
GAG	WMTSNPPIV	270	10	16	25	7278
GAG	GPAATLHEMM	362	10	16	25	7279
GAG	LLETSEGCROI	52	11	16	25	7280
GAG	ALGPAATLEEM	360	11	16	25	7281
GAG	GPIPPGQM	242	8	17	27	7282
GAG	DIYKRWI	284	8	17	27	7283
GAG	PVGDIYKRWI	281	10	17	27	7284
GAG	PVGDIYKRWI	281	11	17	27	7285
GAG	ALGPGATLEEM	360	11	17	27	7286
GAG	QIGWMTNPPPI	267	11	18	29	7287
GAG	KLDWKEI	12	8	18	28	7288
GAG	TQEVKNWM	334	8	18	28	7289
GAG	PVGDIYKRW	281	9	18	28	7290
GAG	GPGATLEEM	362	9	18	28	7291
GAG	EQATQEVKNW	331	10	18	28	7292
GAG	GPGATLEEM	362	10	18	28	7293
GAG	EQATQEVKNWM	331	11	18	28	7294
GAG	GPIAPGQM	242	8	19	30	7295
GAG	GPSHKARV	379	8	19	30	7296
GAG	DIKQPKPEF	308	10	19	30	7297
GAG	IWWASRELERF	35	11	19	30	7298
GAG	GVGGPSHKARV	376	11	19	30	7299
GAG	WMTNPPPI	270	8	20	31	7300
GAG	WMTNPPPIV	270	10	20	31	7301
GAG	EPTAPPEESF	494	10	20	31	7302
GAG	YPIVQNAQGM	153	11	20	31	7303
GAG	VIEEKAFSPEV	179	11	20	31	7304
GAG	VQNAQGM	156	8	21	33	7305
GAG	KQPKPEF	310	8	21	33	7306
GAG	IVQNAQGM	155	9	21	33	7307
GAG	PIVQNAQGM	154	10	21	33	7308
GAG	KQPKPEFRDY	310	11	21	33	7309
GAG	SQVSQNYPI	146	9	22	44	7310

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
GAG	SQVSNYPV	146	10	22	44	7311
GAG	WMTDTLLV	340	8	22	34	7312
GAG	SLYNTVATLY	79	10	22	34	7313
GAG	RLIPVHAGPI	235	10	22	34	7314
GAG	WPSIKRPGNF	474	11	23	36	7315
GAG	KVIEKAF	178	8	24	38	7316
GAG	WVKVIEKAF	176	10	24	38	7317
GAG	TLRAEQATQEV	327	11	24	38	7318
GAG	LVWASRELERF	35	11	25	39	7319
GAG	MQMLKETI	219	8	26	41	7320
GAG	AMQMLKETI	218	9	26	41	7321
GAG	QVSNYPV	148	8	27	48	7322
GAG	QVSNYPV	148	9	27	48	7323
GAG	TLQEQIGW	263	8	27	42	7324
GAG	IMMQRGNF	408	8	27	42	7325
GAG	TLQEQIGW	263	9	27	42	7326
GAG	GQMVIQAI	161	8	28	44	7327
GAG	KVIEKAF	178	8	28	44	7328
GAG	WVKVIEKAF	176	10	28	44	7329
GAG	VVEKAFSPV	179	11	28	44	7330
GAG	EPFRDYVDRFY	315	11	28	44	7331
GAG	VQNLOGQM	156	8	29	45	7332
GAG	LQEQIGW	264	8	29	45	7333
GAG	IVQNLOGQM	155	9	29	45	7334
GAG	VQNLOGQM	156	9	29	45	7335
GAG	PIVQNLOGQM	154	10	29	45	7336
GAG	IVQNLOGQM	155	10	29	45	7337
GAG	ASPRTLN	167	10	29	45	7338
GAG	YPIVQNLOGQM	153	11	29	45	7339
GAG	PIVQNLOGQM	154	11	29	45	7340
GAG	ASPRTLN	167	11	29	45	7341
GAG	TLN	172	9	30	47	7342
GAG	TLN	172	9	31	48	7343
GAG	MQMLKDTI	219	8	33	52	7344
GAG	AMQMLKDTI	218	9	33	52	7345
GAG	VLAEMSQQ	386	9	33	52	7346
GAG	RVLAEAMSQQ	385	10	33	52	7347
GAG	NPIPVGEI	277	9	34	54	7348
GAG	NPIPVGEI	277	10	34	54	7349
GAG	RLRPGKKKY	20	10	34	53	7350
GAG	IPVGEIYKRW	280	10	34	53	7351
GAG	PIPVGEIYKRW	279	11	34	53	7352
GAG	IPVGEIYKRW	280	11	34	53	7353
GAG	RPGKKKY	22	8	35	55	7354
GAG	PIPVGEI	278	8	35	55	7355
GAG	PIPVGEI	279	8	35	55	7356
GAG	PIPVGEI	278	9	35	55	7357
GAG	EPFRDYVDRFF	315	11	35	55	7358
GAG	GPCHKARV	379	8	36	56	7359
GAG	GVGPGHKARV	376	11	36	56	7360

Table XIV
HIV-B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
GAG	WMTETLV	340	8	37	58	7361
GAG	HPVHAGPI	237	8	38	59	7362
GAG	RMSPVSILDI	299	11	38	59	7363
GAG	EYKRWII	284	8	39	61	7364
GAG	PVGEIYKRWII	281	11	39	61	7365
GAG	KIVRMYSVSI	296	11	39	61	7366
GAG	RMYSVSI	299	8	40	63	7367
GAG	SPVSILDI	302	8	40	63	7368
GAG	PVGEIYKRW	281	9	40	63	7369
GAG	PVGEIYKRWI	281	10	40	63	7370
GAG	IVRMYSVSI	297	10	40	63	7371
GAG	TVATLYCV	83	8	41	64	7372
GAG	KIVRMYSV	296	9	41	64	7373
GAG	DIRQPKPEF	308	10	41	64	7374
GAG	PDNLNTMLNTV	202	11	41	64	7375
GAG	TTQDLNTM	201	8	42	66	7376
GAG	IVRMYSV	297	8	42	66	7377
GAG	RQPKPEF	310	8	42	66	7378
GAG	DLNTMLNTV	204	9	42	66	7379
GAG	RQPKPEFRDY	310	11	42	66	7380
GAG	QMREPRGSDI	248	10	44	69	7381
GAG	GOMREPRGSDI	247	11	44	69	7382
GAG	VQNPDPCKTI	347	11	45	70	7383
GAG	TVGGHQAAM	211	9	47	73	7384
GAG	TVGGHQAAMQM	211	11	47	73	7385
GAG	TINEEAWE	225	9	53	83	7386
GAG	SPEVIMF	186	8	55	86	7387
GAG	APRKKGCW	440	8	55	86	7388
GAG	SPRTLNAWVKY	169	11	55	86	7389
GAG	RQANFLGKI	465	9	56	88	7390
GAG	RQANFLGKIW	465	10	56	88	7391
GAG	IILGLNKIVRM	290	11	56	88	7392
GAG	SPRTLNAW	169	8	57	89	7393
GAG	IILGLNKI	290	8	57	89	7394
GAG	SPRTLNAWV	169	9	57	89	7395
GAG	WILGLNKI	289	9	57	89	7396
GAG	IILGLNKIV	290	9	57	89	7397
GAG	WILGLNKIV	289	10	57	89	7398
GAG	IILGLNKIVRM	291	10	57	89	7399
GAG	IILGLNKIVRMV	291	11	57	89	7400
GAG	IILGLNKIV	291	8	58	91	7401
GAG	EMMTACQGV	369	9	59	92	7402
GAG	GLNKIVRM	293	8	60	94	7403
GAG	MMTACQGV	370	8	60	94	7404
GAG	GLNKIVRMV	293	9	60	94	7405
GAG	TLNAWVKV	172	8	61	95	7406
GAG	GPKEFRDY	312	9	63	98	7407
GAG	GPKEFRDYV	312	10	63	98	7408
GAG	EPFRDYVDRF	315	10	63	98	7409
NEF	APTAAKGV	34	8	01	33	7410

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
NEF	APTAAGVGAV	34	11	01	33	7411
NEF	KQAEPAAEV	32	10	01	17	7412
NEF	RQAPTAAKGV	32	10	01	17	7413
NEF	QAEPAAAGV	33	10	01	17	7414
NEF	EPAADGVGAV	40	10	04	15	7415
NEF	VPLRPMTF	101	8	10	16	7416
NEF	HPICQHGM	259	8	10	16	7417
NEF	QVPLRPMTF	100	9	10	16	7418
NEF	PQVPLRPMTF	99	10	10	16	7419
NEF	LLHPICQHGM	257	10	10	16	7420
NEF	HMARELIPEY	320	10	10	16	7421
NEF	RQVPLRPMTF	98	11	10	16	7422
NEF	CLLHPMSQHGM	256	11	10	16	7423
NEF	HMARELIPEYY	320	11	10	16	7424
NEF	WQNYTTPRGV	204	10	11	17	7425
NEF	VIVDIPREV	230	8	11	17	7426
NEF	LVPVDIPREV	229	9	11	17	7427
NEF	KLVVDIPREV	228	10	11	17	7428
NEF	PMTYKGAF	105	8	12	19	7429
NEF	HPMSQHGM	259	8	12	19	7430
NEF	RPMTYKGAF	104	9	12	19	7431
NEF	LLHPMSQHGM	257	10	12	19	7432
NEF	PLRPMTYKGAF	102	11	12	19	7433
NEF	SQKRODILDW	177	11	12	19	7434
NEF	WVYHTQGF	191	8	13	20	7435
NEF	TPGPGTRF	208	8	13	20	7436
NEF	GIRYPLTF	213	8	13	20	7437
NEF	WVYHTQGF	191	9	13	20	7438
NEF	DLWVYHTQGF	188	10	13	20	7439
NEF	GPGRYPLTF	210	10	13	20	7440
NEF	GPGRYPLTF	210	10	13	20	7441
NEF	GIRYPLTFGW	213	10	13	20	7442
NEF	DLWVYHTQGF	188	11	13	20	7443
NEF	DLEKHGAI	57	8	14	22	7444
NEF	WLEAQEEVEV	79	10	15	24	7445
NEF	AQEEVEVGF	83	9	17	27	7446
NEF	AQEEVEVGFV	83	11	17	27	7447
NEF	TPGGRY	208	8	17	27	7448
NEF	FPLTFGWCF	217	9	17	27	7449
NEF	TQGFPPDWQNY	195	11	17	27	7450
NEF	WQNYTPGPI	204	10	18	29	7451
NEF	LIYSKKRQEI	174	10	18	28	7452
NEF	GLIYSKKRQEI	173	11	18	28	7453
NEF	DILDWVY	185	8	20	31	7454
NEF	RQDILDWV	182	9	20	31	7455
NEF	RQDILDWVY	182	10	20	31	7456
NEF	WVYHTQGY	191	8	21	33	7457
NEF	WVYHTQGYF	191	9	21	33	7458
NEF	DLWVYHTQGY	188	10	21	33	7459
NEF	DLWVYHTQGYF	188	11	21	33	7460

Table XIV
HIV B62-Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
NEF	TQGFPPDW	195	8	22	34	7461
NEF	YPLTFGWCF	217	9	24	38	7462
NEF	RODILDW	182	8	25	39	7463
NEF	RQEILDWVY	182	10	32	50	7464
NEF	EILDWVY	185	8	33	52	7465
NEF	RQEILDWV	182	9	35	55	7466
NEF	PLTFGWCFKV	219	11	35	55	7467
NEF	RQVPLRPMTY	98	11	36	56	7468
NEF	TQGYFPDWQNY	195	11	36	56	7469
NEF	ROEILDW	182	8	37	58	7470
NEF	TQGYFPDW	195	8	37	58	7471
NEF	EVGFVPRQV	91	10	40	63	7472
NEF	PLTFGWCF	219	8	43	67	7473
NEF	PQVPLRPMTY	99	10	45	70	7474
NEF	VPLRPMTY	101	8	46	73	7475
NEF	QVPLRPMTY	100	9	46	72	7476
NEF	RQVPLRPM	98	9	47	73	7477
NEF	PVRPQVPLRPM	95	11	47	73	7478
NEF	PQVPLRPM	99	8	56	88	7479
POL	SPTSRELQV	35	9	01	33	7480
POL	AISSLTQI	80	9	01	33	7481
POL	SPSSRELQV	38	9	01	50	7482
POL	GPERALSV	70	8	01	20	7483
POL	VPTFNFPQI	79	9	01	17	7484
POL	EPGEDRELSV	69	10	01	17	7485
POL	GQRQGTVLSLF	69	11	01	17	7486
POL	POGEAREF	9	8	10	16	7487
POL	FPQGEAREF	8	9	10	16	7488
POL	LIEICGHKAI	150	10	10	16	7489
POL	AVQKIATESI	563	10	10	16	7490
POL	MLTQLGCTLNF	176	11	10	16	7491
POL	AVQKIATESIV	563	11	10	16	7492
POL	AVKAAACWWAGI	877	11	10	16	7493
POL	IQTKELOKQII	960	11	10	16	7494
POL	RIGPENPY	238	8	11	17	7495
POL	YQLETEPI	619	8	11	17	7496
POL	AQEDIEKY	760	8	11	17	7497
POL	GIQQEFGI	886	8	11	17	7498
POL	KVVPKRKV	1011	8	11	17	7499
POL	VPRRKVKI	1013	8	11	17	7500
POL	VPRRKVKI	1012	9	11	17	7501
POL	VPRRKVKII	1013	9	11	17	7502
POL	IKDYGKQM	1020	9	11	17	7503
POL	GIQQEFGIPY	886	10	11	17	7504
POL	KVVPKRKVYKI	1011	10	11	17	7505
POL	VPRRKVKII	1012	10	11	17	7506
POL	KIKDYGKQM	1019	10	11	17	7507
POL	KISRIGPENPY	235	11	11	17	7508
POL	IPSTNNETPGI	321	11	11	17	7509
POL	KLWYQLETEPI	616	11	11	17	7510

Table XIV
 HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	KVPRRKVKII	1011	11	11	17	7511
POL	KQIKIONF	967	9	12	19	7512
POL	IKIONFRV	969	9	12	19	7513
POL	IKIONFRVY	969	10	12	19	7514
POL	KQIKIONFRV	967	11	12	19	7515
POL	IKIONFRVY	969	11	12	19	7516
POL	RPLVTVKI	95	8	12	19	7517
POL	EINLPKW	122	8	12	19	7518
POL	QIKIONF	968	8	12	19	7519
POL	VIQNSEI	1003	8	12	19	7520
POL	RQHLLRWGF	395	9	12	19	7521
POL	NQKTELHAI	666	9	12	19	7522
POL	IIDIASDI	952	9	12	19	7523
POL	IVDIIATDI	952	9	12	19	7524
POL	VVIQNSEI	1002	9	12	19	7525
POL	IQDNSEIKV	1004	9	12	19	7526
POL	WQRPLTVKI	93	10	12	19	7527
POL	RQYDQPIEI	144	10	12	19	7528
POL	GQDQWYQIY	525	10	12	19	7529
POL	RMRGATINDV	548	10	12	19	7530
POL	NQKTELQAIY	666	10	12	19	7531
POL	RIDIASDI	951	10	12	19	7532
POL	RIVDIIATDI	951	10	12	19	7533
POL	QIKIONFRV	968	10	12	19	7534
POL	AVVIQDNSEI	1000	10	12	19	7535
POL	VIQDNSEIKV	1003	10	12	19	7536
POL	IQDNSEIKV	1004	10	12	19	7537
POL	VLEEINLPKW	119	11	12	19	7538
POL	ELRQHLLRWGF	393	11	12	19	7539
POL	HPDKWTVQPIV	424	11	12	19	7540
POL	IQKQGQDQWY	521	11	12	19	7541
POL	LQKQIKIONF	965	11	12	19	7542
POL	QIKIONFRVY	968	11	12	19	7543
POL	VVIQDNSEIKV	1002	11	12	19	7544
POL	VIQDNSEIKV	1003	11	12	19	7545
POL	ELQKQIKI	964	9	13	21	7546
POL	NLKTGYARM	540	10	13	21	7547
POL	DINLPKW	122	8	13	20	7548
POL	ROYDQPI	144	8	13	20	7549
POL	QLPEKDSW	434	8	13	20	7550
POL	VLPEKDSW	434	8	13	20	7551
POL	LQKQIKI	965	8	13	20	7552
POL	IQLEKDSW	433	9	13	20	7553
POL	IVLPEKDSW	433	9	13	20	7554
POL	IQKQGQDQW	521	9	13	20	7555
POL	GQDQWYQI	525	9	13	20	7556
POL	SPTRELOVW	29	10	13	20	7557
POL	KVRQYDQPI	142	10	13	20	7558
POL	LIEICGKAI	150	10	13	20	7559
POL	PIQLPEKDSW	432	10	13	20	7560

Table XIV
 CHY B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	PIVLPEKDSW	432	10	13	20	7561
POL	QLPEKDSWTV	434	10	13	20	7562
POL	VLPEKDSWTV	434	10	13	20	7563
POL	ELQKQGDQW	520	10	13	20	7564
POL	EOAEHLKTAV	919	10	13	20	7565
POL	VLEDINLPKRW	119	11	13	20	7566
POL	ILIEICGRKAI	149	11	13	20	7567
POL	QPIQLPEKDSW	431	11	13	20	7568
POL	QPIVLPEKDSW	431	11	13	20	7569
POL	IOLPEKDSWTV	433	11	13	20	7570
POL	IVLPEKDSWTV	433	11	13	20	7571
POL	KQGQDQWYQI	523	11	13	20	7572
POL	LIKKEKVYLSW	717	11	13	20	7573
POL	KLGRWPVKTI	855	11	13	20	7574
POL	RPLVTIKI	95	8	14	22	7575
POL	KQNPDI VI	362	8	14	22	7576
POL	KIATESIV	566	8	14	22	7577
POL	YQLEKDP I	619	8	14	22	7578
POL	SPTRRELQV	29	9	14	22	7579
POL	KQNPDI VI	362	9	14	22	7580
POL	VQKIATESI	564	9	14	22	7581
POL	KIATESIV	566	9	14	22	7582
POL	WORPLVTIKI	93	10	14	22	7583
POL	VQKIATESIV	564	10	14	22	7584
POL	KIATESIV	566	10	14	22	7585
POL	TIHTDNGSNF	864	10	14	22	7586
POL	EPFRKQNPDI V	358	11	14	22	7587
POL	KQNPDI VI YQY	362	11	14	22	7588
POL	ELREHLKKGWF	393	11	14	22	7589
POL	VQKIATESIV	564	11	14	22	7590
POL	KLWYQLEKDPH	616	11	14	22	7591
POL	LVEICTEM	221	8	15	24	7592
POL	KIKALVEI	217	8	15	23	7593
POL	TQLGCTLNF	178	9	15	23	7594
POL	ALVEICTEM	220	9	15	23	7595
POL	ELRQHLLRW	393	9	15	23	7596
POL	IQKQGGQW	521	9	15	23	7597
POL	KQGQDQWY	523	9	15	23	7598
POL	IQKETWEAW	585	9	15	23	7599
POL	LVSAGIRKV	743	9	15	23	7600
POL	LPGRWPKPMI	125	10	15	23	7601
POL	ELQKQGGQW	520	10	15	23	7602
POL	PIQKETWEAW	584	10	15	23	7603
POL	IQKETWEAW	585	10	15	23	7604
POL	QVDKLV SAGI	739	10	15	23	7605
POL	KLVSAGIRKV	742	10	15	23	7606
POL	TQLGCTLNFPI	178	11	15	23	7607
POL	PLTEEKIKALV	212	11	15	23	7608
POL	IQKQGGQWY	521	11	15	23	7609
POL	LPIQKETWEAW	583	11	15	23	7610

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	PIKETWEAWW	584	11	15	23	7611
POL	HILALQDSGLEV	675	11	15	23	7612
POL	EQVDKLYSAGI	738	11	15	23	7613
POL	LVSAGIRKVLV	743	11	15	23	7614
POL	QLGCTLNF	179	8	16	25	7615
POL	QLEKEPIV	620	8	16	25	7616
POL	AQEEHERY	760	8	16	25	7617
POL	LPGRWPKPM	125	9	16	25	7618
POL	YOLEKEPIV	619	9	16	25	7619
POL	IQQEFQIPY	887	9	16	25	7620
POL	QLGCTLNFPI	179	10	16	25	7621
POL	EPFRKQNPDI	358	10	16	25	7622
POL	TPKFKLPI	578	8	17	27	7623
POL	NPDIYQY	364	9	17	27	7624
POL	ELREHLLKW	393	9	17	27	7625
POL	NPDIYVQYM	364	10	17	27	7626
POL	MLTQIGCTLNF	176	11	17	27	7627
POL	NLKTGKYAKM	540	10	18	29	7628
POL	SVPLDKDF	306	8	18	28	7629
POL	DIVIYQYM	366	8	18	28	7630
POL	TLWQRPLVTI	91	10	18	28	7631
POL	IIGRNMLTQI	171	10	18	28	7632
POL	VPLDKDFRKY	307	10	18	28	7633
POL	NIIGRNMLTQI	170	11	18	28	7634
POL	SVPLDKDFRKY	306	11	18	28	7635
POL	LLRGTKALTEV	471	11	18	28	7636
POL	ELVNOHIEQLI	708	11	18	28	7637
POL	AMASDFNLPHI	773	11	18	28	7638
POL	PLWKGPAKLLW	985	11	18	28	7639
POL	PLDKDFRKY	308	9	19	30	7640
POL	WQRPLVTI	93	8	19	30	7641
POL	EICGHKAI	152	8	19	30	7642
POL	LVNQHIEQLI	709	10	19	30	7643
POL	LVSQHIEQLI	709	10	19	30	7644
POL	EICGHKAIGTV	152	11	19	30	7645
POL	ELVSQHIEQLI	708	11	19	30	7646
POL	QQEFGIPY	888	8	20	32	7647
POL	QYDQILI	144	8	20	31	7648
POL	SQHIEQLI	711	8	20	31	7649
POL	KLPQKETW	582	9	20	31	7650
POL	KVRQYDQILI	142	10	20	31	7651
POL	ROYDQILIEI	144	10	20	31	7652
POL	DLEIGHRTKI	381	11	20	31	7653
POL	LIKKEKYYLAW	717	11	20	31	7654
POL	TVKAACWWAGI	877	11	20	31	7655
POL	KVIHTDGSNF	863	11	21	33	7656
POL	WQRPLVTI	93	8	21	33	7657
POL	EIGHRTKI	383	9	21	33	7658
POL	EPVGAETI	624	9	21	33	7659
POL	TLWQRPLVTI	91	10	21	33	7660

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	IIGRNLLTOI	171	10	21	33	7661
POL	EPVGAETFY	624	10	21	33	7662
POL	NIIGRNLLTOI	170	11	21	33	7663
POL	LLTQIGCTLNF	176	11	21	33	7664
POL	EPVGAETFYV	624	11	21	33	7665
POL	DQWTYQIY	527	8	22	34	7666
POL	GIKQEFGI	886	8	22	34	7667
POL	GIKQEFGI	886	10	22	34	7668
POL	LLRGAKALTDI	471	11	22	34	7669
POL	YLAWVPAHKG	724	11	22	34	7670
POL	KLGRWPVKVI	855	11	22	34	7671
POL	NPEIVYQY	364	9	23	36	7672
POL	HLEGKVLV	819	9	23	36	7673
POL	KVILVAVHV	823	9	23	36	7674
POL	NPEIVYQYM	364	10	23	36	7675
POL	EICGKKAIGTV	152	11	23	36	7676
POL	HLEGKVLVAV	819	11	23	36	7677
POL	EICGKKAI	152	8	24	38	7678
POL	NPYNTPIF	243	8	24	38	7679
POL	EIVYQYM	366	8	24	38	7680
POL	NOHEQLI	711	8	24	38	7681
POL	VILVAVIV	824	8	24	38	7682
POL	TVKAAACW	877	8	24	38	7683
POL	PVNIIGRNM	168	9	24	38	7684
POL	TPVNIIGRNM	167	10	24	38	7685
POL	GPENPYNTPI	240	10	24	38	7686
POL	NPYNTPIF	243	10	24	38	7687
POL	GQGQWTYQIY	525	10	24	38	7688
POL	VIHTDNGSNF	864	10	24	38	7689
POL	GPENPYNTPIF	240	11	24	38	7690
POL	LQDSGSEV	678	8	25	39	7691
POL	LLKLAGRW	853	8	25	39	7692
POL	KQGQGWYTY	523	9	25	39	7693
POL	GQGQWTYQI	525	9	25	39	7694
POL	ALQDSGSEV	677	9	25	39	7695
POL	FLKLAGRW	852	9	25	39	7696
POL	LQDSGSEVNI	678	10	25	39	7697
POL	LLKLAGRWVP	853	10	25	39	7698
POL	KQGQGWYTYQI	523	11	25	39	7699
POL	LQDSGSEVNI	677	11	25	39	7700
POL	LQDSGSEVNI	678	11	25	39	7701
POL	AMASDFNLPPV	773	11	25	39	7702
POL	FLKLAGRWVP	852	11	25	39	7703
POL	QLDCTHLEGV	814	11	26	41	7704
POL	PVAKIV	782	8	26	41	7705
POL	EIGQHRAKI	383	9	26	41	7706
POL	RLPIQKETW	582	9	26	41	7707
POL	LVSSGIRKV	743	9	26	41	7708
POL	PPIVAKIV	781	9	26	41	7709
POL	DPSKDLIAEI	512	10	26	41	7710

Table XIV
 HLXB62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	KLVSSGIRKV	742	10	26	41	7711
POL	NLPPIVAKEI	779	10	26	41	7712
POL	LPPVAKEIV	780	10	26	41	7713
POL	DLEIGHORAKI	381	11	26	41	7714
POL	LVSSGIRKVLV	743	11	26	41	7715
POL	NLPPIVAKEIV	779	11	26	41	7716
POL	QIYAGIKV	458	8	27	43	7717
POL	QIYPGIV	458	8	27	43	7718
POL	LQDSGLEV	678	8	27	42	7719
POL	AQEEHEKY	760	8	27	42	7720
POL	PPIVAKEI	781	8	27	42	7721
POL	SQIYAGIKV	457	9	27	42	7722
POL	SQIYPGIV	457	9	27	42	7723
POL	IQKETWETW	585	9	27	42	7724
POL	ALQDSGLEV	677	9	27	42	7725
POL	LPPVAKEI	780	9	27	42	7726
POL	PIQKETWETW	584	10	27	42	7727
POL	IQKETWETWW	585	10	27	42	7728
POL	LQDSGLEVNI	678	10	27	42	7729
POL	NLPPVAKEI	779	10	27	42	7730
POL	LPPVAKEIV	780	10	27	42	7731
POL	LPIQKETWETW	583	11	27	42	7732
POL	PIQKETWETWW	584	11	27	42	7733
POL	YVTDGRQKV	649	11	27	42	7734
POL	ALQDSGLEVNI	677	11	27	42	7735
POL	LQDSGLEVNIV	678	11	27	42	7736
POL	NLPPVAKEIV	779	11	27	42	7737
POL	KQEFGIPY	888	8	28	44	7738
POL	KIKALTEI	217	8	28	44	7739
POL	PIVGAETF	625	8	28	44	7740
POL	IVGAETFY	626	8	28	44	7741
POL	QLIKKEKV	716	8	28	44	7742
POL	PVVAKEIV	782	8	28	44	7743
POL	PIVGAETFY	625	9	28	44	7744
POL	IVGAETFYV	626	9	28	44	7745
POL	EQLIKKEKV	715	9	28	44	7746
POL	QLIKKEKVY	716	9	28	44	7747
POL	LPPVAKEI	780	9	28	44	7748
POL	PPVAKEIV	781	9	28	44	7749
POL	PIVGAETFYV	625	10	28	44	7750
POL	EQLIKKEKVY	715	10	28	44	7751
POL	IEQLIKKEKV	713	11	28	44	7752
POL	PPVAKEI	781	8	29	45	7753
POL	IIDIATDI	952	9	29	45	7754
POL	YVTDGRQKV	649	10	29	45	7755
POL	QVDKLVSSGI	739	10	29	45	7756
POL	RIDIATDI	951	10	29	45	7757
POL	EQVDKLVSSGI	738	11	29	45	7758
POL	TPKFLPI	578	8	30	47	7759
POL	IILVAVHIV	824	8	30	47	7760

Table XIV
 HIV-1 B2 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	KILVAVHV	823	9	30	47	7761
POL	KLGRWPVKV	855	10	30	47	7762
POL	GQWTYQIY	527	8	31	48	7763
POL	YQLEKEPI	619	8	31	48	7764
POL	GOETAYFI	846	8	31	48	7765
POL	HLEGKILV	819	9	31	48	7766
POL	IPSINNETPGI	321	11	31	48	7767
POL	GVYYDPSKDLI	508	11	31	48	7768
POL	KLWYQLEKEPI	616	11	31	48	7769
POL	HLEGKILVAV	819	11	31	48	7770
POL	KOLTEAVOKI	558	10	32	51	7771
POL	AVKAAACWW	877	8	32	50	7772
POL	SINNETPGI	323	9	32	50	7773
POL	FILKLAGRW	852	9	32	50	7774
POL	EMEKEGKISKI	229	11	32	50	7775
POL	SINNETPGIRY	323	11	32	50	7776
POL	FILKLAGRWPV	852	11	32	50	7777
POL	QLDCTHLEGKI	814	11	33	52	7778
POL	DVKQLTEAV	556	9	33	52	7779
POL	ELQKQITKI	964	9	34	54	7780
POL	KQITKIQNF	967	9	34	54	7781
POL	KQITKIQNFRV	967	11	34	54	7782
POL	ILKLAGRW	853	8	34	53	7783
POL	QLTEAVQKI	559	9	34	53	7784
POL	ILKLAGRWPV	853	10	34	53	7785
POL	LQKQITKIQNF	965	11	34	53	7786
POL	RVYYNDSRDIPI	976	11	34	53	7787
POL	LIKKEKVV	717	8	35	55	7788
POL	QITKIQNF	968	8	35	55	7789
POL	NLPKWKPKM	124	10	35	55	7790
POL	QITKIQNFRV	968	10	35	55	7791
POL	NLPKWKPKMI	124	11	35	55	7792
POL	QITKIQNFRVY	968	11	35	55	7793
POL	PIWKGPAKLLW	985	11	35	55	7794
POL	KLGRAGYV	643	8	36	56	7795
POL	LQKQITKI	965	8	36	56	7796
POL	AIFQSSMTKI	347	10	36	56	7797
POL	AOPDKSESELV	700	11	36	56	7798
POL	VIQDNSDI	1003	8	37	58	7799
POL	VVIQDNSDI	1002	9	37	58	7800
POL	NPYNTVPFAI	243	10	37	58	7801
POL	QPDKSESELV	701	10	37	58	7802
POL	AVVIQDNSDI	1000	10	37	58	7803
POL	VIQDNSDIKV	1003	10	37	58	7804
POL	YLSWVPAHKGII	724	11	37	58	7805
POL	VVIQDNSDIKV	1002	11	37	58	7806
POL	VVIQDNSDIKV	1003	11	37	58	7807
POL	NPYNTVPF	243	8	38	59	7808
POL	FQSSMTKI	349	8	38	59	7809
POL	IQDNSDIKV	1004	9	38	59	7810

Table XIV
HIV-1 B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	GPENPYNTPV	240	10	38	59	7811
POL	IQDNSDIKVV	1004	10	38	59	7812
POL	GPENPYNTPVF	240	11	38	59	7813
POL	ILKEPVHGVVY	498	11	38	59	7814
POL	LPGKWKPKM	125	9	39	61	7815
POL	LPGKWKPKMI	125	10	39	61	7816
POL	LPEKDSWTV	435	9	40	63	7817
POL	ILKEPVHGVY	498	10	40	63	7818
POL	EILKEPVHGVY	497	11	40	63	7819
POL	KVRQYDQI	142	8	41	64	7820
POL	QIGCTLNF	179	8	41	64	7821
POL	EPVHGYY	504	8	41	64	7822
POL	TQIGCTLNF	178	9	41	64	7823
POL	ILKEPVHGV	498	9	41	64	7824
POL	FIKVRQYDQI	140	10	41	64	7825
POL	QIGCTLNFI	179	10	41	64	7826
POL	EILKEPVHGV	497	11	41	64	7827
POL	TQIGCTLNFI	178	11	41	64	7828
POL	KISKIGPENPY	235	11	41	64	7829
POL	SIVIWGKTPKF	571	11	41	64	7830
POL	EMEKEGKI	229	8	42	66	7831
POL	SPAIFQSSM	345	9	42	66	7832
POL	NQTELOAI	666	9	42	66	7833
POL	IVIYQYMDILY	367	11	42	66	7834
POL	YQIYQEPF	531	8	43	67	7835
POL	SMTKILEPF	352	9	43	67	7836
POL	QIYQYMDILY	1027	8	44	69	7837
POL	QIYQYMDILY	1026	9	44	69	7838
POL	QIYQYMDILY	1026	10	44	69	7839
POL	QIYQYMDILY	1026	11	44	69	7840
POL	QIYQYMDILY	1026	11	44	69	7841
POL	QIYQYMDILY	1026	11	44	69	7842
POL	QIYQYMDILY	1026	11	44	69	7843
POL	QIYQYMDILY	1026	11	44	69	7844
POL	QIYQYMDILY	1026	11	44	69	7845
POL	QIYQYMDILY	1026	11	44	69	7846
POL	QIYQYMDILY	1026	11	44	69	7847
POL	QIYQYMDILY	1026	11	44	69	7848
POL	QIYQYMDILY	1026	11	44	69	7849
POL	QIYQYMDILY	1026	11	44	69	7850
POL	QIYQYMDILY	1026	11	44	69	7851
POL	QIYQYMDILY	1026	11	44	69	7852
POL	QIYQYMDILY	1026	11	44	69	7853
POL	QIYQYMDILY	1026	11	44	69	7854
POL	QIYQYMDILY	1026	11	44	69	7855
POL	QIYQYMDILY	1026	11	44	69	7856
POL	QIYQYMDILY	1026	11	44	69	7857
POL	QIYQYMDILY	1026	11	44	69	7858
POL	QIYQYMDILY	1026	11	44	69	7859
POL	QIYQYMDILY	1026	11	44	69	7860

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	VPRRKAKI	1013	8	51	80	7861
POL	KPGMDGPKV	199	9	51	80	7862
POL	VVPRRKAKI	1012	9	51	80	7863
POL	GMDGPKVKQW	201	10	51	80	7864
POL	TPGIRYQYNV	328	10	51	80	7865
POL	VYQYMDLKY	368	10	51	80	7866
POL	KVPRRKAKI	1011	10	51	80	7867
POL	VLVGPTPVNII	162	11	51	80	7868
POL	VYQYMDLKY	368	11	51	80	7869
POL	WIPEWFEV	602	8	52	84	7870
POL	IQNFRVYY	972	8	52	84	7871
POL	GLKKKKS	288	8	52	81	7872
POL	TPGIRYQY	328	8	52	81	7873
POL	GIRYQYNV	330	8	52	81	7874
POL	KIQNFRVY	971	8	52	81	7875
POL	KIQNFRVYY	971	9	52	81	7876
POL	LVGPTPVNII	163	10	52	81	7877
POL	WQATWIPEWFE	598	11	52	81	7878
POL	HVASGYIEAEV	830	11	52	81	7879
POL	VLVGPTPV	162	8	53	83	7880
POL	CQLKGEAM	795	8	53	83	7881
POL	SQGVVFSM	899	8	53	83	7882
POL	TVLVGPTPV	161	9	53	83	7883
POL	AVIIVASGYI	828	9	53	83	7884
POL	SMNKELKKI	905	9	53	83	7885
POL	VLVGPTPVNI	162	10	53	83	7886
POL	HPDKWTVOPI	424	10	53	83	7887
POL	ELELAENREI	489	10	53	83	7888
POL	LVAVHVASGY	826	10	53	83	7889
POL	POSQGVVFSM	897	10	53	83	7890
POL	SMNKELKKII	905	10	53	83	7891
POL	GIGGFIVRQY	136	11	53	83	7892
POL	TVLVGPTPVNI	161	11	53	83	7893
POL	VLDVGDAYFSV	297	11	53	83	7894
POL	QLKGEAMHGQV	796	11	53	83	7895
POL	ILVAVIIVASGY	825	11	53	83	7896
POL	NPQSQGVVFSM	896	11	53	83	7897
POL	FVNTPLV	608	8	54	86	7898
POL	FVNTPLVKLW	608	11	54	86	7899
POL	GPTPVNII	165	8	54	84	7900
POL	LVGPTPVNI	163	9	54	84	7901
POL	DVGDAYFSV	299	9	54	84	7902
POL	WQATWIPEW	598	9	54	84	7903
POL	TVPVKLKPGM	193	10	54	84	7904
POL	FPISPIETVPV	186	11	55	86	7905
POL	TQDFWEVQLGI	273	11	55	86	7906
POL	SPIETVPV	189	8	56	88	7907
POL	PVKLKPGM	195	8	56	88	7908
POL	WPLTEEKI	211	8	56	88	7909
POL	FPISPIETV	186	9	56	88	7910

Table XIV
HY B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	VPVKLKPGM	194	9	56	88	7911
POL	PSPIETVPV	187	10	56	88	7912
POL	KQWPLTEKI	209	10	56	88	7913
POL	SVTVLDVGDAY	294	11	56	88	7914
POL	PSPIETV	187	8	57	89	7915
POL	ELAENREI	491	8	57	89	7916
POL	TPPLVKLW	611	8	57	89	7917
POL	PPLVKLWY	612	8	57	89	7918
POL	QVDCSPGI	805	8	57	89	7919
POL	HLKTAVQM	923	8	57	89	7920
POL	ELNKRTODF	268	9	57	89	7921
POL	TVLDVGDAY	296	9	57	89	7922
POL	TPPLVKLWY	611	9	57	89	7923
POL	GOVDCSPGI	804	9	57	89	7924
POL	QVDCSPGIW	805	9	57	89	7925
POL	ELKKIIGOV	909	9	57	89	7926
POL	AIKKKDKTW	251	10	57	89	7927
POL	ELNKRTODFW	268	10	57	89	7928
POL	TVLDVGDAYF	296	10	57	89	7929
POL	GOVDCSPGIW	804	10	57	89	7930
POL	HLKTAVQMAV	923	10	57	89	7931
POL	HLKTAVQMAVF	923	11	57	89	7932
POL	GIGGYSAGERI	942	11	57	89	7933
POL	LPQGWKGSPI	338	11	58	92	7934
POL	YVGSDLFI	377	8	58	91	7935
POL	DLVYVGSLEI	375	10	58	91	7936
POL	IVTDSQYALGI	687	11	58	91	7937
POL	IPAEITQETAY	841	11	58	91	7938
POL	FIHNFKRKGGI	933	11	58	91	7939
POL	SQYALGII	691	8	59	92	7940
POL	GIGGNEQV	733	8	59	92	7941
POL	AVHVASGY	828	8	59	92	7942
POL	KLGRWPV	855	8	59	92	7943
POL	NPQSQGVV	896	8	59	92	7944
POL	PQGWKGSPI	339	10	59	92	7945
POL	EVNIVTDSQY	684	10	59	92	7946
POL	PQGWKGSPIF	339	11	59	92	7947
POL	IPYNPQSQGVV	893	11	59	92	7948
POL	KLLWKGEAVV	992	11	59	92	7949
POL	LLWKGEAVVI	993	11	59	92	7950
POL	KPKMIGGI	130	8	60	94	7951
POL	VLDVGDAY	297	8	60	94	7952
POL	AVQMAVEI	927	8	60	94	7953
POL	VLDVGDAYF	297	9	60	94	7954
POL	ELHPDKWTV	422	9	60	94	7955
POL	KLNWASQIY	452	9	60	94	7956
POL	QMAVFIHNF	929	9	60	94	7957
POL	VQMAVFIHNF	928	10	60	94	7958
POL	KLLWKGEAV	992	10	60	94	7959
POL	KPKMIGGIGGF	130	11	60	94	7960

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
POL	WMGYELHPDKW	418	11	60	94	7961
POL	LVGKLNWASQI	449	11	60	94	7962
POL	AVQMAVFHINF	927	11	60	94	7963
POL	TLNFPISI	183	9	61	97	7964
POL	YQYMDLKY	370	8	61	95	7965
POL	KNWASQI	452	8	61	95	7966
POL	YQYMDLKY	370	9	61	95	7967
POL	TVNDIQKLV	442	9	61	95	7968
POL	LLWKGEQAVV	993	10	61	95	7969
POL	ALLDTGADDTV	109	11	61	95	7970
POL	MIGGIGGF	133	8	62	97	7971
POL	KLVGKLNW	448	8	62	97	7972
POL	NIVTDSQY	686	8	62	97	7973
POL	KMIGGIGGF	132	9	62	97	7974
POL	MIGGIGGF	133	9	62	97	7975
POL	HQKEPFLW	410	9	62	97	7976
POL	LLWKGEQAV	993	9	62	97	7977
POL	KMIGGIGGF	132	10	62	97	7978
POL	HQKEPFLWM	410	10	62	97	7979
POL	IQKLVGKLNW	446	10	62	97	7980
POL	MIGGIGGF	133	11	62	97	7981
POL	DIQKLVGKLNW	445	11	62	97	7982
POL	WVPAHKGH	727	8	63	98	7983
POL	EPFLWMGY	413	9	63	98	7984
POL	LLDTGADDTV	110	10	63	98	7985
POL	YQYNVLPQGW	333	10	63	98	7986
POL	IPYNPQSQV	893	10	63	98	7987
POL	GIPYNPQSQV	892	11	63	98	7988
POL	GIGGFIKV	136	8	64	100	7989
POL	PPFLWMGY	414	8	64	100	7990
REV	PQGTETGV	101	8	05	18	7991
REV	SQGTETGV	101	8	05	18	7992
REV	QPQGTETGV	100	9	05	18	7993
REV	CLGRPAEPV	67	9	10	16	7994
REV	TQGVGSFQI	98	9	11	18	7995
REV	LLKTVRLI	12	8	11	17	7996
REV	RQRIHSI	52	8	11	17	7997
REV	VPQLPPI	75	8	11	17	7998
REV	VPVPLPPI	74	9	11	17	7999
REV	EPVPLPPI	73	10	11	17	8000
REV	AVRIKILY	17	9	13	20	8001
REV	ROARKNRNRW	39	11	16	25	8002
REV	IKILYQSNPY	20	11	18	25	8003
REV	KILYQSNPY	22	9	26	41	8004
REV	ILYQSNPY	23	8	27	42	8005
REV	RQARNRNRW	39	11	38	59	8006
TAT	GPESKSKKV	90	9	13	20	8007
TAT	EPVDPRLPWP	2	10	13	20	8008
TAT	FLNKGLGI	41	8	14	22	8009
TAT	PVDPRLPWP	3	9	14	22	8010

Table XIV
 C-HLY B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
TAT	EPVDPNLEPW	2	10	14	22	8011
TAT	FLNKGGLGISY	41	10	14	22	8012
TAT	PVDPNLEPW	3	9	20	31	8013
VIF	ALIKPKKI	157	8	10	16	8014
VIF	PLGEARLVI	58	9	10	16	8015
VIF	QVDRMRINTW	12	10	10	16	8016
VIF	HIPLGDARLV	56	10	10	16	8017
VIF	IPLGEARLVI	57	10	10	16	8018
VIF	WQVDRMRINTW	11	11	10	16	8019
VIF	HIPLGEARLVI	56	11	10	16	8020
VIF	GVSEWRRLRY	87	11	10	16	8021
VIF	QIDPDLADQLI	102	11	10	16	8022
VIF	PLGDARLV	58	8	11	17	8023
VIF	IPLGDARLV	57	9	11	17	8024
VIF	SIEWRLRY	89	9	11	17	8025
VIF	GLADQLIHIMHY	106	11	11	17	8026
VIF	RLVITTYW	65	8	12	19	8027
VIF	LQTGERDW	74	8	12	19	8028
VIF	KIRTWNSLV	17	9	12	19	8029
VIF	GLOTGERDW	73	9	12	19	8030
VIF	IVWQVDRMKI	9	10	12	19	8031
VIF	QVDRMKIRTW	12	10	12	19	8032
VIF	WQVDRMKIRTW	11	11	12	19	8033
VIF	RMKIRTWNSLV	15	11	12	19	8034
VIF	WQVDRMKI	11	8	13	20	8035
VIF	HPKISSEV	48	8	13	20	8036
VIF	HPRISSEV	48	8	13	20	8037
VIF	DQLIHIMHY	109	8	13	20	8038
VIF	DQLIHIMHYF	109	9	13	20	8039
VIF	HPKISSEVHI	48	10	13	20	8040
VIF	HPRISSEVHI	48	10	13	20	8041
VIF	SVKKLTEDRW	174	10	13	20	8042
VIF	QLIHLYYFDCF	110	11	13	20	8043
VIF	DQLIHLYY	109	8	14	22	8044
VIF	QLIHLYYF	110	8	14	22	8045
VIF	QLIHIMHYF	110	8	14	22	8046
VIF	IVSPRCEY	133	8	14	22	8047
VIF	DQLIHLYYF	109	9	14	22	8048
VIF	QVDPGLADQLI	102	11	14	22	8049
VIF	QLIHIMHYFDCF	110	11	14	22	8050
VIF	KISSEVHI	50	8	15	23	8051
VIF	RISSEVHI	50	8	15	23	8052
VIF	HMHYFDCF	113	8	15	23	8053
VIF	RIRTWKS LV	17	9	15	23	8054
VIF	RIRTWNSLV	17	9	15	23	8055
VIF	GLADQLIHIM	106	10	15	23	8056
VIF	LHMHYFDCF	111	11	15	23	8057
VIF	RMRTWKS LV	15	11	15	23	8058
VIF	RMRTWNSLV	15	11	15	23	8059
VIF	HLIYYFDCF	113	8	16	25	8060

Table XIV
HIV B62 Super-Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
VIF	LHLVYFDCF	111	10	16	25	8061
VIF	LVKHIIMYI	24	8	19	30	8062
VIF	HPKVSSEV	48	8	19	30	8063
VIF	PLGEARLV	58	8	19	30	8064
VIF	SLVKHHMYI	23	9	19	30	8065
VIF	IPLGEARLV	57	9	19	30	8066
VIF	DPDLADQLI	104	9	19	30	8067
VIF	KIKPPLPSV	164	9	19	30	8068
VIF	HPKVSSEVHI	48	10	19	30	8069
VIF	HIPLGEARLV	56	10	19	30	8070
VIF	KVSSEVHI	50	8	20	31	8071
VIF	LVKHIIMYV	24	8	21	33	8072
VIF	SLVKHHMYV	23	9	21	33	8073
VIF	GLIITGERDW	73	9	22	34	8074
VIF	HLGHGVS	83	8	25	39	8075
VIF	HLGHGVSIEW	83	10	25	39	8076
VIF	HLGQGSV	83	8	26	41	8077
VIF	GQGVSEW	85	8	26	41	8078
VIF	HLGQGSVSEW	83	10	26	41	8079
VIF	SLQYLALTALI	149	11	27	42	8080
VIF	YLALTALI	152	8	28	44	8081
VIF	LOYLALTALI	150	10	28	44	8082
VIF	QVDRMRITW	12	10	31	48	8083
VIF	WQVDRMRITW	11	11	31	48	8084
VIF	YOAGHNKV	140	8	38	59	8085
VIF	QVMIVWQV	6	8	43	67	8086
VIF	WQVMIVWQV	5	9	43	67	8087
VIF	QVMIVWQVDRM	6	11	43	67	8088
VIF	MIVWQVDRM	8	11	43	67	8089
VIF	SLVKHHMY	23	8	44	69	8090
VIF	VMIVWQVDRM	7	10	44	69	8091
VIF	MIVWQVDRM	9	9	46	72	8092
VIF	IVWQVDRMRI	8	10	47	73	8093
VIF	WQVDRMRI	11	8	48	75	8094
VIF	IVWQVDRM	9	8	59	92	8095
VIF	RPWLHGLGQY	36	10	10	16	8096
VPR	QQLLFVHF	65	8	10	16	8097
VPR	LOQLLFVHF	64	9	10	16	8098
VPR	QQLLFVHFRI	66	9	10	16	8099
VPR	QQLLFVHFRI	65	10	10	16	8100
VPR	LOQLLFVHFRI	64	11	10	16	8101
VPR	KQEAVRHF	27	8	11	17	8102
VPR	WLHGLGQY	38	8	11	17	8103
VPR	RIGCRHSRIGI	74	11	11	17	8104
VPR	RPWLHGLGQHI	36	11	12	19	8105
VPR	LLEVFHRI	67	8	12	19	8106
VPR	RIGCRHSRI	74	9	12	19	8107
VPR	GQHIYNTY	43	8	13	20	8108
VPR	AVRHFPRI	30	8	14	22	8109
VPR						8110

Table XIV
HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
VPR	GQYIYETY	43	8	14	22	8111
VPR	AVRHPRPW	30	9	14	22	8112
VPR	HIYNTYGDW	45	10	14	22	8113
VPR	YIYTYGDTW	45	10	14	22	8114
VPR	ELKSEAVRHF	25	10	15	23	8115
VPR	CQHSRIGI	77	9	16	25	8116
VPR	LLEELKSEAV	22	10	16	25	8117
VPR	ELLEELKNEAV	21	11	16	25	8118
VPR	ELLEELKSEAV	21	11	16	25	8119
VPR	GQHIYETY	43	8	17	27	8120
VPR	LLEELKNEAV	22	10	17	27	8121
VPR	ELKNEAVRHF	25	10	17	27	8122
VPR	HIYTYGDTW	45	10	17	27	8123
VPR	WLHGLGQIII	38	9	20	31	8124
VPR	WLHGLGQIIY	38	10	20	31	8125
VPR	IRILQQLLFI	60	11	33	52	8126
VPR	GVEAIRI	56	8	34	53	8127
VPR	AVRHPRPW	30	9	34	53	8128
VPR	RILQQLLFHIF	62	11	34	53	8129
VPR	ILQQLLFHIF	63	10	35	55	8130
VPR	RILQQLLFI	62	9	36	56	8131
VPR	ILQQLLFI	63	8	37	58	8132
VPR	PQREPYNEW	10	9	37	58	8133
VPR	GQREPYNEW	9	10	37	58	8134
VPR	AIRILQQLLF	59	11	38	59	8135
VPR	DQGPQREPY	7	9	41	64	8136
VPR	IRILQQLLF	60	10	41	64	8137
VPR	QQLLFHIF	65	8	44	69	8138
VPR	LLFIHIFRI	67	8	44	69	8139
VPR	LQQLLFHIF	64	9	44	69	8140
VPR	QQLLFHIFRI	65	10	44	69	8141
VPR	LQQLLFHIFRI	65	11	44	69	8142
VPR	LQQLLFHIFRI	64	11	44	69	8143
VPR	RILQQLLF	62	8	45	70	8144
VPR	CQHSRIGI	77	8	45	70	8145
VPR	RIGCQHSRIGI	74	11	45	70	8146
VPR	RIGCQHSRI	74	9	47	73	8147
VPU	KVDYRIVI	7	8	01	33	8148
VPU	KVDYRLGV	7	8	01	33	8149
VPU	RIDYRLGV	7	8	01	33	8150
VPU	KVDYRIVIV	7	9	01	33	8151
VPU	KVDYRIVIVAF	7	11	01	33	8152
VPU	GVEMGHHPAP	91	10	01	50	8153
VPU	RIKEIRDDSDY	64	11	01	50	8154
VPU	RIKEIRDDSDY	64	11	01	50	8155
VPU	LIIVVW	26	8	10	16	8156
VPU	DQEELSALV	79	9	11	17	8157
VPU	ILAIIVLVV	12	9	11	17	8158
VPU	EMGHIAIPW	89	8	11	17	8159
VPU	ILAIIVLV	12	8	12	19	8160

Table XIV
 HIV B62 Super Motif Peptides

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	SEQ ID NO.
VPV	IVFIEYRKI	36	9	12	19	8161
VPV	VVWTVFIEY	31	10	12	19	8162
VPV	IVVWTVFIEY	30	11	12	19	8163
VPV	ILRQRKIDRLI	46	11	13	20	8164
VPV	AIVVWTVF	29	9	14	22	8165
VPV	KIDRLIDRI	52	9	14	22	8166
VPV	AIVVWTVFI	29	10	14	22	8167
VPV	IVVWTVF	30	8	15	23	8168
VPV	VVWTVFI	31	8	15	23	8169
VPV	KILRQRKI	45	8	15	23	8170
VPV	IVVWTVFI	30	9	15	23	8171
VPV	RQRKIDRLI	48	9	17	27	8172
VPV	IIAIVVWTV	27	10	20	31	8173
VPV	IIAIVVWTV	27	9	23	36	8174
VPV	AIVVWTV	29	8	29	45	8175

Table XV
HIV-1 A01 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0101	SEQ ID NO.
ENV	IGSGQAFY	361	8	01	25		8176
ENV	GKDLWTVY	42	9	01	33		8177
ENV	GKDLWTVYY	42	10	01	33		8178
ENV	NTSPSRVAY	376	10	01	33		8179
ENV	GTAGNSSRAA	375	11	01	33		8180
ENV	DSSNSTGNY	218	9	01	20		8181
ENV	TNSSTNDTY	458	10	01	17		8182
ENV	WFDITNLWL	767	10	10	16		8183
ENV	WMEWERIDN	723	11	10	16		8184
ENV	EWEREIDNY	725	9	11	17		8185
ENV	NMAWQEVGKA	494	11	15	23		8186
ENV	HSFNCRGEFFY	434	11	16	25		8187
ENV	WQEVGKAMY	496	9	18	28		8188
ENV	VSEFPIPIIY	253	10	28	44		8189
ENV	KVSFPIPIIY	252	11	28	44		8190
ENV	SFEPIPIIY	254	9	31	48		8191
ENV	LQARLAVLR	662	11	33	52		8192
ENV	LSIVNRVROQY	797	11	34	53		8193
ENV	RSLCLFSY	858	8	35	55		8194
ENV	LRLCLFSY	857	9	35	55		8195
ENV	HSFNCRGEFFY	434	11	35	55		8196
ENV	DMRDNRWSEL	552	11	37	58		8197
ENV	MIRDNRWSELY	553	10	40	63	0.0010	8198
ENV	CASDAKAY	67	8	42	66		8199
ENV	FCASDAKAY	66	9	42	66		8200
ENV	WRSELYKY	557	8	54	84		8201
GAG	ETIDKDL	537	8	01	25		8202
GAG	EKEEKGLY	538	8	01	25		8203
GAG	KQEPIDKELY	535	10	01	25		8204
GAG	KQETIDKDL	535	10	01	25		8205
GAG	AADKGVSONY	130	10	01	50		8206
GAG	ASAOQDLKGG	392	11	01	50		8207
GAG	ATAQQDLKGG	392	11	01	50		8208
GAG	AADKGVSON	129	11	02	18		8209
GAG	EADKGVSONY	129	10	04	36		8210
GAG	GNSQVSONY	140	10	12	23		8211
GAG	KQEPIDKELY	531	10	12	19		8212
GAG	SEELKSLY	74	8	12	19		8213
GAG	GSEELKSLY	73	9	12	19		8214
GAG	TGSEELKSLY	72	10	12	19		8215
GAG	NSSQVSONY	144	9	14	31		8216
GAG	SSQVSONY	145	8	15	31		8217
GAG	RSLYNTVATL	78	11	15	24		8218
GAG	FRDYVDREY	317	9	29	45	0.0900	8219
GAG	PKEPRDY	313	8	63	98		8220
GAG	HMARELHPEY	320	10	10	16		8221
NEF	HMARELHPEY	320	11	10	16		8222
NEF	ARELIHPEY	322	9	11	17		8223
NEF	YTPPGIRY	207	9	17	27		8224
NEF	RQDILDLWVY	182	10	20	31		8225

Table XV
HIV-1 A01 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101	SEQ ID NO.
NEF	ARELHPEYY	322	9	21	33		8226
NEF	ARELHPEY	322	8	24	38		8227
NEF	RQELDLWVY	182	10	32	50		8228
POL	TWETWTDY	589	9	10	16		8229
POL	TWETWTEY	589	9	10	16		8230
POL	ETWETWTD	588	10	10	16		8232
POL	ETWETWTE	588	10	10	16		8233
POL	AOEDHEKY	760	8	11	17		8234
POL	ISRGIPENPY	236	10	11	17		8235
POL	KISRGIPENPY	235	11	11	17		8236
POL	STNETPGIRY	323	11	11	17		8237
POL	KTELQAIY	668	8	12	19		8238
POL	GQDQWYTYQY	525	10	15	23		8239
POL	DKAQEEHERY	758	10	15	23		8240
POL	AOEEHERY	760	8	16	25	0.0011	8241
POL	NPDIVIYQY	364	9	17	27		8242
POL	PLDKDFRKY	308	9	19	30		8243
POL	QOEFGIPY	888	8	20	32		8244
POL	NPEIYIYQY	364	9	23	36		8245
POL	DKAQEEHEKY	758	10	25	39		8246
POL	AOEEHEKY	760	8	27	42		8247
POL	KQEFGIPY	888	8	28	44		8248
POL	NRETKLGKAG	639	11	28	44		8249
POL	ETKLGKAGY	641	9	35	55	0.0010	8250
POL	ITKIQNFRVY	969	10	36	57	0.0010	8251
POL	ITKIQNFRVY	969	11	36	57	0.0110	8252
POL	LKEPVHGVY	502	10	39	61	0.0010	8253
POL	LKEPVHGVY	502	9	41	64	0.0007	8254
POL	RKAKIIRDY	1016	9	41	64		8255
POL	KISKIGPENPY	235	11	41	64	0.0130	8256
POL	ISKIGPENPY	236	10	42	66	0.0007	8257
POL	NNETPGIRY	325	9	51	80	0.0004	8258
POL	NNETPGIRYQY	325	11	51	81	0.0052	8259
POL	ETPGIRYQY	327	9	52	83	0.0390	8260
POL	LVAVHVASGY	826	10	53	88	0.2800	8261
POL	VTVDVGDY	295	10	56	88	0.0041	8262
POL	NTPLVLKLY	610	10	57	89	0.0130	8263
POL	PAETQETAY	842	10	58	91		8264
POL	PAETQETAY	841	11	58	91		8265
POL	ETQETAY	844	8	59	92		8266
POL	VLDVGDY	297	8	60	94		8267
POL	QKEPFLWMG	411	11	63	98	0.0004	8268
VIF	GVSIEWRLRR	87	10	60	16		8269
VIF	SIEWRLRRY	89	9	11	17		8270
VIF	VSIEWRLRRY	88	10	11	17		8271
VIF	GLADQLIHMH	106	11	11	17		8272
VIF	LADQLIHMHY	107	10	13	20		8273
VIF	IVSPRCEY	133	8	14	22		8274
VIF	LADQLIHLY	107	10	14	22		8275
VIF	LADQLIHLY	107	9	15	23		8275

Table XV
HIV-1 Amino Acid Sequences with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0101	SEQ ID NO.
VIF	KSLVKHHMY	22	9	18	28		8276
VIF	WKSIVKHHM	21	10	18	28		8277
VIF	NSLVKHHMY	22	9	24	38		8278
VIF	WNSLVKHHM	21	10	24	38		8279
VPR	PEDQGPQREPY	5	11	37	58		8280
VPU	WTIVFIEY	34	8	12	19		8281

Table XVI
HIV-A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
ENV	GIGPGQTF	360	8	01	33		8282
ENV	SIGSGQAF	360	8	01	33		8283
ENV	IGPGQTFY	361	8	01	25		8284
ENV	IGSQAFY	361	8	01	25		8285
ENV	GTAGNSSR	375	8	01	33		8286
ENV	TAGNSSRA	376	8	01	33		8287
ENV	KLREIRQF	405	8	01	25		8288
ENV	ADNLWVTVY	42	9	01	33		8289
ENV	GIGPGQTFY	360	9	01	33		8290
ENV	SIGSGQAFY	360	9	01	33		8291
ENV	IGPGQTFYA	361	9	01	25		8292
ENV	GTAGNSSRA	375	9	01	33		8293
ENV	NTSPRSRVA	376	9	01	33		8294
ENV	TAGNSSRAA	376	9	01	33		8295
ENV	ADNLWVTVYY	42	10	01	33		8296
ENV	EGKNEINDTY	217	10	01	33		8297
ENV	GIGPGQTFYA	360	10	01	33		8298
ENV	GTAGNSSRAA	375	10	01	33		8299
ENV	NTSPRSRVAY	376	10	01	33		8300
ENV	TAGNSSRAAY	376	10	01	33		8301
ENV	FGLGALFLGF	597	10	01	33		8302
ENV	VGLGAVFLGF	597	10	01	33		8303
ENV	GTAGNSSRAA	375	11	01	25		8304
ENV	KLREIRQFENK	405	11	01	50		8305
ENV	QLYATVYA	34	8	01	50		8306
ENV	IINIHTPH	584	8	01	50		8307
ENV	VISTRTHR	584	8	01	50		8308
ENV	STRTHREK	586	8	01	50		8309
ENV	NANITPCR	478	9	01	50		8310
ENV	IINIHTPHR	584	9	01	50		8311
ENV	ISTRTHREK	585	9	01	50		8312
ENV	NIHTPHREK	586	9	01	50		8313
ENV	STRTHREKR	586	9	01	50		8314
ENV	VISTRTHREK	584	10	01	50		8315
ENV	ISTRTHREKR	585	10	01	50		8316
ENV	NIHTPHREKR	586	10	01	50		8317
ENV	STRTHREKRA	586	10	01	50		8318
ENV	ITEGNTLQCR	478	11	01	50		8319
ENV	NANITPCRK	584	11	01	50		8320
ENV	IINIHTPHREK	584	11	01	50		8321
ENV	VISTRTHREKR	585	11	01	50		8322
ENV	ISTRTHREKRA	585	11	01	50		8323
ENV	NIHTPHREKRA	586	11	01	50		8324
ENV	VISTGNSA	161	8	01	20		8325
ENV	DSSNSTGNY	218	9	01	20		8326
ENV	STNGTETF	537	8	01	17		8327
ENV	STNGTETFR	537	9	01	17		8328
ENV	NDTENNTIEF	537	10	01	17		8329
ENV	NTEINKTETF	537	10	01	17		8330
ENV	NTTGNNTETF	537	10	01	17		8331

Table XVI
HIV-A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
ENV	NDTENNTETFR	537	11	01	17		8332
ENV	NTEINKTETFR	537	11	01	17		8333
ENV	NTTGNITETFR	537	11	01	17		8334
ENV	NGSENGTETFR	537	10	02	33		8335
ENV	NGSENGTETFR	537	11	02	33		8336
ENV	GSENGTETFR	538	9	02	18		8337
ENV	GSENGTETFR	538	10	02	18		8338
ENV	TIGAMFLGF	599	9	03	27		8339
ENV	NDTITLPCR	477	9	03	20		8340
ENV	NDTITLPCR	477	11	03	20		8341
ENV	MLGAMFLGF	599	9	04	36		8342
ENV	RGWEALKY	895	8	06	19		8343
ENV	KGLRLGWEGFL	891	11	08	27		8344
ENV	LGWEGLY	895	8	09	29		8345
ENV	RLGWEGLY	894	9	09	29		8346
ENV	GLRLGWEGLY	892	11	09	29		8347
ENV	LGRRGWEGLY	883	10	09	15		8348
ENV	LGRRGWEGLY	882	11	09	15		8349
ENV	LGRRGWEGLY	882	11	09	15		8350
ENV	LGRRGWEGLY	372	9	09	15		8351
ENV	LGRRGWEGLY	21	11	09	15		8352
ENV	LGRRGWEGLY	370	11	09	15		8353
ENV	LGRRGWEGLY	894	8	10	32		8354
ENV	LGRRGWEGLY	892	10	10	32		8355
ENV	LGRRGWEGLY	883	8	10	16		8356
ENV	LGRRGWEGLY	882	9	10	16		8357
ENV	LGRRGWEGLY	372	10	10	16		8358
ENV	LGRRGWEGLY	881	10	10	16		8359
ENV	LGRRGWEGLY	370	11	10	16		8360
ENV	LGRRGWEGLY	28	8	10	16		8361
ENV	LGRRGWEGLY	498	8	10	16		8362
ENV	LGRRGWEGLY	571	8	10	16		8363
ENV	LGRRGWEGLY	572	8	10	16		8364
ENV	LGRRGWEGLY	769	8	10	16		8365
ENV	LGRRGWEGLY	869	8	10	16		8366
ENV	LGRRGWEGLY	870	8	10	16		8367
ENV	LGRRGWEGLY	923	8	10	16		8368
ENV	LGRRGWEGLY	27	9	10	16		8369
ENV	LGRRGWEGLY	243	9	10	16		8370
ENV	LGRRGWEGLY	358	9	10	16		8371
ENV	LGRRGWEGLY	768	9	10	16		8372
ENV	LGRRGWEGLY	869	9	10	16		8373
ENV	LGRRGWEGLY	916	9	10	16		8374
ENV	LGRRGWEGLY	26	10	10	16		8375
ENV	LGRRGWEGLY	26	10	10	16		8376
ENV	LGRRGWEGLY	260	10	10	16		8377
ENV	LGRRGWEGLY	269	10	10	16		8378
ENV	LGRRGWEGLY	357	10	10	16		8379
ENV	LGRRGWEGLY	651	10	10	16		8380
ENV	LGRRGWEGLY	665	10	10	16		8381
ENV	LGRRGWEGLY	767	10	10	16		8382

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
ENV	EGIEEGGER	828	10	10	16		8382
ENV	PIIYCTPAGFA	260	11	10	16		8383
ENV	GFAILKNDKK	268	11	10	16		8384
ENV	FAILKNDKKF	269	11	10	16		8385
ENV	GDIIGDIRQAH	371	11	10	16		8386
ENV	NVPWNSSWSN	693	11	10	16		8387
ENV	WMEWEREIDN	723	11	10	16		8388
ENV	NSAVSLLNAT	916	11	10	16		8389
ENV	IAIAVAEGTDR	925	11	10	16		8390
ENV	RGWEALKY	886	8	11	18		8391
ENV	GIGAVFLGF	598	9	11	18		8392
ENV	KLWVTVY	44	8	11	17		8393
ENV	AVGIGAVF	595	8	11	17		8394
ENV	AVGIGAVF	594	9	11	17		8395
ENV	AVGIGAVFLGF	595	9	11	17		8396
ENV	TITQACPK	244	11	11	17		8397
ENV	YCTPAGFA	263	8	11	17		8398
ENV	RIGPGQTF	357	8	11	17		8399
ENV	RIGPGQTF	358	8	11	17		8400
ENV	IGPGQTF	603	8	11	17		8401
ENV	LFLGPLGA	667	8	11	17		8402
ENV	LAVERYLR	859	8	11	17		8403
ENV	NLCFLSYH	917	8	11	17		8404
ENV	SAVSLNNA	919	8	11	17		8405
ENV	VSLNATA	919	8	11	17		8406
ENV	LGMLMICA	27	9	11	17		8407
ENV	RIGPGQTF	357	9	11	17		8408
ENV	ITTHSFNCR	431	9	11	17		8409
ENV	NITLPCRIK	482	9	11	17		8410
ENV	ALFLGFLGA	602	9	11	17		8411
ENV	LFLGFLGAA	603	9	11	17		8412
ENV	VLAVERYLR	666	9	11	17		8413
ENV	ISNLWYIK	770	9	11	17		8414
ENV	NLCFSYHR	859	9	11	17		8415
ENV	AVSLNATA	918	9	11	17		8416
ENV	GDIIGDIRQA	371	10	11	17		8417
ENV	EITTHSFNCR	430	10	11	17		8418
ENV	VGIGAVFLGF	596	10	11	17		8419
ENV	GALFLGFLGA	601	10	11	17		8420
ENV	ALFLGFLGAA	602	10	11	17		8421
ENV	SAVSLNATA	917	10	11	17		8422
ENV	VSLNATAIA	919	10	11	17		8423
ENV	YATGDIIGDIR	368	11	11	17		8424
ENV	GALFLGFLGAA	601	11	11	17		8425
ENV	ISNLWYIKIF	770	11	11	17		8426
ENV	DLRNLCLFSYH	856	11	11	17		8427
ENV	NLCFSYHRLR	859	11	11	17		8428
ENV	AVSLNATAIA	918	11	11	17		8429
ENV	PTRIRQGLERA	951	11	11	17		8430
ENV	TGDIIGDIR	370	9	12	19		8431
ENV	DIIGDIRQA	372	9	12	19		8431

Table XVI
HIV-1 gp120 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
ENV	EAQQHLK	646	8	12	19		8432
ENV	GMLMCSA	28	8	12	19		8433
ENV	ILKCNDDK	271	8	12	19		8434
ENV	TTHSFNCR	432	8	12	19		8435
ENV	IGAVFLGF	600	8	12	19		8436
ENV	MTWMEWER	721	8	12	19		8437
ENV	GGERDRDR	834	8	12	19		8438
ENV	AILKCNDDK	270	9	12	19		8439
ENV	ILKCNDDKFF	271	9	12	19		8440
ENV	LAEEVVIR	312	9	12	19	0.0002	8441
ENV	AMFLGFLGA	602	9	12	19		8442
ENV	NMTWMEWER	720	9	12	19		8443
ENV	GIEEGGER	829	9	12	19		8444
ENV	EGGERDRDR	833	9	12	19		8445
ENV	RSIRLVNGF	841	9	12	19		8446
ENV	WGQELKNSA	910	9	12	19		8447
ENV	WSQELKNSA	910	9	12	19		8448
ENV	KTLFLCASDA	60	10	12	19		8449
ENV	AILKCNDDKFF	270	10	12	19		8450
ENV	SLAEEVVIR	311	10	12	19		8451
ENV	ATGDHIGDIR	369	10	12	19		8452
ENV	IINMWQEVGK	492	10	12	19		8453
ENV	AMFLGFLGA	601	10	12	19		8454
ENV	AMFLGFLGA	602	10	12	19		8455
ENV	AIEAQQHLK	644	10	12	19		8456
ENV	QDLALDKWA	753	10	12	19		8457
ENV	SIRLVSGFLA	842	10	12	19		8458
ENV	LLQYWSQELK	906	10	12	19		8459
ENV	AILHIPRRIR	946	10	12	19		8460
ENV	PTRIQGLER	951	10	12	19		8461
ENV	KTLFLCASDA	60	11	12	19		8462
ENV	GSLAEEVVIR	310	11	12	19		8463
ENV	TTHSFNCRGE	432	11	12	19		8464
ENV	QINMWQEVG	491	11	12	19		8465
ENV	IINMWQEVGK	492	11	12	19		8466
ENV	GAMFLGFLGA	601	11	12	19		8467
ENV	ITKWLWYIKIF	770	11	12	19		8468
ENV	GIEEGGERDR	829	11	12	19		8469
ENV	RSIRLVSGFLA	841	11	12	19		8470
ENV	NLLQYWSQEL	905	11	12	19		8471
ENV	RAILHIPRRIR	945	11	12	19		8472
ENV	NTSVITQA	241	8	13	20		8473
ENV	SVEINCTR	340	8	13	20		8474
ENV	GDIIGDIR	371	8	13	20		8475
ENV	MFLGFLGA	603	8	13	20		8476
ENV	KLTVWGK	653	8	13	20		8477
ENV	SIRLVNGF	842	8	13	20		8478
ENV	SIRLVSGF	842	8	13	20		8479
ENV	RLVNGFLA	844	8	13	20		8480
ENV	RAILHIPR	945	8	13	20		8481

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
ENV	ALHPRR	946	8	13	20		8482
ENV	KAKRRVVQR	579	9	13	20		8483
ENV	MFLGFLGAA	603	9	13	20	0.0002	8484
ENV	RSRLVSGF	841	9	13	20		8485
ENV	RAILHIPRR	945	9	13	20		8486
ENV	ILHIPRRIR	947	9	13	20		8487
ENV	SGGDPFIVMHI	425	10	13	20		8488
ENV	LLKLTWVGK	651	10	13	20		8489
ENV	NTSVITQACPK	241	11	13	20		8490
ENV	CTNVSTVQCT	285	11	13	20		8491
ENV	SSGGDLFITH	424	11	13	20		8492
ENV	SSGGDPFIVMHI	424	11	13	20		8493
ENV	VMHSFNCGE	432	11	13	20		8494
ENV	PTKAKRRVVQ	576	11	13	20		8495
ENV	KAKRRVVQRE	579	11	13	20		8496
ENV	IILLKLTWGI	650	11	13	20		8497
ENV	VGLGLRIIF	784	11	13	20		8498
ENV	SLLNATAIAVA	920	11	14	23		8500
ENV	TGEIGDIR	370	9	14	22		8501
ENV	NTSAITQA	241	8	14	22		8502
ENV	AITQACPK	244	8	14	22		8503
ENV	GDPEIVMHI	427	8	14	22		8504
ENV	QDLLALDK	753	8	14	22		8505
ENV	NATAIAVA	923	8	14	22		8506
ENV	SAITQACPK	243	9	14	22	0.0002	8507
ENV	FAILKCNDK	269	9	14	22		8508
ENV	GGDPFIVMHI	426	9	14	22		8509
ENV	TITLPCRIK	482	9	14	22		8510
ENV	SLLNATAIA	920	9	14	22		8511
ENV	NCNTSAITQA	239	10	14	22		8512
ENV	TSAITQACPK	242	10	14	22		8513
ENV	TSVITQACPK	242	10	14	22		8514
ENV	GFAILKCNDK	268	10	14	22		8515
ENV	GDPEIVMHSF	427	10	14	22		8516
ENV	IFAVLSIVNR	793	10	14	22		8517
ENV	LLNATAIAVA	921	10	14	22		8518
ENV	NTSAITQACPK	241	11	14	22		8519
ENV	VITQACPKVSF	244	11	14	22		8520
ENV	AGFAILKCNDK	267	11	14	22		8521
ENV	GGDPFIVMHSF	426	11	14	22		8522
ENV	ITNWLWYIKIF	770	11	14	22		8523
ENV	IFAVLSIVNR	792	11	14	24		8524
ENV	KIEPLGVAPT	568	11	15	23		8525
ENV	FDPIPIHY	255	8	15	23		8526
ENV	PAGYAILK	266	8	15	23		8527
ENV	NMWQEVGK	494	8	15	23		8528
ENV	LNATAIA	921	8	15	23		8529
ENV	NMWQEVGKA	494	9	15	23		8530
ENV	DLLALDKWA	754	9	15	23		8531
ENV	ITNWLWYIK	770	9	15	23		8531

Table XVI
HIV-A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
ENV	GLIGLRIIF	786	9	15	23		8532
ENV	DDLRLNCLF	855	9	15	23		8533
ENV	SGGDLEITH	425	10	15	23		8534
ENV	IFRPGGDMR	545	10	15	23		8535
ENV	GGLIGLRIIF	785	10	15	23		8536
ENV	GLIGLRIIFA	786	10	15	23		8537
ENV	WDDLRLNCLF	854	10	15	23		8538
ENV	NMWQEVGKA	494	11	15	23		8539
ENV	BIFRPGGDMR	544	11	15	23		8540
ENV	GGLIGLRIIFA	785	11	15	23		8541
ENV	DDLRLNCLFSY	855	11	15	23		8542
ENV	SFNCRGEF	437	8	16	25		8543
ENV	LIGLRIIF	787	8	16	25		8544
ENV	VSGFLALA	846	8	16	25		8545
ENV	HSFNCRGEF	434	9	16	25		8546
ENV	SFNCRGEFF	437	9	16	25		8547
ENV	ITKWLWYIK	770	9	16	25		8548
ENV	LIGLRIIFA	787	9	16	25		8549
ENV	LVSGLALA	845	9	16	25		8550
ENV	HSFNCRGEFF	434	10	16	25		8551
ENV	SFNCRGEFF	437	10	16	25		8552
ENV	RLVSGFLALA	844	10	16	25		8553
ENV	DLRLNCLFSY	856	10	16	25		8554
ENV	TTTISFNCGE	432	11	16	25		8555
ENV	HSFNCRGEFF	434	11	16	25		8556
ENV	RLINCNTSA	236	9	17	27		8557
ENV	KAYDTEVH	72	8	17	27		8558
ENV	LINCNTSA	237	8	17	27		8559
ENV	VITQACPK	244	8	17	27	0.0003	8560
ENV	RVQREKR	587	8	17	27		8561
ENV	RVQREKRA	588	8	17	27		8562
ENV	IGLRIIFA	788	8	17	27		8563
ENV	DLRLNCLF	856	8	17	27		8564
ENV	SVITQACPK	243	9	17	27		8565
ENV	VAPTAKRR	574	9	17	27	0.0002	8566
ENV	RVQREKRA	587	9	17	27		8567
ENV	DAKAYDTEVII	70	10	17	27		8568
ENV	YDTEVINVWA	74	10	17	27		8569
ENV	GVAPTAKRR	573	10	17	27		8570
ENV	VFAVLSIVNR	793	10	17	27		8571
ENV	SDAKAYDTEV	69	11	17	27		8572
ENV	DTEVHNVWAT	75	11	17	27		8573
ENV	NCTRPNNTR	344	11	17	27		8574
ENV	LGVAPTAKRR	572	11	17	27		8575
ENV	IVFAVLSIVNR	792	11	17	27		8576
ENV	PIHYCTPA	260	8	18	28		8577
ENV	EVGKAMYA	498	8	18	28		8578
ENV	DTEVINVWA	75	9	18	28		8579
ENV	VLAVERYLK	666	9	18	28		8580
ENV	ELLELDKWA	754	9	18	28		8581

Table XVI
HIV-A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
ENV	FSYHRLRDF	863	9	18	28		8582
ENV	PIPIHYCTPA	258	10	18	28		8583
ENV	RVLAVERYLK	665	10	18	28		8584
ENV	LFSYHRLRDF	862	10	18	28		8585
ENV	CLFSYHRLRDF	861	11	18	28		8586
ENV	NCRGEFFY	439	8	19	30		8587
ENV	GVAPTKAK	573	8	19	30		8588
ENV	VAPTKAKR	574	8	19	30		8589
ENV	VFLGFLGA	603	8	19	30		8590
ENV	LLALDKWA	755	8	19	30		8591
ENV	LGVAPTKAK	572	9	19	30		8592
ENV	GVAPTKAKR	573	9	19	30		8593
ENV	AVFLGFLGA	602	9	19	30		8594
ENV	VFLGFLGAA	603	9	19	30		8595
ENV	SGKLICTTA	685	9	19	30		8596
ENV	PLGVAPTKAK	571	10	19	30		8597
ENV	LGVAPTKAKR	572	10	19	30		8598
ENV	GAVFLGFLGA	601	10	19	30		8599
ENV	AVFLGFLGAA	602	10	19	30		8600
ENV	CSGKLICTTA	684	10	19	30		8601
ENV	SSNITGLLTR	516	11	19	30		8602
ENV	PLGVAPTKAK	571	11	19	30		8603
ENV	GAVFLGFLGA	601	11	19	30		8604
ENV	GCSGKLICTTA	683	11	19	30		8605
ENV	AILKCNDK	270	8	20	31		8606
ENV	RLVSGFLA	844	8	20	31		8607
ENV	ETFRPGGGDM	544	11	20	31		8608
ENV	LIEESQNQOEK	740	11	20	31		8609
ENV	GDLEITH	427	8	21	33		8610
ENV	YCNTSGLF	446	8	21	33		8611
ENV	LLELDKWA	755	8	21	33		8612
ENV	GGDLEITH	426	9	21	33		8613
ENV	DLEITHSF	428	9	21	33		8614
ENV	LIGLRIVFA	787	9	21	33		8615
ENV	GDLEITHSF	427	10	21	33		8616
ENV	PFYCNTSGLF	444	10	21	33		8617
ENV	GLIGLRIVFA	786	10	21	33		8618
ENV	SFEPIHYCA	254	11	21	33		8619
ENV	GGDLEITHSF	426	11	21	33		8620
ENV	EFFYCNTSGLF	443	11	21	33		8621
ENV	GGIGLRIVFA	785	11	21	33		8622
ENV	TAIAVAEGTDR	925	11	21	33		8623
ENV	IGLRIVFA	788	8	22	34		8624
ENV	RIVELLGR	878	8	22	34		8625
ENV	IVELLGRR	879	8	22	34	0.0550	8626
ENV	RIVELLGRR	878	9	22	34		8627
ENV	NCTRPNNNTR	344	10	22	34		8628
ENV	CTRPNNNTRK	345	10	22	34		8629
ENV	PVWKEATTTL	54	11	22	34		8630
ENV	TTTLFCASDA	60	11	22	34		8631

Table XVI
HIV-A63 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
ENV	KIEPLGVA	568	8	23	37		8632
ENV	LGVAPTKA	572	8	23	36		8633
ENV	TVQCTHGIR	290	9	23	36	0.0008	8634
ENV	PLGVAPTKA	571	9	23	36		8635
ENV	STVQCTHGIR	289	10	23	36		8636
ENV	VVKIEPLGVA	566	10	23	36		8637
ENV	QSNLLRAIEA	638	10	23	36		8638
ENV	ATTTLCASD	59	11	23	36		8639
ENV	VSTVQCTHGIR	288	11	23	36		8640
ENV	KVKIEPLGVA	565	11	23	36		8641
ENV	ATTTLFCA	59	8	24	38		8642
ENV	EATTLFCA	58	9	24	38		8643
ENV	TTTLFCASDA	60	10	24	38		8644
ENV	TRPGGGDMR	545	10	24	38		8645
ENV	ALAWDDL	851	8	25	39		8646
ENV	LALAWDDL	850	9	25	39	0.0024	8647
ENV	IVQQNNLLR	634	10	25	39		8648
ENV	FLALAWDDL	849	10	25	39		8649
ENV	GIVQQNNLLR	633	11	25	39		8650
ENV	IVQQNNLLRA	634	11	25	39		8651
ENV	GFLALAWDDL	848	11	25	39		8652
ENV	ITLPCRK	483	8	26	41		8653
ENV	PLGVAPTK	571	8	26	41		8654
ENV	LAVERYLK	667	8	26	41		8655
ENV	IVQQSNLLR	634	10	26	41		8656
ENV	GIVQQSNLLR	633	11	26	41		8657
ENV	IVQQSNLLRA	634	11	26	41		8658
ENV	LDKWSLWN	758	11	26	41		8659
ENV	IGDIRQAH	377	9	27	44		8660
ENV	ESQNOQEK	743	8	27	42		8661
ENV	PIIYCAPAGF	260	10	27	42		8662
ENV	PIIYCAPAGFA	260	11	27	42		8663
ENV	VGGLGLRIVF	784	11	27	42		8664
ENV	IGDIRQAH	378	8	28	44		8665
ENV	YCAPAGFA	263	8	28	44		8666
ENV	TVQCTHGIR	290	9	28	44	0.0021	8667
ENV	CTRPNNTR	345	9	28	44		8668
ENV	ASITLTVOA	619	9	28	44		8669
ENV	VSFEPIHY	253	10	28	44		8670
ENV	STVQCTHGIR	289	10	28	44		8671
ENV	AASITLTVOA	618	10	28	44		8672
ENV	ASITLTVOAR	619	10	28	44		8673
ENV	KVSFEPIHY	252	11	28	44		8674
ENV	YCAPAGFAILK	263	11	28	44		8675
ENV	VSTVQCTHGIR	288	11	28	44		8676
ENV	GAASITLTVOA	617	11	28	44		8677
ENV	AASITLTVOAR	618	11	28	44		8678
ENV	LIGLRIVF	787	8	29	45		8679
ENV	VSFEPIHY	253	9	29	45		8680
ENV	GLIGLRIVF	786	9	29	45		8681

Table XVI
HIV-A03: Most Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
ENV	ITOACPKVSF	245	10	29	45		8682
ENV	KVSFEPIPIH	252	10	29	45		8683
ENV	CAPAGFAILK	264	10	29	45		8684
ENV	GGILGLRIVF	785	10	29	45		8685
ENV	RSELYKYKVV	558	11	29	45		8686
ENV	IIGDIRQA	377	8	30	49		8687
ENV	WASLWNWF	761	8	30	47		8688
ENV	AVLSIVNR	795	8	31	48		8689
ENV	AVAEGTDR	928	8	31	48		8690
ENV	VTFNFMWK	102	9	31	48		8691
ENV	SFEPIPIH	254	9	31	48		8692
ENV	FAVLSIVNR	794	9	31	48		8693
ENV	SLCLFSYHR	859	9	31	48		8694
ENV	IATAEGTDR	927	9	31	48	0.0004	8695
ENV	NVTENFMW	101	10	31	48		8696
ENV	AVLSIVNRVR	795	10	31	48		8697
ENV	RSCLFSYHR	858	10	31	48		8698
ENV	AIATAEGTDR	926	10	31	48		8699
ENV	FAVLSIVNRVR	794	11	31	48		8700
ENV	DDLSLCLFSY	855	11	31	48		8701
ENV	SLCLFSYIHLR	859	11	31	48		8702
ENV	ELYKYKVVK	560	9	32	51		8703
ENV	RVVEREKR	587	8	32	50		8704
ENV	VVEREKRA	588	8	32	50		8705
ENV	SITLIVQA	620	8	32	50		8706
ENV	ITLTVQAR	621	8	32	50		8707
ENV	SLCLFSYH	859	8	32	50		8708
ENV	RVVEREKRA	587	9	32	50		8709
ENV	SITLTVQAR	620	9	32	50		8710
ENV	RSCLFSYH	858	9	32	50		8711
ENV	DLRSCLFSYH	856	11	32	50		8712
ENV	SFEPIPIH	254	8	33	52		8713
ENV	RVLAVERY	665	8	33	52	0.0009	8714
ENV	QARVLAVR	663	9	33	52		8715
ENV	DDLRSCLF	855	9	33	52		8716
ENV	QARVLAVRY	663	10	33	52		8717
ENV	WDDLRSCLF	854	10	33	52		8718
ENV	QLQARVLAVE	661	11	33	52		8719
ENV	IMVGGILGLR	781	11	34	54		8720
ENV	GVVWKEA	52	8	34	53		8721
ENV	YGVVWKEA	51	9	34	53		8722
ENV	RIRQLERA	953	9	34	53	0.0055	8723
ENV	LLQLTVWGIK	651	10	34	53		8724
ENV	HLQLTVWGI	650	11	34	53		8725
ENV	LSIVNRVRQGY	797	11	34	53		8726
ENV	NLWVTVYY	44	8	35	56		8727
ENV	NCGGEFFY	439	8	35	55		8728
ENV	RSCLFSY	858	8	35	55		8729
ENV	EVHNVWATH	77	9	35	55		8730
ENV	SFNCGGEFF	437	9	35	55		8731

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
ENV	NITGLLLTR	519	9	35	55	0.0004	8732
ENV	EVINWATHA	77	10	35	55		8733
ENV	IISFNCGGEFF	434	10	35	55		8734
ENV	SFNCGGEFF	437	10	35	55		8735
ENV	DLRSLCLFSY	856	10	35	55		8736
ENV	HSFNCGGEFF	434	11	35	55		8737
ENV	SFNCGGEF	437	8	36	56		8738
ENV	IISFNCGGEF	434	9	36	56		8739
ENV	PIPIHYCAPA	258	10	36	56		8740
ENV	GGGDMRDNW	549	10	36	56		8741
ENV	MIVGGLIGLR	782	10	36	56		8742
ENV	SIVNRVROGY	798	10	36	56		8743
ENV	PGGDMRDN	548	11	36	56	0.0008	8744
ENV	PIHYCAPA	260	8	37	58		8745
ENV	ITGLLLTR	520	8	37	58		8746
ENV	DMRDNRSEL	552	11	37	58		8747
ENV	PAGFAILK	266	8	38	59		8748
ENV	LSIVNRVR	797	8	38	59		8749
ENV	DLRSLCLF	856	8	38	59		8750
ENV	VLSIVNRVR	796	9	38	59		8751
ENV	IVNRVROGY	799	9	38	59		8752
ENV	IISLWDQSLK	121	10	38	59	0.0410	8753
ENV	DIISLWDQSLK	120	11	38	59		8754
ENV	GDMRDNR	551	8	39	61		8755
ENV	GGDMRDNR	550	9	39	61		8756
ENV	QACPKVSF	248	8	40	63		8757
ENV	PIPIHYCA	258	8	40	63		8758
ENV	RDNWRSELY	554	9	40	63	0.0003	8759
ENV	RDNWRSELYK	554	10	40	63	0.0008	8760
ENV	TLFCASDAKA	64	11	40	63		8761
ENV	RDNWRSELYK	554	11	40	63		8762
ENV	GIKQARVLA	658	11	40	63		8763
ENV	QLOARVLA	661	8	41	64		8764
ENV	TVYYGVVVK	48	10	41	64	3.8000	8765
ENV	VTYYGVVVK	47	11	41	64	0.8600	8766
ENV	CASDAKAY	67	8	42	66		8767
ENV	LCLFSYHR	860	8	42	66		8768
ENV	FCASDAKAY	66	9	42	66		8769
ENV	IVGGLIGLR	783	9	42	66		8770
ENV	CLFSYHRLR	861	9	42	66		8771
ENV	LFCASDAKAY	65	10	42	66	0.0004	8772
ENV	GAAGSTMGA	610	10	42	66		8773
ENV	LCLFSYHRLR	860	10	42	66		8774
ENV	LGAAGSTMGA	609	11	42	66		8775
ENV	VGGLIGLR	784	8	43	67		8776
ENV	QLTVWGK	653	8	44	69		8777
ENV	LFSYHRLR	862	8	44	69		8778
ENV	RIRQGLER	953	8	44	69		8779
ENV	TTLFCASDAK	61	11	44	69		8780
ENV	AAGSTMGA	611	9	45	70		8781

Table XVI
HIV-1 A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
ENV	TLFCASDAKA	64	10	46	72		8782
ENV	SLWDQSLK	123	8	47	75		8783
ENV	ISLWDQSLK	122	9	47	73	0.0048	8784
ENV	WDQSLKPCVK	125	10	47	73		8785
ENV	RVROGYSPLSF	802	11	47	73		8786
ENV	QSLKPCVK	127	8	48	75		8787
ENV	FLFLGAA	604	8	48	75		8788
ENV	QGYSPLSF	805	8	48	75		8789
ENV	TVWGIKQLQA	655	11	48	75		8790
ENV	GKQLQAR	658	8	49	77	0.0004	8791
ENV	WGKQLQAR	657	9	49	77		8792
ENV	TVWGIKQLQA	655	10	49	77		8793
ENV	LTWGIKQLQ	654	11	49	77		8794
ENV	FCASDAKA	66	8	50	78		8795
ENV	AGSTMGA	612	8	50	78		8796
ENV	WLYWIKIF	773	8	50	78		8797
ENV	LFCASDAKA	65	9	50	78		8798
ENV	LGIWGCSGK	679	9	50	78	0.0097	8799
ENV	TLFCASDAK	61	10	50	78	0.1200	8800
ENV	LLGIWGCSGK	678	10	50	78		8801
ENV	NLLRAIEAQH	640	11	50	78		8802
ENV	QLLGIWGCSG	677	11	50	78		8803
ENV	VSTVOCTH	288	8	51	80		8804
ENV	NLLRAIEA	640	8	51	80		8805
ENV	RAIEAQH	643	8	51	80		8806
ENV	WGKQLQA	657	8	51	80		8807
ENV	NVSTVQCTH	287	9	51	80		8808
ENV	LLRAIEAQH	641	10	51	80		8809
ENV	GIWGCSGK	680	8	52	81		8810
ENV	TLFCASDA	61	9	52	81	0.0930	8811
ENV	TLFCASDAK	64	9	52	81		8812
ENV	TLFCASDA	64	8	54	84		8813
ENV	RSELYKYK	558	8	54	84		8814
ENV	LLNGSLA	306	8	55	86		8815
ENV	QLLLNGSLA	305	9	55	86		8816
ENV	GAAGSTMGA	610	9	55	86		8817
ENV	LGAAGSTMGA	609	10	55	86		8818
ENV	STQLLLNGSLA	303	11	55	86		8819
ENV	FLGAAGSTMG	608	11	55	86		8820
ENV	LFCASDAK	65	8	57	89		8821
ENV	AAGSTMGA	611	8	58	91		8822
ENV	EDTSARQA	133	8	01	33		8823
GAG	AAAIMMQK	405	8	01	25		8824
GAG	SATIMMQK	405	8	01	25		8825
GAG	TAPPESF	508	8	01	33		8826
GAG	KDKDKELY	535	8	01	25		8827
GAG	ETIDKELY	537	8	01	25		8828
GAG	NSATIMMQK	404	9	01	33		8829
GAG	PTAPPESF	507	9	01	33		8830
GAG	TAPPESFR	508	9	01	33		8831

Table XVI
HIV X03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
GAG	NGQANFLGK	461	10	01	25		8832
GAG	NGQANFLGK	461	10	01	25		8833
GAG	PTAPPESFR	507	10	01	33		8834
GAG	TAPPESFR	508	10	01	33		8835
GAG	TIDKDLTYPLA	538	10	01	25		8836
GAG	AAAIMMOKSN	405	11	01	25		8837
GAG	SATIMMORGN	405	11	01	25		8838
GAG	NGQANFLGK	461	11	01	25		8839
GAG	NGQANFLGK	461	11	01	33		8840
GAG	PTAPPESFR	507	11	01	33		8841
GAG	KDKKELYPL	535	11	01	25		8842
GAG	ETIDKDLTYPLA	537	11	01	25		8843
GAG	PAADKEK	123	8	01	50		8844
GAG	ASAQODLK	392	8	01	50		8845
GAG	ATAQODLK	392	8	01	50		8846
GAG	PAEPTAIPA	492	9	01	50		8847
GAG	AAADKGVSONY	130	10	01	50		8848
GAG	SAQODLKGGY	393	10	01	50		8849
GAG	TAQODLKGGY	393	10	01	50		8850
GAG	GTRPGNYVQK	480	10	01	50		8851
GAG	GTRPGNYVQR	480	10	01	50		8852
GAG	ITSLPKQEQK	526	10	01	50		8853
GAG	PAAADKEKDS	123	11	01	50		8854
GAG	GANSIPVGDYI	276	11	01	50		8855
GAG	ASAQODLKGG	392	11	01	50		8856
GAG	ATAQODLKGG	392	11	01	50		8857
GAG	EITSLPKQEQK	525	11	01	50		8858
GAG	YTAVFMQR	405	8	02	50		8859
GAG	TAPPAESF	508	8	02	67		8860
GAG	PTAPPAESF	507	9	02	67		8861
GAG	TAPPAESFR	508	9	02	67		8862
GAG	PTAPPAESFR	507	10	02	67		8863
GAG	TAPPAESFR	508	10	02	67		8864
GAG	PTAPPAESFR	507	11	02	67		8865
GAG	EGROANFLGK	462	10	02	100		8866
GAG	AADKGVSONY	129	11	02	18		8867
GAG	EADGVSONY	129	10	04	36		8868
GAG	AAAIMMOK	400	8	04	19		8869
GAG	AAIMMOKSNF	406	10	06	15		8870
GAG	AAIMMOKSNF	406	11	06	15		8871
GAG	KTVKCFNCGK	421	10	08	16		8872
GAG	NIMMQRGNF	407	9	10	17		8873
GAG	GARASILR	2	8	10	16		8874
GAG	PGNFPQSR	483	8	10	16		8875
GAG	MGARASILR	1	9	10	16		8876
GAG	KIWPSSKGR	472	9	10	16		8877
GAG	TGNSSQVSON	139	11	10	16		8878
GAG	NFLGKIWPSSK	468	11	10	16		8879
GAG	NFLQNRPEPTA	485	11	10	16		8880
GAG	PVATQGMQR	243	8	10	16		8881

Table XVI
HIV-A03-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Λ^*0301	SEQ ID NO.
GAG	MMQSNFK	409	8	10	16		8882
GAG	MMQGNFK	409	8	10	16		8883
GAG	KLDKWEKIR	12	9	10	16		8884
GAG	GGKKYKLLK	24	9	10	16	0.0001	8885
GAG	RDTEALDK	97	9	10	16		8886
GAG	ALSPRLNA	167	9	10	16		8887
GAG	IMMQSNFK	408	9	10	16		8888
GAG	LGIWPSSK	470	9	10	16		8889
GAG	PGKKKYKLLK	23	10	10	16		8890
GAG	GGKKYKLLKH	24	10	10	16		8891
GAG	QALSPRLNA	166	10	10	16		8892
GAG	AGPVAPQMR	241	10	10	16		8893
GAG	GASLEEMMTA	364	10	10	16		8894
GAG	FLGIWPSK	469	10	10	16		8895
GAG	FLQNRPEPTA	486	10	10	16		8896
GAG	TAPPALSEFG	496	10	10	16		8897
GAG	KLDKWEKIRL	12	11	10	16		8898
GAG	PGKKKYKLLK	23	11	10	16		8899
GAG	LGIWPSKGR	470	11	10	16		8900
GAG	PTAPPALSEFG	495	11	11	28		8901
GAG	ATIMMQRGNF	406	11	11	28		8902
GAG	ATIMMQRGNF	406	11	11	18		8903
GAG	PSQKQEPIDK	528	10	11	18		8904
GAG	SSKGRFGNF	476	9	11	17		8905
GAG	TTSTLQEQIA	260	10	11	17		8906
GAG	DVKDTKEA	95	8	11	17		8907
GAG	PIPVGDIY	279	8	11	17		8908
GAG	SLEEMMTA	366	8	11	17		8909
GAG	MSQVTNSA	391	8	11	17		8910
GAG	IMMQSNF	408	8	11	17		8911
GAG	IDV'KDTKEA	94	9	11	17		8912
GAG	ASLEEMMTA	365	9	11	17		8913
GAG	AMSOVTNSA	390	9	11	17		8914
GAG	TIKCFNCGK	422	9	11	17		8915
GAG	TVKCFNCGK	422	9	11	17		8916
GAG	EAMSOVTNSA	389	10	11	17		8917
GAG	PSSKGRFGNF	475	10	11	17		8918
GAG	GTTSTLQEQIA	259	11	11	17		8919
GAG	TIMMQRGNF	407	10	12	21		8920
GAG	QTGSEELR	71	8	12	19		8921
GAG	KSKKKAQQA	112	10	12	19		8922
GAG	KSKKKAQQA	112	11	12	19		8923
GAG	PGKKKYK	23	8	12	19		8924
GAG	TYCVHOK	86	8	12	19		8925
GAG	DTKEALEK	98	8	12	19		8926
GAG	MLNIVGGH	208	8	12	19		8927
GAG	NIVGGHQA	210	8	12	19		8928
GAG	IVGGHQA	211	8	12	19		8929
GAG	STLQEQIA	262	8	12	19		8930
GAG	PTSILDIR	303	8	12	19		8931

Table XVI
 HIV-1 A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
GAG	LTSLSLF	549	8	12	19		8932
GAG	GSEELRSY	73	9	12	19		8933
GAG	ATLYCVHOK	85	9	12	19		8934
GAG	KDTEALEK	97	9	12	19		8935
GAG	MMLNIVGGH	207	9	12	19		8936
GAG	NIVGGHQA	210	9	12	19		8937
GAG	TSTLQEQIA	261	9	12	19		8938
GAG	PLTSLKSLF	548	9	12	19		8939
GAG	PLTSLRSF	548	9	12	19		8940
GAG	TGSEELRSY	72	10	12	19		8941
GAG	VATLYCVHOK	84	10	12	19		8942
GAG	NAQGMVHQA	158	10	12	19		8943
GAG	NMMLNIVGGH	206	10	12	19		8944
GAG	MMLNIVGGH	208	10	12	19		8945
GAG	MLNIVGGHQA	301	10	12	19		8946
GAG	YSPTSILDIR	329	10	12	19		8947
GAG	RAEQASQEVK	20	11	12	19		8948
GAG	RLRPGGKKY	83	11	12	19		8949
GAG	TVATLYCVHOK	207	11	12	19		8950
GAG	MMLNIVGGHQA	208	11	12	19		8951
GAG	MLNIVGGHQA	304	11	12	19		8952
GAG	TSILDIROGPK	407	11	13	22		8953
GAG	TIMMORGNF	483	8	13	21		8954
GAG	PGNFLQNR	434	9	13	21		8955
GAG	IARNCRAPR	472	9	13	21		8956
GAG	KIWPNSKGR	427	10	13	21		8957
GAG	NCGKFGHIAR	434	10	13	21		8958
GAG	IARNCRAPRK	434	11	13	21		8959
GAG	NFLGKIWPNSK	468	11	13	21		8960
GAG	KGRPGNFLO	478	11	13	21		8961
GAG	KLKHIVWA	31	8	13	20		8962
GAG	RIEVKDTK	93	8	13	20		8963
GAG	HIARNCR	433	8	13	20		8964
GAG	LTSLSLF	549	8	13	20		8965
GAG	IVKCFNCK	422	9	13	20		8966
GAG	CGKEGHIAR	428	9	13	20		8967
GAG	EGHIARNCR	431	9	13	20		8968
GAG	LGKIWPNSK	470	9	13	20		8969
GAG	KLKHIVWASR	31	10	13	20		8970
GAG	RIEVKDTKEA	93	10	13	20		8971
GAG	TILRALGPGA	356	10	13	20		8972
GAG	EGHIARNCR	431	10	13	20		8973
GAG	HIARNCRAPR	433	10	13	20		8974
GAG	FLGKIWPNSK	469	10	13	20		8975
GAG	EVDKTEALD	95	11	13	20		8976
GAG	FSPEVPMFTA	185	11	13	20		8977
GAG	AAEWDRVHPV	230	11	13	20		8978
GAG	KTILRALGPGA	355	11	13	20		8979
GAG	HIARNCRAPRK	433	11	13	20		8980
GAG	LGKIWPNSKG	470	11	13	20		8981

Table XVI
HIV-1 X03-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
GAG	NSSQVSQNY	144	9	14	31		8982
GAG	KSKKKAQQA	112	9	14	22		8983
GAG	NCGKEGIIAK	427	10	14	22		8984
GAG	IAKNCRAPRKK	434	11	14	22		8985
GAG	EVIPMFTA	188	8	14	22		8986
GAG	RGNFRNQRK	412	9	14	22		8987
GAG	CGKEGIIAK	428	9	14	22		8988
GAG	EGHIAKNCR	431	10	14	22		8989
GAG	EGHIAKNCR	431	10	14	22		8990
GAG	PSNKGKPGNF	475	10	14	22		8991
GAG	TAPPEESFRF	496	10	14	22		8992
GAG	TVATLYCVIIQ	83	11	14	22		8993
GAG	IVQNAQGMV	155	11	14	22		8994
GAG	PTAPPEESFRF	495	11	14	22		8995
GAG	SSOVSONY	145	8	15	31		8996
GAG	VSONYPIVQNA	149	11	15	26		8997
GAG	RSLYNTVATL	78	11	15	24		8998
GAG	TYLCVHQH	86	8	15	23		8999
GAG	FTALSEGA	193	8	15	23		9000
GAG	AAFWDRVII	230	8	15	23		9001
GAG	WDRVIIPVII	233	8	15	23		9002
GAG	RGNFRNQR	412	8	15	23		9003
GAG	TAPPEESF	496	8	15	23		9004
GAG	LASLKSFL	549	8	15	23		9005
GAG	VLSGGKLDA	7	9	15	23		9006
GAG	LFNTVATLY	80	9	15	23	0.0150	9007
GAG	ATLYCVIIHQ	85	9	15	23		9008
GAG	MFTALSEGA	192	9	15	23		9009
GAG	EAAEWDRVIH	229	9	15	23		9010
GAG	WDRVIIPVIA	233	9	15	23		9011
GAG	PTAPPEESF	495	9	15	23		9012
GAG	TAPPEESFR	496	9	15	23		9013
GAG	PLASLKSFL	548	9	15	23		9014
GAG	SVLSGGKLDA	6	10	15	23		9015
GAG	SGGKLDAWEK	9	10	15	23		9016
GAG	ELRSLYNTVA	76	10	15	23		9017
GAG	SLFNTVATLY	79	10	15	23		9018
GAG	VATLYCVIIHQ	84	10	15	23		9019
GAG	KIEEQNKSK	105	10	15	23		9020
GAG	PMFTALSEGA	191	10	15	23		9021
GAG	RAEQATODVK	329	10	15	23		9022
GAG	PTAPPEESFR	495	10	15	23		9023
GAG	ASVLSGGKLD	5	11	15	23		9024
GAG	LSGOKLDWE	8	11	15	23		9025
GAG	PGLLETSEGR	50	11	15	23		9026
GAG	KIEEQNKSKK	105	11	15	23		9027
GAG	RLHPVHAGPIA	235	11	15	23		9028
GAG	MMQGNFRN	409	11	15	23		9029
GAG	IAKNCRAPRK	434	10	16	25		9030
GAG	LSGGKLDA	8	8	16	25		9031

Table XVI
HIV-A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
GAG	LDWEKIR	13	8	16	25		9032
GAG	NAQGMVH	158	8	16	25		9033
GAG	PVSILDIK	303	8	16	25		9034
GAG	ILKALGPA	357	8	16	25		9035
GAG	KLDWEKIR	12	9	16	25		9036
GAG	GGKKKYRLK	24	9	16	25		9037
GAG	TILKALGPA	356	9	16	25		9038
GAG	ILKALGPA	357	9	16	25	0.0003	9039
GAG	VLAEMSQA	386	9	16	25		9040
GAG	LDWEKIRL	13	10	16	25		9041
GAG	PGKKKYRLK	23	10	16	25		9042
GAG	GGKKKYRLK	24	10	16	25		9043
GAG	GLLETSEGR	51	10	16	25		9044
GAG	YSPVSILDIK	301	10	16	25		9045
GAG	KTILKALGPA	355	10	16	25	0.0045	9046
GAG	TILKALGPA	356	10	16	25		9047
GAG	AATLEEMMTA	364	10	16	25		9048
GAG	RVLAEAMSQA	385	10	16	25		9049
GAG	GGKLDWEKI	10	11	16	25		9050
GAG	KLDWEKIRL	12	11	16	25		9051
GAG	PGKKKYRLK	23	11	16	25		9052
GAG	VSILDIKQPK	304	11	16	25		9053
GAG	KTILKALGPA	355	11	16	25		9054
GAG	PAATLEEMMT	363	11	16	25		9055
GAG	HIANKRPRK	433	11	16	25		9056
GAG	LAEAMSQA	387	8	17	27		9057
GAG	RLKHLVWA	31	8	17	27		9058
GAG	LSPTLNA	168	8	17	27		9059
GAG	PIPPQMR	243	8	17	27		9060
GAG	GGKLDWEK	10	9	17	27		9061
GAG	DAWEKIRL	14	9	17	27		9062
GAG	LLETSEGR	52	9	17	27		9063
GAG	RLKHLVWASR	31	10	17	27		9064
GAG	LDKIEEQNK	103	10	17	27		9065
GAG	AGPIPPQMR	241	10	17	27		9066
GAG	ALDKIEEQNK	102	11	17	27		9067
GAG	LSPTLNAV	168	11	17	27		9068
GAG	HAGPIPPQMR	240	11	17	27		9069
GAG	PIPPQMRPR	243	11	17	27		9070
GAG	PGATLEEMMT	363	11	17	27		9071
GAG	RSLYNTVA	78	8	18	29	0.0009	9072
GAG	IAKNCRAPR	434	9	18	28		9073
GAG	LDKWEKIR	13	8	18	28		9074
GAG	PVGDIYKR	281	8	18	28		9075
GAG	PDCKTILR	352	8	18	28		9076
GAG	DCKTILRA	353	8	18	28		9077
GAG	HIANKCRA	433	8	18	28		9078
GAG	PDCKTILRA	352	9	18	28		9079
GAG	ILRALGPA	357	9	18	28		9080
GAG	LDKWEKIRL	13	10	18	28		9081

Table XVI
HIV X03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
GAG	SILDIKQGP	305	10	18	28		9082
GAG	HIANKCRAPR	433	10	18	28		9083
GAG	HAGPIAPGOM	240	11	18	28		9084
GAG	NANPCKTILR	349	11	18	28		9085
GAG	LARNCRAPRK	434	11	19	30		9086
GAG	PVIAGPIA	238	8	19	30		9087
GAG	PIAPGOMR	243	8	19	30		9088
GAG	LDIKQGP	307	8	19	30		9089
GAG	ILDIKQGP	306	9	19	30		9090
GAG	PSIHKARVLA	380	9	19	30		9091
GAG	AGPIAPGOMR	241	10	19	30		9092
GAG	IAPGOMREPR	244	10	19	30		9093
GAG	DIKQGPKEPF	308	10	19	30		9094
GAG	RLRPGGKKY	20	11	19	30		9095
GAG	IVWASRELERF	35	11	19	30		9096
GAG	PIAPGOMREPR	243	11	19	30		9097
GAG	LDIKQGPKEPF	307	11	19	30		9098
GAG	DIKQGPKEPF	308	11	19	30		9099
GAG	GGPSHKARVL	378	11	19	30		9100
GAG	PSIHKARVLA	380	11	19	30		9101
GAG	LARNCRAPR	434	9	20	32		9102
GAG	LARNCRAPRK	434	10	20	32		9103
GAG	PGGKKYR	23	8	20	31		9104
GAG	TAPPAESF	496	8	20	31		9105
GAG	IMMORGNER	408	9	20	31		9106
GAG	PTAPPAESF	495	9	20	31	0.0099	9107
GAG	IVWASRELER	35	10	20	31		9108
GAG	HLARNCRAPR	433	10	20	31		9109
GAG	HLARNCRAPR	433	11	20	31		9110
GAG	HLARNCRAPR	433	11	20	31		9111
GAG	HLARNCRAPR	433	8	21	33		9112
GAG	EGHLARNCR	431	9	21	33		9113
GAG	NLQGMVHQA	158	10	21	33		9114
GAG	EGHLARNCR	431	10	21	33		9115
GAG	QSRPEPTAPPA	488	11	21	33		9116
GAG	KIWPCHKGR	472	9	22	35		9117
GAG	EVKDTKEA	95	8	22	34	0.0770	9118
GAG	ETINEEAA	224	8	22	34		9119
GAG	DTLLVQNA	343	8	22	34		9120
GAG	GGPSHKAR	378	8	22	34		9121
GAG	TDLLVQNA	342	9	22	34		9122
GAG	VGGPSHKAR	377	9	22	34		9123
GAG	SLYNTVATLY	79	10	22	34		9124
GAG	MLKETINEEA	221	10	22	34		9125
GAG	MTDTLLVQNA	341	10	22	34		9126
GAG	GVGGPSHKAR	376	10	22	34		9127
GAG	QMLKETINEEA	220	11	22	34		9128
GAG	MLKETINEEA	221	11	22	34		9129
GAG	WMTDTLLVQ	340	11	22	34		9130
GAG	QGVGGPSHKA	375	11	22	34		9131

Table XVI
HIV-A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
GAG	LGIKIWPISHK	470	11	22	34		9132
GAG	NFLGKIWPISHK	468	11	23	37		9133
GAG	KIEEQNK	105	8	23	36		9134
GAG	QGVGGPISH	375	8	23	36		9135
GAG	GVGGPISHK	376	8	23	36		9136
GAG	VGGPISHK	377	8	23	36		9137
GAG	MMQRGNFR	409	8	23	36		9138
GAG	QGVGGPISHK	375	9	23	36		9139
GAG	GVGGPISHK	376	9	23	36		9140
GAG	LGIKIWPISHK	470	9	23	36		9141
GAG	ACQVGGPISH	373	10	23	36		9142
GAG	QGVGGPISHK	375	10	23	36		9143
GAG	FLGIKIWPISHK	469	10	23	36	0.0200	9144
GAG	PSHKRPGNF	475	10	23	36		9145
GAG	TACQVGGPIS	372	11	23	36		9146
GAG	ACQVGGPISH	373	11	23	36		9147
GAG	NCGKEGHLAR	427	10	24	38		9148
GAG	KVIEKAF	178	8	24	38		9149
GAG	CGKEGHLAR	428	9	24	38		9150
GAG	WVKVIEKAF	176	10	24	38		9151
GAG	YSPVSILDIR	301	10	24	38		9152
GAG	NFLGKIWPISH	468	10	25	40		9153
GAG	PVSILDIR	303	8	25	39		9154
GAG	LGIKIWPISH	470	8	25	39		9155
GAG	KDTKEALDK	97	9	25	39		9156
GAG	WVKVIEKA	176	9	25	39		9157
GAG	FLGIKIWPISH	469	9	25	39		9158
GAG	LVWASRELER	35	11	25	39		9159
GAG	NAWVKVIEK	174	11	25	39		9160
GAG	VSILDIRQPK	304	11	25	41		9161
GAG	LVWASRELER	35	10	26	41		9162
GAG	HLVWASRELE	34	11	26	41		9163
GAG	CFNCGKEGIIIA	425	9	27	43		9164
GAG	NCGKEGIIIA	427	9	27	43		9165
GAG	NCGKEGIIIA	427	8	27	42		9166
GAG	RFFKTLRA	323	8	27	42		9167
GAG	IMMQRGNF	408	8	27	42		9168
GAG	CGKEGIIIA	428	8	27	42	0.1800	9169
GAG	CGKEGIIIA	428	8	27	42		9170
GAG	MVHQIAISPR	163	9	27	42		9171
GAG	VDREFKTLR	321	9	27	42	0.0260	9172
GAG	QMVHQIAISPR	162	10	27	42		9173
GAG	YVDREFKTLR	320	10	27	42		9174
GAG	VDREFKTLR	321	10	27	42		9175
GAG	FFKTLRAEQ	324	10	27	42		9176
GAG	RAEQATQEVK	329	10	27	42		9177
GAG	NAWVKVIEK	174	11	27	42		9178
GAG	YVDREFKTLR	320	11	27	42		9179
GAG	RFFKTLRAEQ	323	11	27	42		9180
GAG	RFFKTLRAEQ	323	11	27	42		9181

Table XVI
HIV-A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
GAG	NANPCKTILK	349	11	27	42		9182
GAG	CFNCKEGHIL	425	11	27	42		9183
GAG	KGRPNFLOS	478	11	28	44		9184
GAG	NFLOSREPTA	485	11	28	44		9185
GAG	KVVEEKAF	178	8	28	44		9186
GAG	RFYKTLRA	323	8	28	44		9187
GAG	PDCKTILK	352	8	28	44		9188
GAG	DCKTILKA	353	8	28	44		9189
GAG	WVKVVEEKA	176	9	28	44		9190
GAG	VDRFYKTLR	321	9	28	44		9191
GAG	PDCKTILKA	352	9	28	44		9192
GAG	WVKVVEEKAF	176	10	28	44		9193
GAG	PRDYVDRFY	316	10	28	44	0.0003	9194
GAG	YVDRFYKTLR	320	10	28	44		9195
GAG	VDRFYKTLRA	321	10	28	44		9196
GAG	GATLEEMMTA	364	10	28	44		9197
GAG	FLOSREPTA	486	10	28	44		9198
GAG	PRDYVDRFY	316	11	28	44	0.0005	9199
GAG	YVDRFYKTLR	320	11	28	44		9200
GAG	GARASVLSGG	2	11	29	46		9201
GAG	ASVLSGGK	5	8	29	45		9202
GAG	NLOQGMVH	158	8	29	45		9203
GAG	WVKVVEEK	176	8	29	45		9204
GAG	WDRHPVH	233	8	29	45		9205
GAG	ROYVDRFY	318	8	29	45		9206
GAG	RASVLSGGK	4	9	29	45	0.0050	9207
GAG	ASPRTLNA	167	9	29	45	0.0007	9208
GAG	WDRHPVHA	233	9	29	45		9209
GAG	ROYVDRFYK	318	9	29	45		9210
GAG	QAISPRTLNA	166	10	29	45		9211
GAG	NAWKVVEEK	174	10	29	45		9212
GAG	IVQNLOQGMV	155	11	29	45		9213
GAG	AAEWDRHPV	230	11	29	45		9214
GAG	PGNFQSR	483	8	30	48	0.0004	9215
GAG	NAWKVVEEK	174	10	30	47		9216
GAG	KIRLRPGKKK	18	11	30	47	0.0003	9217
GAG	WVKVVEEK	176	8	31	48		9218
GAG	MLKDTINEEA	221	10	32	50		9219
GAG	QMLKDTINEEA	220	11	32	50		9220
GAG	MLKDTINEEA	221	11	32	50		9221
GAG	KDTINEEA	223	8	33	52		9222
GAG	DTINEEA	224	8	33	52		9223
GAG	KDTINEEA	223	9	33	52		9224
GAG	RDYVDRFFK	318	9	33	52		9225
GAG	PRDYVDRFF	316	11	33	52		9226
GAG	RLRPGKKKK	20	9	34	53		9227
GAG	RLRPGKKKKY	20	10	34	53		9228
GAG	PIPVGEIYKR	279	10	34	53	0.0003	9229
GAG	PIPVGEIY	279	8	35	55		9230
GAG	RDYVDRFF	318	8	35	55		9231

Table XVI
HIV-A63 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
GAG	PIPVGEIYK	279	9	35	55	0.0002	9232
GAG	PGHKARVLA	380	9	35	55		9233
GAG	PFRDYVDRFF	316	10	35	55		9234
GAG	WMTETLLVQN	340	11	35	55		9235
GAG	GGPGHKARVL	378	11	35	55		9236
GAG	PGHKARVLAE	380	11	35	55		9237
GAG	DTKEALDK	98	8	36	56	0.0003	9238
GAG	ISPTLNA	168	8	36	56		9239
GAG	QGVGGPGH	375	8	36	56		9240
GAG	QSRPEPTA	488	8	36	56	0.0004	9241
GAG	QGVGGPGHK	375	9	36	56		9242
GAG	MTETLLVQNA	341	10	36	56		9243
GAG	ACQGVGGPGH	373	10	36	56		9244
GAG	QGVGGPGHKA	375	10	36	56		9245
GAG	ISPTLNAVW	168	11	36	56		9246
GAG	TACQGVGGPG	372	11	36	56	0.0001	9247
GAG	ACQGVGGPGH	373	11	36	56		9248
GAG	QGVGGPGHKA	375	11	36	56		9249
GAG	QGVGGPGHKA	375	11	37	58		9250
GAG	QGVGGPGHKA	160	8	37	58	0.0012	9251
GAG	ETLLVQNA	343	8	37	58		9252
GAG	GVGGPGHK	376	8	37	58		9253
GAG	GVGGPGHKA	377	8	37	58		9254
GAG	GVGGPGHKA	378	8	37	58		9255
GAG	GVGGPGHKA	376	9	37	58		9256
GAG	GVGGPGHKA	377	9	37	58	0.0003	9257
GAG	GVGGPGHKA	376	10	37	61		9258
GAG	AAEWDRLLH	230	8	39	61		9259
GAG	AAEWDRLLH	229	9	39	61	0.0003	9260
GAG	PVGEIYKR	281	8	40	63		9261
GAG	TVATLYCVH	83	9	40	63		9262
GAG	NTVATLYCVH	82	10	40	63		9263
GAG	SILDIRQGP	305	10	40	63	0.3100	9264
GAG	FSPEVIPMESA	185	11	40	63		9265
GAG	DIRQGPKEPF	308	10	41	64		9266
GAG	LDIROGPK	307	11	41	64		9267
GAG	DIRQGPKEPF	308	11	41	64		9268
GAG	VATLYCVH	84	8	42	66		9269
GAG	LDIROGPK	307	8	42	66	0.0420	9270
GAG	ILDIRQGP	306	9	42	66		9271
GAG	NTMLNTVGGH	206	10	42	66		9272
GAG	TMLNTVGGH	207	9	43	67		9273
GAG	TMLNTVGGH	207	11	43	67		9274
GAG	KGCWKCGK	444	8	44	69		9275
GAG	KIRLRPGGK	18	9	44	69	1.9000	9276
GAG	ASRELERFA	38	9	44	69		9277
GAG	KIRLRPGGK	18	10	44	69		9278
GAG	WASRELERFA	37	10	44	69		9279
GAG	QMPREPRGSDIA	248	11	44	69		9280
GAG	KGCWKCGKEG	444	11	44	69		9281
GAG	FSALSEGA	193	8	45	70		

Table XVI
HIV-1 A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
GAG	PGMREPR	246	8	45	70		9282
GAG	MFSALSEGA	192	9	45	70		9283
GAG	CGKEGHQMK	449	9	45	70		9284
GAG	PMFSALSEGA	191	10	45	70		9285
GAG	KCGKEGHQMK	448	10	45	70		9286
GAG	ASRELERF	38	8	46	72		9287
GAG	EVIPMFSA	188	8	46	72		9288
GAG	TLEEMMTA	366	8	46	72		9289
GAG	WASRELERF	37	9	46	72	0.0003	9290
GAG	ATLEEMMTA	365	9	46	72		9291
GAG	MLNTVGGH	208	8	47	73		9292
GAG	NTVGGHQA	210	8	47	73		9293
GAG	TVGGHQA	211	8	47	73		9294
GAG	NTVGGHQA	210	9	47	73		9295
GAG	MLNTVGGHQA	208	10	47	73		9296
GAG	MLNTVGGHQA	208	11	47	73		9297
GAG	WASRELER	37	8	48	75		9298
GAG	GCWKCKEGH	445	10	48	75		9299
GAG	RLRPGGKK	20	8	49	77		9300
GAG	QMKDCTER	455	8	49	77		9301
GAG	QMKDCTERQA	455	10	49	77		9302
GAG	EGHQMKDCTE	452	11	49	77		9303
GAG	AFSPEVIMF	184	10	50	78	0.0007	9304
GAG	KAFSPEVIMF	183	11	50	78		9305
GAG	RAPRKKGCWK	439	10	51	80		9306
GAG	KDCTERQA	457	8	52	83		9307
GAG	KDCTERQANF	457	10	52	83		9308
GAG	CTERQANFLG	459	11	52	83		9309
GAG	DCTERQANF	458	9	52	81		9310
GAG	NCRAPRKK	437	8	53	84		9311
GAG	TINEEAIEWD	225	11	53	83		9312
GAG	KTLRAEQA	326	8	54	84		9313
GAG	FSPEVIMF	185	9	54	84		9314
GAG	CTERQANF	459	8	55	87		9315
GAG	WIILGLNK	289	8	57	89		9316
GAG	KARVLAE	383	8	57	89		9317
GAG	CFNCGKEGH	425	9	57	89	0.0003	9318
GAG	IILGLNKIVR	290	10	57	89		9319
GAG	KCFNCGKEGH	424	10	57	89		9320
GAG	WIILGLNKIVR	289	11	57	89		9321
GAG	IILGLNKIVRMY	291	11	57	89		9322
GAG	IILGLNKIVR	291	9	58	91	0.0008	9323
GAG	LGLNKIVRMY	292	10	58	91	0.0004	9324
GAG	LLVQANPDC	345	11	58	91		9325
GAG	LGLNKIVR	292	8	59	92	0.0002	9326
GAG	LVQANPDC	346	10	59	92	0.0100	9327
GAG	GLNKIVRMY	293	9	60	94		9328
GAG	QAAMQMLK	216	8	61	95		9329
GAG	GGHOAAQM	213	11	61	95		9330
GAG	RTLNAWVK	171	8	63	98	0.0410	9331

Table XVI
HIV A03-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
GAG	QGPKEPFR	311	8	63	98		9332
GAG	PFRDYVDR	316	8	63	98		9333
GAG	PFRDYVDRF	316	9	63	98		9334
GAG	QGPKEPFRDY	311	10	63	98		9335
NEF	QGPKEPFRDY	34	11	01	33	0.0004	9336
NEF	RAQAEPAAGVG	32	8	01	17		9337
NEF	RAQAEPAAGVG	32	9	01	17		9338
NEF	RAQAEPAAGVG	32	11	01	17		9339
NEF	QTEPAAGVG	32	11	01	17		9340
NEF	RAEPAAGVG	32	11	01	17		9341
NEF	RTEPAAGVG	32	11	01	17		9342
NEF	QAEPAAGVG	33	11	01	17		9343
NEF	QAPTAAGVG	33	11	01	15		9344
NEF	AADGVGAVSR	42	10	09	15		9345
NEF	SSIVGWPA	8	8	09	17		9346
NEF	VGVPAIRER	11	9	10	16		9347
NEF	AAEGVGAA	42	8	10	16		9348
NEF	FDSRLAFH	310	8	10	16		9349
NEF	FDSRLAFHII	310	9	10	16		9350
NEF	DSRLAFHII	311	8	10	16		9351
NEF	AVSQDLK	48	8	10	16		9352
NEF	PLRPMTFK	102	8	10	16		9353
NEF	KGAFDLSF	109	8	10	16		9354
NEF	KGAFDLSF	110	8	10	16		9355
NEF	GAFLSFF	47	9	10	16		9356
NEF	GAVSQDLK	100	9	10	16		9357
NEF	QVPLRPMTF	100	9	10	16		9358
NEF	KGAFDLSF	109	9	10	16		9359
NEF	GLEGLYSK	125	9	10	16		9360
NEF	MARELHPEY	321	9	10	16		9361
NEF	VGAVSQDLK	46	10	10	16		9362
NEF	QVPLRPMTFK	100	10	10	16		9363
NEF	GAFLSFFLK	110	10	10	16		9364
NEF	GGLEGLYSK	124	10	10	16		9365
NEF	CFKLVPVDP	226	10	10	16		9366
NEF	HMARELHPEY	320	10	10	16		9367
NEF	MARELHPEY	321	10	10	16		9368
NEF	GVGAVSQDLK	45	11	10	16		9369
NEF	KGAFDLSFFLK	109	11	10	16		9370
NEF	KGLEGLYSK	122	11	10	16		9371
NEF	WCFKLVPVDP	225	11	10	16		9372
NEF	HMARELHPEY	320	11	10	16		9373
NEF	MARELHPEY	321	11	11	17		9374
NEF	AVSRDLEK	48	8	11	17		9375
NEF	VSRDLEKH	49	8	11	17	0.0002	9376
NEF	KLVVPVDP	228	8	11	17		9377
NEF	GAVSRDLEK	47	9	11	17		9378
NEF	AVSRDLEKH	48	9	11	17		9379
NEF	VGAVSRDLEK	46	10	11	17		9380
NEF	GAVSRDLEKH	47	10	11	17		9381
NEF	VSRDLEKHGA	49	10	11	17		9382
NEF	NSLLHPIQCH	255	10	11	17		9383

Table XVI
HIV-1 A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
NEF	GVGAVSRDLE	45	11	11	17		9382
NEF	VGAVSRDLEK	46	11	11	17		9383
NEF	AVSRDLEKIIG	48	11	11	17		9384
NEF	AATNADCA	70	8	12	22		9385
NEF	ATNADCAWLE	71	11	12	22		9386
NEF	EGENNCLLH	251	9	12	19		9387
NEF	PMTYKGAF	105	8	12	19		9388
NEF	YTPGPGVR	207	8	12	19		9389
NEF	TAATNADCA	69	9	12	19		9390
NEF	DILDWVYII	185	9	12	19		9391
NEF	NTAATNADCA	68	10	12	19		9392
NEF	QDILDWVYH	184	10	12	19		9393
NEF	ITSSNTAATNA	64	11	12	19		9394
NEF	PLRPMYKGA	102	11	12	19		9395
NEF	PGIRYPLTF	211	9	13	21		9396
NEF	PGTRFPLTF	211	9	13	21		9397
NEF	EGENNSLLH	251	9	13	21		9398
NEF	WVYHTQGF	191	8	13	20		9399
NEF	GRYPLTF	213	8	13	20		9400
NEF	GTRFPLTF	213	8	13	20		9401
NEF	SSNTAATNA	66	9	13	20		9402
NEF	WVYHTQGF	191	9	13	20		9403
NEF	YTPGPGTRF	207	9	13	20		9404
NEF	TSSNTAATNA	65	10	13	20		9405
NEF	VDSLHFLKEK	112	10	13	20		9406
NEF	DLWVYHTQGF	188	10	13	20		9407
NEF	AVDSLHFLKEK	111	11	13	20		9408
NEF	LDLWVYHTQG	187	11	13	20		9409
NEF	DLWVYHTQGF	188	11	13	20		9410
NEF	PGGIRYPLTF	209	11	13	20		9411
NEF	PGGTRFPLTF	209	11	13	20		9412
NEF	VDSLHFLK	112	8	14	22		9413
NEF	DGLYSKK	172	8	14	22		9414
NEF	ELHPEFYK	324	8	14	22		9415
NEF	AITSSNTAA	63	9	14	22	0.0003	9416
NEF	AVDSLHFLK	111	9	14	22	0.0740	9417
NEF	LDGLYSKK	171	9	14	22		9418
NEF	DGLYSKKR	172	9	14	22		9419
NEF	SLHPIQHI	256	9	14	22		9420
NEF	GAITSSNTAA	62	10	14	22		9421
NEF	GLDGLYSKK	125	10	14	22		9422
NEF	LDGLYSKKR	171	10	14	22		9423
NEF	HGAITSSNTAA	61	11	14	22		9424
NEF	GGLDGLYSKK	124	11	14	22		9425
NEF	GLDGLYSKKR	125	11	14	22		9426
NEF	PAADGVGA	41	8	15	23		9427
NEF	ITSSNTAA	64	8	15	23		9428
NEF	CLLHPMSQH	256	9	15	23		9429
NEF	NCLLHPMSQH	255	10	15	23		9430
NEF	EAQEEVEVGF	82	10	16	25		9431

Table XVI
HIV-1 X3 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
NEF	RDLEKHGA	51	8	16	25		9432
NEF	LDGLIYK	171	8	16	25		9433
NEF	GLDGLIYK	125	9	16	25		9434
NEF	GGLDGLIYK	124	10	16	25		9435
NEF	KGGLDGLIYK	122	11	16	25		9436
NEF	RPPLTFGWCF	216	10	17	27		9437
NEF	RPPLTFGWCF	216	11	17	27		9438
NEF	ADCAWLEA	74	8	17	27		9439
NEF	FFPDWQNY	199	8	17	27		9440
NEF	LLHPMSQH	257	8	17	27		9441
NEF	NADCAWLEA	73	9	17	27		9442
NEF	GFFPDWQNY	198	9	17	27		9443
NEF	YTPGPGIRY	207	9	17	27		9444
NEF	FDSLFLKEK	112	10	17	27		9445
NEF	QGFPPDWQNY	196	10	17	27		9446
NEF	AFDLSFLKEK	111	11	17	27		9447
NEF	FDSLFLK	112	8	18	28		9448
NEF	LLIPICQH	257	8	18	28		9449
NEF	AFDLSFLK	111	9	18	28		9450
NEF	GGLEGLIY	124	8	19	30		9451
NEF	KGLEGLIY	122	9	19	30		9452
NEF	DILDWVY	185	8	20	31		9453
NEF	YTPGPGIR	207	8	20	31		9454
NEF	QDILDWVY	184	9	20	31		9455
NEF	PLRPMTYKAA	102	10	20	31		9456
NEF	QVPLRPMTYK	100	11	20	31		9457
NEF	PAEGVGA	41	8	21	33		9458
NEF	GGLDGLIY	124	8	21	33		9459
NEF	WVYHTQGY	191	8	21	33		9460
NEF	YTPGPGTR	207	8	21	33		9461
NEF	PLRPMTYKA	102	9	21	33		9462
NEF	KGGLDGLIY	122	9	21	33		9463
NEF	WVYHTQGYF	191	9	21	33		9464
NEF	DLWVYHTQGY	188	10	21	33		9465
NEF	LDLWVYHTQG	187	11	21	33		9466
NEF	DLWVYHTQGY	188	11	21	33		9467
NEF	LSFLKEK	114	8	22	34		9468
NEF	ELIPEYYK	324	8	22	34		9469
NEF	DLSEFLKEK	113	9	22	34		9470
NEF	EILDWVYH	185	9	22	34		9471
NEF	GLYSKKR	173	8	23	36		9472
NEF	PLRPMTYKGA	102	10	25	39		9473
NEF	AITSSNTA	63	8	27	42		9474
NEF	LSHFLKEK	114	8	27	42		9475
NEF	GAITSSNTA	62	9	27	42		9476
NEF	DLSEFLKEK	113	9	27	42		9477
NEF	HGAITSSNTA	61	10	27	42		9478
NEF	EILDWVY	185	8	33	52		9479
NEF	ILDWVYH	186	8	34	53		9480
NEF	YFPDWQNY	199	8	36	56		9481

Table XVI
HIV X03 Motif Peptides With Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*0301	SEQ ID NO.
NEF	QGYFDWQNY	196	10	36	56		9482
NEF	LTFGWCFK	221	8	39	61	0.0004	9483
NEF	PLTFGWCFK	219	9	39	61		9484
NEF	PLTFGWCF	219	8	43	67		9485
NEF	QVPLRPMTY	100	9	46	72		9486
NEF	QVPLRPMTYK	100	10	46	72	0.6100	9487
NEF	PVRPQVPLR	95	9	48	75		9488
NEF	GFVRPQVPLR	93	11	48	75		9489
NEF	PLRPMTYK	102	8	49	77	0.0010	9490
POL	STNSPTSR	32	8	01	33		9491
POL	RANSPSSR	35	8	01	33		9492
POL	NSNSPTSR	31	9	01	33		9493
POL	PSRELOVR	36	9	01	33		9494
POL	QTRANSRSSR	33	10	01	33		9495
POL	QTRANSPTTR	35	10	01	33		9496
POL	NSPTSRELOVR	34	11	01	33		9497
POL	RANSPTR	37	8	01	50		9498
POL	PSSRELOVR	39	9	01	50		9499
POL	PSRANSPTR	24	10	01	50		9500
POL	NSPSSRELOVR	37	11	01	50		9501
POL	NSPTTRELQV	39	11	01	50		9502
POL	ADROGIVSF	71	9	01	20		9503
POL	DDRQGPVSF	71	9	01	20		9504
POL	GADROGIVSF	70	10	01	20		9505
POL	GDDRQGPVSF	70	10	01	20		9506
POL	ADROGIVSFNF	71	11	01	20		9507
POL	DDRQGPVSFSEF	69	11	01	17		9508
POL	AGADROGIVSF	69	11	01	17		9509
POL	AGDDRQGPVS	69	11	01	17		9510
POL	GTTLNFQITF	79	11	01	17		9511
POL	NLAFPOGEA	5	9	10	16		9512
POL	NLAFPOGEAR	5	10	10	16		9513
POL	KTGYAKMRT	542	11	10	16		9514
POL	ILIEICGH	149	8	10	16		9515
POL	LIEICGHK	150	8	10	16		9516
POL	YAKMRTAH	546	8	10	16		9517
POL	LIEICGHKA	150	9	10	16		9518
POL	RSAHTNDVK	550	9	10	16		9519
POL	AFPOGEAREF	7	10	10	16		9520
POL	LIEALLDTGA	106	10	10	16		9521
POL	TGKYAKMRTA	543	10	10	16		9522
POL	ETWETWTD	588	10	10	16		9523
POL	ETWETWTE	588	10	10	16		9524
POL	ETWWTYQQ	591	10	10	16		9525
POL	VSLDTTNQK	659	10	10	16		9526
POL	LAFPOGEAREF	6	11	10	16		9527
POL	QLIEALLDTGA	105	11	10	16		9528
POL	MLTQLGCTLN	176	11	10	16		9529
POL	TGKYAKMRTA	543	11	10	16		9530
POL	VVSLDTTNQ	658	11	10	16		9531

Table XVI
HIV-103 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	QTKELQKQIK	961	11	10	16		9532
POL	QTRANSPTRR	21	10	11	18		9533
POL	LDGDKAQEDH	754	11	11	17		9534
POL	IGGFIKVK	137	8	11	17		9535
POL	RIGPENPY	238	8	11	17		9536
POL	VIPLTEEA	481	8	11	17		9537
POL	TAHTNDVK	551	8	11	17		9538
POL	QLTEVVQK	559	8	11	17		9539
POL	IDKAQEDH	757	8	11	17		9540
POL	WAGIQQEF	884	8	11	17		9541
POL	VVPRKVK	1012	8	11	17		9542
POL	KIKDYGK	1019	8	11	17		9543
POL	GIGGFIKVK	136	9	11	17		9544
POL	EVIPLTEEA	480	9	11	17		9545
POL	SLDTTNQK	660	9	11	17		9546
POL	GDKAQEDH	756	9	11	17		9547
POL	KVPRKVK	1011	9	11	17		9548
POL	GGIGGFIKVK	135	10	11	17		9549
POL	ISRIGPENPY	236	10	11	17		9550
POL	STNNETGIR	323	10	11	17		9551
POL	ESWTVNDIQK	439	10	11	17		9552
POL	ETTNQKTELH	663	10	11	17		9553
POL	DGDKAQEDH	755	10	11	17		9554
POL	GSNFTSTTVK	870	10	11	17		9555
POL	GIQQEFGIPY	886	10	11	17		9556
POL	SDIQTKELQK	958	10	11	17		9557
POL	1020		10	11	17		9558
POL	IKDYGKQMA	134	11	11	17		9559
POL	IGGIGGFIKVK	235	11	11	17		9560
POL	KISRIGPENPY	322	11	11	17		9561
POL	PSNNETGIR	323	11	11	17		9562
POL	STNNETGIRY	478	11	11	17		9563
POL	LTEVIPLTEEA	658	11	11	17		9564
POL	VVSLTETTNQ	663	11	11	17		9565
POL	ETTNQKTELH	869	11	11	17		9566
POL	NGSNFTSTTV	870	11	11	17		9567
POL	GSNFTSTTVK	881	11	11	17		9568
POL	ACWWAGIQQE	885	11	11	17		9569
POL	AGIQQEFGIPY	953	11	11	17		9570
POL	IDIASDIQTK	953	11	11	17		9571
POL	VDIATDIQTK	957	11	11	17		9572
POL	ASDIQTKELQK	1007	11	11	17		9573
POL	NSEIKVVPRKK	1019	11	11	17		9574
POL	KIKDYGKQMA	60	8	12	20		9575
POL	NSLSEAGA	21	10	12	19		9576
POL	QTRANSPTSR	969	8	12	19		9577
POL	IKIQNFR	458	9	12	19		9578
POL	QIYPGKVK	526	9	12	19		9579
POL	ODQWTYQIY	969	10	12	19		9580
POL	IKIQNFRVY	456	11	12	19		9581
POL	ASQIYPGKVK						

Table XVI
HIV A03-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	IIKIQNFRVYY	969	11	12	19		9582
POL	LAFPOGEA	6	8	12	19		9583
POL	LAFPOGKA	6	8	12	19		9584
POL	AFPOGEAR	7	8	12	19		9585
POL	KTELOAIY	668	8	12	19		9586
POL	ELQAIYLA	670	8	12	19		9587
POL	QIKIQNF	968	8	12	19		9588
POL	KDYGQMA	1022	8	12	19		9589
POL	LAFPOGEAR	6	9	12	19		9590
POL	EINLPKWK	122	9	12	19		9591
POL	TTNOKTELIH	664	9	12	19		9592
POL	QIKIQNFR	968	9	12	19		9593
POL	VIODNSEIK	1003	9	12	19		9594
POL	NSEIKVVPR	1007	9	12	19		9595
POL	VLEEINLPK	119	10	12	19		9596
POL	TTNOKTELIH	664	10	12	19		9597
POL	KTELOAIYLA	668	10	12	19		9598
POL	VVIONNSEIK	1002	10	12	19		9599
POL	NSEIKVVPR	1007	10	12	19		9600
POL	TVLEINLPK	118	11	12	19		9601
POL	EINLPKWKPK	122	11	12	19		9602
POL	ELRQILLRWG	393	11	12	19		9603
POL	QGQDQWYQI	524	11	12	19		9604
POL	RMGAHTNDV	548	11	12	19		9605
POL	QIKIQNFRVY	968	11	12	19		9606
POL	AVVIONNSEIK	1000	11	12	19		9607
POL	QDNSEIKVVPR	1005	11	12	19		9608
POL	ELQKQIK	964	8	13	21		9609
POL	EFSEQTRA	16	9	13	21		9610
POL	KTGKYARMR	542	9	13	21		9611
POL	NLKTGYARM	540	11	13	21		9612
POL	KTGKYARMRG	542	11	13	21		9613
POL	EDINLPK	121	8	13	20		9614
POL	IVPLTEEA	481	8	13	20		9615
POL	TKYARMR	543	8	13	20		9616
POL	YARMRGH	546	8	13	20		9617
POL	IGOVREQA	914	8	13	20		9618
POL	QVREQAEH	916	8	13	20		9619
POL	DINLPKWK	122	9	13	20		9620
POL	LIEICGKKA	150	9	13	20		9621
POL	DIVPLTEEA	480	9	13	20		9622
POL	IIGOVREQA	913	9	13	20		9623
POL	VLEDINLPK	119	10	13	20		9624
POL	EDINLPKWK	121	10	13	20		9625
POL	ILIEICGKKA	149	10	13	20		9626
POL	RAKIEELREH	388	10	13	20		9627
POL	TVQPIVLPEK	429	10	13	20		9628
POL	TDIVPLTEEA	479	10	13	20		9629
POL	TGYARMRGA	543	10	13	20		9630
POL	AGRWPVKTHI	857	10	13	20	0.1600	9631

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	KIQGVREQA	912	10	13	20		9632
POL	IGQVREQA	914	10	13	20		9633
POL	QVREQA	916	10	13	20		9634
POL	EIKVVRKA	1009	10	13	20		9635
POL	TLVQRPLVTV	91	11	13	20		9636
POL	LVTKIGGQK	97	11	13	20		9637
POL	TVLEDINLQK	118	11	13	20		9638
POL	DINLPKWK	122	11	13	20		9639
POL	QILIECGKA	148	11	13	20		9640
POL	KIELREHLK	390	11	13	20		9641
POL	WTVOPIVLPEK	428	11	13	20		9642
POL	LTDIVPLTEA	478	11	13	20	0.0011	9643
POL	TGKYARMGA	543	11	13	20		9644
POL	LAGRWPKTI	856	11	13	20		9645
POL	IIGQVREQA	913	11	13	20		9646
POL	DSRDPLWKG	981	11	13	20		9647
POL	EIKVVRKAK	1009	11	13	20		9648
POL	EFSEQTR	16	8	14	22		9649
POL	QIYPIKVR	458	9	14	22		9650
POL	ASQIYPIKVR	456	11	14	22		9651
POL	IATESIVIWGK	567	11	14	22		9652
POL	ILIECGK	149	8	14	22		9653
POL	LEICGKK	150	8	14	22		9654
POL	NFTSTTVK	872	8	14	22		9655
POL	FISTTVKA	873	8	14	22		9656
POL	TSTTVKAA	874	8	14	22		9657
POL	IASDIQTK	956	8	14	22		9658
POL	DSRDPLWK	981	8	14	22		9659
POL	ILIECGK	148	9	14	22		9660
POL	NFTSTTVKA	872	9	14	22		9661
POL	FISTTVKAA	873	9	14	22	0.0003	9662
POL	IASDIQTK	955	9	14	22		9663
POL	RDSRDPLWK	980	9	14	22		9664
POL	RDPLWKGPA	983	9	14	22		9665
POL	QILIECGKK	148	10	14	22		9666
POL	RTKIELRQH	388	10	14	22		9667
POL	PGIKVRLCK	461	10	14	22		9668
POL	TIHTDNGSNF	864	10	14	22		9669
POL	NFTSTTVKAA	872	10	14	22		9670
POL	TTVKAACWW	876	10	14	22	0.0006	9671
POL	AGERIVDIA	948	10	14	22		9672
POL	DIASDIQTK	954	10	14	22		9673
POL	RDPLWKGPAK	983	10	14	22		9674
POL	FSFQITLWQR	85	11	14	22		9675
POL	YDQILIECGK	146	11	14	22		9676
POL	ELREHLKWK	393	11	14	22		9677
POL	KTPKFLPIQK	577	11	14	22		9678
POL	GIDKAQEEHER	756	11	14	22		9679
POL	STTVKAACW	875	11	14	22		9680
							9681

Table XVI
HIV-1 gp120 Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	SAGERIVDIIA	947	11	14	22		9682
POL	QTRANSPTTR	21	9	15	24		9683
POL	LVEICTEMEK	221	10	15	24	0.0002	9684
POL	FFREDLAF	1	8	15	23		9685
POL	FSSEQTRA	17	8	15	23		9686
POL	ELRQHLLR	393	8	15	23		9687
POL	OGQDOWTY	524	8	15	23		9688
POL	KTELQAIH	668	8	15	23		9689
POL	AGIRKVLV	746	8	15	23		9690
POL	PIKETWEA	584	9	15	23		9691
POL	SAGIRKVLV	745	9	15	23		9692
POL	EIKVVPRK	1009	9	15	23		9693
POL	LTQLGCTLNF	177	10	15	23		9694
POL	KTELQAIHLA	668	10	15	23		9695
POL	LCHQAQPD	695	10	15	23		9696
POL	VDKLVSAGIR	740	10	15	23		9697
POL	VSAGIRKVLV	744	10	15	23		9698
POL	IDKAEHER	757	10	15	23		9699
POL	ALVEICTEMEK	220	11	15	23		9700
POL	KIELRQHLLR	390	11	15	23		9701
POL	ALGHQAQPD	694	11	15	23		9702
POL	LVNQHIEQLK	709	11	15	23		9703
POL	QVDKLVSAGIR	739	11	15	23		9704
POL	VDKLVSAGIR	740	11	15	23		9705
POL	LVSAGIRKVLV	743	11	15	23		9706
POL	IDKAEHER	757	11	15	23		9707
POL	KAQEEHER	759	8	16	25		9708
POL	NLAFOQGEA	5	9	16	25		9709
POL	KAQEEHER	759	9	16	25		9710
POL	NLAFOQGEAR	5	10	16	25		9711
POL	KAQEEHERVH	759	10	16	25		9712
POL	LAFQOGEA	6	8	16	25		9713
POL	AFQOGEAR	7	8	16	25		9714
POL	RANSPTTR	26	8	16	25		9715
POL	QLGCTLNF	179	8	16	25		9716
POL	SAITNDVK	551	8	16	25		9717
POL	ELQAIHLA	670	8	16	25		9718
POL	IIQAQPD	697	8	16	25		9719
POL	QVDKLVS	739	8	16	25		9720
POL	KLVSAGIR	742	8	16	25		9721
POL	LVSAGIRK	743	8	16	25		9722
POL	EIKVVPRR	1009	8	16	25	0.0091	9723
POL	LAFQOGEAR	6	9	16	25		9724
POL	GIQAQPD	696	9	16	25		9725
POL	KLVSAGIRK	742	9	16	25	0.1300	9726
POL	OLEKEPIVGA	620	10	16	25		9727
POL	RANSPTSR	26	8	17	27		9728
POL	KIELRQH	390	8	17	27		9729
POL	ELREHLK	393	8	17	27		9730
POL	WGKTPKFK	575	8	17	27		9731

Table XVI
HIV X03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	TIKIGQLK	99	9	17	27	0.2700	9732
POL	VTIKIGQLK	98	10	17	27	0.0370	9733
POL	TVQPIQLPEK	429	10	17	27		9734
POL	VIWGTKPKFK	573	10	17	27		9735
POL	TLWQRPLVTI	91	11	17	27		9736
POL	TIKIGQLKEA	99	11	17	27		9737
POL	MLTOIGCTLNF	176	11	17	27		9738
POL	WTVQPIQLPEK	428	11	17	27		9739
POL	IVIWGTKPKFK	572	11	17	27		9740
POL	ETTNQKTELQ	663	11	17	27		9741
POL	KDFRKYTAF	311	9	18	29		9742
POL	YFSVPLDKDF	304	10	18	29		9743
POL	YFSVPLDKDFR	304	11	18	29		9744
POL	YFSVPLDKDFR	540	11	18	29		9745
POL	NLKTGKYAKM	306	8	18	28		9746
POL	SVPLDKDF	365	8	18	28		9747
POL	PDIVYQY	305	9	18	28		9748
POL	FSPVPLDKDF	306	9	18	28		9749
POL	SVPLDKDFR	305	10	18	28		9750
POL	SVPLDKDFR	306	10	18	28		9751
POL	AGIKVKQLCK	461	11	18	28		9752
POL	FSPVPLDKDFR	305	11	18	28		9753
POL	SVPLDKDFR	306	11	18	28		9754
POL	LDKDFRKYTA	309	11	18	28		9755
POL	YAGIKVKQLCK	460	11	18	28		9756
POL	LVSQIEQLIK	709	11	18	28		9757
POL	PLDKDFR	308	8	19	30		9758
POL	KDFRKYTA	311	8	19	30		9759
POL	PLDKDFRKY	308	9	19	30		9760
POL	KTGKYAKMR	542	9	19	30		9761
POL	PLDKDFRKYT	308	11	19	30		9762
POL	LDKDFRKY	309	8	19	30		9763
POL	KIELREH	390	8	19	30		9764
POL	TGKYAKMR	543	8	19	30		9765
POL	GAHTNDVK	551	8	19	30		9766
POL	LTDTTNOK	661	8	19	30		9767
POL	PLWKGPAK	985	8	19	30		9768
POL	GIKVRQLCK	462	9	19	30		9769
POL	RGHTNDVK	550	9	19	30		9770
POL	LDKDFRKYTA	309	10	19	30		9771
POL	KVRQLCKLLR	464	10	19	30		9772
POL	ATESVIWVK	568	10	19	30		9773
POL	VSQIEQLIK	710	10	19	30	0.0007	9774
POL	MAGDDCVASR	1028	10	19	30		9775
POL	VSQIEQLIK	710	11	19	30		9776
POL	QLIKKEKVVLA	716	11	19	30		9777
POL	QMAGDDCVAS	1027	11	19	30		9778
POL	QIYAGIKVK	458	9	20	32	0.0750	9779
POL	KVYLAWVPA	722	9	20	32	0.0280	9780
POL	KVYLAWVPAH	722	10	20	32		9781

Table XVI
HIV-1 A05-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	KAACWWAGIK	879	10	20	32	0.0300	9782
POL	ASQIYAGIKVK	456	11	20	32		9783
POL	KVYLAWVPAH	722	11	20	32	8.6000	9784
POL	KFKLPIQK	580	8	20	31		9785
POL	GDDCVASR	1030	8	20	31		9786
POL	AGDDCVASR	1029	9	20	31		9787
POL	VSLTETTNQK	659	10	20	31		9788
POL	LIKKEKVYLA	717	10	20	31		9789
POL	LLKLAGRWPV	853	11	20	31		9790
POL	YFSVPLDK	304	8	21	33		9791
POL	KVIHTDNGSNF	863	11	21	33		9792
POL	ACWWAGIK	881	8	21	33		9793
POL	WAGIKQEF	884	8	21	33		9794
POL	SLTETTNQK	660	9	21	33		9795
POL	AACWWAGIK	880	9	21	33	0.0130	9796
POL	DAYESVPLDK	302	10	21	33		9797
POL	DLEIGQIRTK	381	10	21	33		9798
POL	QLCKLLRGTK	467	10	21	33		9799
POL	SDFNLPPIVA	776	10	21	33		9800
POL	LLYQIGCTLNF	176	11	21	33		9801
POL	IFAIRKKDSTK	249	11	21	33		9802
POL	GDAYESVPLD	301	11	21	33		9803
POL	SDLEIGQIRTK	380	11	21	33		9804
POL	QLCKLLRGTK	467	11	21	33		9805
POL	ASDFNLPPIVA	775	11	21	33		9806
POL	SDFNLPPIVAK	776	11	21	33		9807
POL	ACWWAGIKQE	881	11	21	33		9808
POL	AGIKQEFGIPY	885	11	21	33		9809
POL	EDFRKYTA	311	8	22	35		9810
POL	EDFRKYTAF	311	9	22	35		9811
POL	EIGQIRTK	383	8	22	34		9812
POL	RTKIELR	388	8	22	34		9813
POL	YLAWVPAH	724	8	22	34		9814
POL	YLAWVPAHK	725	8	22	34	0.0770	9815
POL	YLAWVPAHK	724	9	22	34		9816
POL	NFQITLWQR	86	10	22	34		9817
POL	MTKILEPERK	353	10	22	34	0.0150	9818
POL	KVILVAVHVA	823	10	22	34		9819
POL	AGRWPKVVIH	857	10	22	34	0.0002	9820
POL	GKQEFGIPY	886	10	22	34		9821
POL	SMTKILEPERK	352	11	22	34		9822
POL	KTPKRLPIQK	577	11	22	34		9823
POL	LAGRWPKVVI	856	11	22	34		9824
POL	KVYLSWVPA	722	9	23	37		9825
POL	KVYLSWVPAH	722	10	23	37		9826
POL	KVYLSWVPAH	722	11	23	37		9827
POL	KILEPERK	355	8	23	36		9828
POL	EGKVILVA	821	8	23	36		9829
POL	KVILVAVH	823	8	23	36		9830
POL	KIGGQLKEA	101	9	23	36		9831

Table XVI
HIV-1 Mod Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	DENLPIVA	777	9	23	36		9832
POL	VILVAHVA	824	9	23	36		9833
POL	TVKAAACWVA	877	9	23	36		9834
POL	SEPOITLWOR	86	10	23	36		9835
POL	DFNLPIVAK	777	10	23	36		9836
POL	HLEKGVILVA	819	10	23	36		9837
POL	EGKVLVAVII	821	10	23	36		9838
POL	LLKVGFTTPD	398	11	23	36		9839
POL	LLRWGFTTPD	398	11	23	36		9840
POL	IDIATDIQTK	953	11	23	36		9841
POL	KLLRGTKA	470	8	24	38		9842
POL	NTPIFAIK	246	8	24	38		9843
POL	GDDCVAGR	1030	8	24	38		9844
POL	NTPIFAIKK	246	9	24	38	0.0004	9845
POL	LCKLLRGTK	468	9	24	38		9846
POL	AGDDCVAGR	1029	9	24	38		9847
POL	NTPIFAIKKK	246	10	24	38		9848
POL	LCKLLRGTKA	468	10	24	38		9849
POL	VIIHDNGSNF	864	10	24	38		9850
POL	MAGDDCVAGR	1028	10	24	38		9851
POL	QLCKLLRGAK	467	11	24	38		9852
POL	QGQGWYQI	524	11	24	38		9853
POL	KLKAGYVTD	643	11	24	38		9854
POL	TAYFLKLAG	849	11	24	38		9855
POL	QMGDDCVAG	1027	11	24	38		9856
POL	KLLRGAKA	470	8	25	40		9857
POL	QGQWYQIY	526	8	25	40	0.0004	9858
POL	IGGQLKEA	102	8	25	39		9859
POL	PIFAIKKK	248	8	25	39		9860
POL	QGQGWY	524	8	25	39		9861
POL	FLKLAGR	852	8	25	39		9862
POL	QLCKLLRGA	467	9	25	39		9863
POL	PIVAKEIVA	782	9	25	39		9864
POL	YFLKLAGR	851	9	25	39		9865
POL	QLCKLLRGAK	467	10	25	39		9866
POL	LCKLLRGAKA	468	10	25	39		9867
POL	LKAGYVTD	644	10	25	39		9868
POL	IDKAEHEK	757	10	25	39		9869
POL	SDFNLPPVA	776	10	25	39		9870
POL	PSKDLIAEIQK	513	11	25	39		9871
POL	DTINQTELO	663	11	25	39		9872
POL	GIDKAEHEK	756	11	25	39		9873
POL	IDKAEHEKY	757	11	25	39		9874
POL	ASDFNLPPVA	775	11	25	39		9875
POL	SDFNLPPVAK	776	11	25	39		9876
POL	RAKIEELR	388	8	26	41		9877
POL	LCKLLRGA	468	8	26	41		9878
POL	KFLRPIQK	580	8	26	41		9879
POL	NLPIVAK	779	8	26	41		9880
POL	IVAKEIVA	783	8	26	41		9881

Table XVI
HIV-1 gp120 Motif Repeats with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	LCKLLRGAK	468	9	26	41		9882
POL	LTEAVOKIA	560	9	26	41		9883
POL	SSGIRKVLV	745	9	26	41		9884
POL	DFNLPIVVA	777	9	26	41		9885
POL	QLTEAVOKIA	559	10	26	41		9886
POL	VSSGIRKVLV	744	10	26	41		9887
POL	DFNLPPVAK	777	10	26	41		9888
POL	GSNFTSAAVK	870	10	26	41		9889
POL	LVSSGIRKVLV	743	11	26	41		9890
POL	TGOETAYFLL	845	11	26	41		9891
POL	NGSNFTSAAV	869	11	26	41		9892
POL	GSNFTSAAVK	870	11	26	41		9893
POL	KAQEEIEK	759	8	27	43	0.0013	9894
POL	ASQIYAGIK	456	9	27	43		9895
POL	KAQEEIEKY	759	9	27	43		9896
POL	KAQEEIEKYII	759	10	27	43		9897
POL	EICTEMEK	223	8	27	42		9898
POL	EIQHIRAK	383	8	27	42		9899
POL	LVSSGIRK	743	8	27	42		9900
POL	SGIRKVLV	746	8	27	42		9901
POL	NLPPVAK	779	8	27	42	0.0037	9902
POL	ETAYFLLK	848	8	27	42		9903
POL	TSAAVKAA	874	8	27	42		9904
POL	KLVSIGIRK	742	9	27	42	0.0027	9905
POL	TAYFLLKLA	849	9	27	42		9906
POL	FTSAVKAA	873	9	27	42		9907
POL	DLEIGQHRAK	381	10	27	42	0.0052	9908
POL	KLNWASQIYA	452	10	27	42		9909
POL	WASQIYAGIK	455	10	27	42		9910
POL	KVQLCKLLR	464	10	27	42		9911
POL	ETAYFLLKLA	848	10	27	42		9912
POL	NFTSAVKAA	872	10	27	42		9913
POL	EICTEMEKEGK	223	11	27	42		9914
POL	SDLEIGQHRAK	380	11	27	42		9915
POL	VDKLVSSGIRK	740	11	27	42		9916
POL	ASQIYPGIK	456	9	28	44		9917
POL	KDLIAEQK	515	9	28	44		9918
POL	NLKTGYAK	540	9	28	44		9919
POL	DLIAEQK	516	8	28	44		9920
POL	PIVGAETF	625	8	28	44		9921
POL	IVGAETFY	626	8	28	44		9922
POL	GSNFTSAA	870	8	28	44		9923
POL	NFTSAAVK	872	8	28	44		9924
POL	FTSAAVKA	873	8	28	44	0.0002	9925
POL	CTEMEKECK	225	9	28	44		9926
POL	DLEIGQHRA	381	9	28	44		9927
POL	GIKVKQLCK	462	9	28	44		9928
POL	PIVGAETFY	625	9	28	44		9929
POL	QLIKKEKVV	716	9	28	44		9930
POL	PVVAKEIVA	782	9	28	44		9931

Table XVI
HIV-1 gp120 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	NGSNFTSAA	869	9	28	44		9932
POL	NFTSAAVKA	872	9	28	44		9933
POL	ICTEMEKEGK	224	10	28	44		9934
POL	SDLEIGHORA	380	10	28	44		9935
POL	WASQVPGIK	455	10	28	44		9936
POL	AAVKAACWW	876	10	28	44		9937
POL	GSDLEIGHORA	379	11	28	44		9938
POL	VGAETFYVGG	627	11	28	44		9939
POL	TNGSNFTSA	867	11	28	44		9940
POL	SAAVKAACW	875	11	28	44	0.0008	9941
POL	NLTKGYAR	540	9	29	46		9942
POL	KLVSSGIR	742	8	29	45		9943
POL	VIWGTTPKFR	573	10	29	45		9944
POL	VDKLVSSGIR	740	10	29	45		9945
POL	PLTEAELELA	483	11	29	45		9946
POL	IVWGTTPKFR	572	11	29	45		9947
POL	QVDKLVSSGIR	739	11	29	45		9948
POL	WGKTPKFR	575	8	30	47		9949
POL	LTETTNQK	661	8	30	47		9950
POL	IILVAVIIVA	824	9	30	47		9951
POL	AAANRETKLQK	637	10	30	47	0.0007	9952
POL	IEQLIKKEK	713	10	30	47	0.0004	9953
POL	KIILVAVIIVA	823	10	30	47		9954
POL	GAANRETKLG	636	11	30	47		9955
POL	AAANRETKLQK	637	11	30	47		9956
POL	QIEQLIKKEK	712	11	30	47		9957
POL	ILKLAGRWPV	853	11	30	47		9958
POL	VVAKEIVA	783	8	31	48		9959
POL	EGKILVA	821	8	31	48		9960
POL	KIILVAVIH	823	8	31	48		9961
POL	ETAYFILK	848	8	31	48		9962
POL	YFILKLAGR	851	9	31	48		9963
POL	HLEGHILVA	819	10	31	48		9964
POL	EGKILVAVH	821	10	31	48		9965
POL	ETAYFILKLA	848	10	31	48		9966
POL	PSINNETPGIR	322	11	31	48		9967
POL	TGQETAYFILK	845	11	31	48		9968
POL	TAYFILKLAGR	849	11	31	48		9969
POL	FILKLAGR	852	8	32	50		9970
POL	NDVKQLTEA	555	9	32	50		9971
POL	TAYFIUKLA	849	9	32	50		9972
POL	AVKACWVA	877	9	32	50		9973
POL	SINNETPGIR	323	10	32	50		9974
POL	SINNETPGIRY	323	11	32	50		9975
POL	SSMTKILEPFR	351	11	32	50		9976
POL	HTNDVKQLTE	553	11	32	50		9977
POL	HSNWRAMAS	768	11	32	50		9978
POL	QTKELQKQITK	961	11	32	50		9979
POL	DVKQLTEA	556	8	33	52	0.0050	9980
POL	NGSNFTSA	869	8	33	52		9981

Table XVI
HIV A93-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	EMEKECKISK	229	10	33	52	0.0004	9982
POL	SSMTKILEPF	351	10	33	52	0.0004	9983
POL	TDNGSNFTSA	867	10	33	52		9984
POL	QSSMTKILEPF	350	11	33	52		9985
POL	DVKQLTEAVQ	556	11	33	52	0.0048	9986
POL	HTDNGSNFTS	866	11	33	52		9987
POL	YDPSKDLIA	511	9	34	53		9988
POL	DIATDIQTK	954	10	34	53	0.0056	9989
POL	QLKEALLDTG	105	11	34	53		9990
POL	ELQKQITK	964	8	35	56		9991
POL	LIKKEKVV	717	8	35	55		9992
POL	QITKIQNF	968	8	35	55		9993
POL	DSRDPWIK	981	8	35	55		9994
POL	ETKLGRAGY	641	9	35	55	0.0250	9995
POL	IATDIQTK	955	9	35	55	0.0021	9996
POL	QITKIQNF	968	9	35	55		9997
POL	RDSRDPWIK	980	9	35	55		9998
POL	TDIQTKELOK	958	10	35	55	0.0007	9999
POL	RDPWIKGP	983	10	35	55		10000
POL	ATDIQTELOK	957	11	35	55	0.0051	10001
POL	QITKIQNFVY	981	11	35	55		10002
POL	DSRDPWIKGP	981	11	35	55		10003
POL	SDIKVVPKKA	1008	11	35	55		10004
POL	ITKIQNF	969	8	36	57	0.0016	10005
POL	ITKIQNFVY	969	10	36	57		10006
POL	ITKIQNFVY	956	11	36	57		10007
POL	IATDIQTK	985	8	36	56		10008
POL	PIWKGPAK	985	8	36	56		10009
POL	NLPKWPK	124	9	36	56	1.1000	10010
POL	AIQSSMTK	347	9	36	56	0.0760	10011
POL	PAIQSSMTK	346	10	36	56		10012
POL	LTEAELELA	484	10	36	56		10013
POL	VFAIKKKDSTK	249	11	36	56		10014
POL	NTPVFAIK	246	8	37	58	0.0003	10015
POL	PVFAIKKK	248	8	37	58	0.0003	10016
POL	QLTEAVQK	559	8	37	58		10017
POL	QIEQLIK	712	8	37	58		10018
POL	IEQLIK	713	8	37	58		10019
POL	YLSWVPAH	724	8	37	58		10020
POL	LSWVPAIK	725	8	37	58		10021
POL	NTPVFAIK	246	9	37	58	0.0330	10022
POL	QIEQLIK	712	9	37	58	0.0091	10023
POL	YLSWVPAIK	724	9	37	58		10024
POL	RDPWIKGPA	983	9	37	58		10025
POL	VIQDNDIK	1003	9	37	58	0.0009	10026
POL	NTPVFAIKK	246	10	37	58	0.0006	10027
POL	VVIQDNDIK	1002	10	37	58	0.0005	10028
POL	AVVIQDNDIK	1000	11	37	58	0.0004	10029
POL	IFQSSMTK	348	8	38	59	0.0055	10030
POL	ILKEPVHGVY	498	11	38	59		10031

Table XVI
HIV-A03 Monopeptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	LDGDKAQEEH	754	11	39	62		10032
POL	HSNWRAMA	768	8	39	61		10033
POL	AGYVTDGR	647	9	39	61	0.0011	10034
POL	YVTDGRGK	649	9	39	61		10035
POL	KAGYVTDGR	646	10	39	61	0.0007	10036
POL	LGIIQAQPDK	695	10	39	61		10037
POL	DGIDKAQEEH	755	10	39	61		10038
POL	DIKVVPRKA	1009	10	39	61		10039
POL	PVHGYYDPS	505	11	39	61		10040
POL	AGYVTDGRQ	647	11	39	61		10041
POL	ALGIQAQPDK	694	11	39	61		10042
POL	DIKVVPRKAK	1009	11	39	61	0.0090	10043
POL	VTDRGRQK	650	8	40	63		10044
POL	IIQAQPDK	697	8	40	63	0.0009	10045
POL	GIQAQPDK	696	9	40	63		10046
POL	GIDKAQEEH	756	9	40	63		10047
POL	NSDIKVVPR	1007	9	40	63		10048
POL	ILKEPVHGVY	498	10	40	63	0.0007	10049
POL	NSDIKVVPRR	1007	10	40	63		10050
POL	EILKEPVHGVY	497	11	40	63		10051
POL	WTYQIYQEPF	529	11	40	63	0.9200	10052
POL	QIYQEPKLNK	532	11	40	63	0.2800	10053
POL	SAGERIIDIA	947	11	40	63		10054
POL	QDNSDIKVVPR	1005	11	40	63		10055
POL	NSDIKVVPRRK	1007	11	40	63		10056
POL	ESIVIWGKTPK	570	11	41	65		10057
POL	FFRENLA	1	8	41	64		10058
POL	QIGCTLNF	179	8	41	64	0.0010	10059
POL	QIYQEPK	532	8	41	64		10060
POL	IDKAQEEH	757	8	41	64		10061
POL	KAKIIRDY	1017	8	41	64	0.0081	10062
POL	LTIQIGCTLNF	177	10	41	64		10063
POL	AGERIIDIA	948	10	41	64	0.0048	10064
POL	KAKIIRDY'GK	1017	10	41	64		10065
POL	KISKIGPENPY	235	11	41	64		10066
POL	SIVIWGKTPKF	571	11	41	64		10067
POL	DFRKYTAF	312	8	42	66		10068
POL	KAGYVTD	646	8	42	66		10069
POL	ISKIGPENPY	236	10	42	66		10070
POL	SMTKILEPFR	352	10	42	66	0.0004	10071
POL	WTYQIYQEPF	529	10	42	66		10072
POL	SIVIWGKTPK	571	10	42	66		10073
POL	TTNQKTELQA	664	10	42	66	0.0004	10074
POL	IVIYQYMDLLY	367	11	42	66		10075
POL	VVPRKAKIIR	1012	11	42	66		10076
POL	GVYYDPSK	508	8	43	67		10077
POL	SCDKCQLK	791	8	43	67	0.0004	10078
POL	SMTKILEPFR	352	9	43	67	0.0008	10079
POL	MTKILEPFR	353	9	43	67	0.0004	10080
POL	HGVYYDPSK	507	9	43	67		10081

Table XVI
 HIV-XO3 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	ASCDKCOLK	790	9	43	67	0.0027	10082
POL	DSWTVDIQK	439	10	43	67	0.0007	10083
POL	TFYVDGAANR	631	10	43	67	0.0003	10084
POL	VASCDKCOLK	789	10	43	67	0.0004	10085
POL	KIIGQVRDQA	912	10	43	67		10086
POL	KDSWTVDIQ	438	11	43	67		10087
POL	ETFYVDGAAN	630	11	43	67		10088
POL	IVASCDKCOLK	788	11	43	67		10089
POL	SCDKCOLKGE	791	11	43	67	0.0970	10090
POL	MTKILEPF	353	8	44	69		10091
POL	IGQVRDQA	914	8	44	69		10092
POL	SDIKVVPR	1008	8	44	69		10093
POL	MAGDDCA	1028	8	44	69		10094
POL	IGQVRDQA	913	9	44	69		10095
POL	SDIKVVPRR	1008	9	44	69	0.0002	10096
POL	QMA GDCA	1027	9	44	69	0.0003	10097
POL	VDGAANRETK	634	10	44	69		10098
POL	IGQVRDQA	914	10	44	69		10099
POL	QVRDQA	916	10	44	69	0.0089	10100
POL	SDIKVVPRR	1008	10	44	69	0.0004	10101
POL	PFKNLTKGY	537	11	44	69		10102
POL	GAETFYVDGA	628	11	44	69		10103
POL	YVDGAANRET	633	11	44	69		10104
POL	IGQVRDQA	913	11	44	69		10105
POL	VAKIVASCDK	784	11	45	70		10106
POL	GAANRETK	636	8	45	70		10107
POL	EIVASCDK	787	8	45	70	0.0004	10108
POL	DGAANRETK	635	9	45	70		10109
POL	PFKNLTKGY	537	10	45	70		10110
POL	RDQA	918	10	45	70		10111
POL	PLV KLWYQLE	613	11	45	70		10112
POL	EILKEPVH	497	8	46	72		10113
POL	KLWYQLEK	616	8	46	72		10114
POL	RDQA	918	8	46	72		10115
POL	PFKNLTKG	537	9	46	72		10116
POL	DIOTKELOK	959	10	46	72	0.0009	10117
POL	LVKLWYQLEK	614	10	46	72	0.0560	10118
POL	KVKQWPLTEE	207	11	46	72	0.0750	10119
POL	VIWGTPTKF	573	9	47	73		10120
POL	VIWGTPTKF	572	10	47	73		10121
POL	VIWGTPTK	573	8	48	75		10122
POL	QVRDQA	916	8	48	75		10123
POL	DIKVVPRR	1009	8	48	75	0.0850	10124
POL	VIWGTPTK	572	9	48	75	0.0002	10125
POL	DIKVVPRR	1009	9	48	75		10126
POL	GAETFYVDGA	628	10	48	75	0.3600	10127
POL	KVFLDGDK	750	10	48	75		10128
POL	CDKCOLKGEA	792	10	48	75		10129
POL	KCOLKGEAMH	794	10	48	75		10130
POL	VVESMNKELK	902	10	48	75		10131

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	KVFLDGDIDKA	750	11	48	75		10132
POL	GVVESMINKEL	901	11	48	75		10133
POL	VVESMINKELK	902	11	48	75		10134
POL	GVVESMINK	901	8	49	77		10135
POL	RDYGRQMA	1022	8	49	77		10136
POL	QGVVESMINK	900	9	49	77	0.3900	10137
POL	KLKPGMDGPK	197	10	49	77		10138
POL	IIRDYGRQMA	1020	10	49	77		10139
POL	QSQGVVESMN	898	11	49	77		10140
POL	KIIRDYGRQMA	1019	11	49	77		10141
POL	ESIVIWGK	570	8	50	79		10142
POL	YVDGAANR	633	8	50	78	0.0003	10143
POL	LAGRWPK	856	8	50	78		10144
POL	KIIRDYGR	1019	8	50	78	2.7000	10145
POL	KLAGRWPVK	855	9	50	78	0.0007	10146
POL	GMDGPKVK	201	8	51	80		10147
POL	KIGPENPY	238	8	51	80		10148
POL	FTTPDKKH	403	8	51	80		10149
POL	TFYVDGAA	631	8	51	80		10150
POL	HTDNGSNF	866	8	51	80	0.0004	10151
POL	PGMDGPKVK	200	9	51	80		10152
POL	GFTTPDKKH	402	9	51	80		10153
POL	ETFYVDGAA	630	9	51	80		10154
POL	VFLDGDIDK	751	9	51	80	0.0380	10155
POL	VYQYMDLDY	368	10	51	80	0.0007	10156
POL	WGFTTPDKKH	401	10	51	80		10157
POL	FTTPDKKHQK	403	10	51	80	0.0002	10158
POL	VFLDGDIDKA	751	10	51	80	0.0004	10159
POL	KSVTVLDVGD	293	11	51	80		10160
POL	GFTTPDKKHQ	402	11	51	80	0.0004	10161
POL	QATWIPEWEF	599	10	52	83		10162
POL	PAGLKKKK	286	8	52	81		10163
POL	SDLEIGQH	380	8	52	81		10164
POL	DLEIGQHR	381	8	52	81		10165
POL	WGFTTPDK	401	8	52	81		10166
POL	GFTTPDKK	402	8	52	81		10167
POL	KCOLKGEA	794	8	52	81		10168
POL	VASGYIEA	831	8	52	81		10169
POL	KIQNFRVY	971	8	52	81		10170
POL	KVPRRKA	1011	8	52	81		10171
POL	VVPRRKA	1012	8	52	81	0.0027	10172
POL	ETPGIRYQY	327	9	52	81		10173
POL	GSDLEIGQH	379	9	52	81	0.0003	10174
POL	SDLEIGQHR	380	9	52	81	0.0004	10175
POL	WGFTTPDKK	401	9	52	81		10176
POL	ATWIPEWEF	600	9	52	81		10177
POL	HVASGYIEA	830	9	52	81	0.0003	10178
POL	KIQNFRVY	971	9	52	81	0.1200	10179
POL	KVPRRKA	1011	9	52	81	0.0290	10180
POL	VGSDLEIGQH	378	10	52	81		10181

Table XVI
HIV X03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	GSDLEIGQHR	379	10	52	81		10182
POL	KIQNFRVYYR	971	10	52	81	0.0320	10183
POL	NFRVYYRDSR	974	10	52	81		10184
POL	IGGIGGFIKVR	134	11	52	81		10185
POL	VGPTPVNIIGR	164	11	52	81		10186
POL	YVGSDEIGQHI	377	11	52	81		10187
POL	VGSDEIGQHR	378	11	52	81		10188
POL	AVIIVASGYIEA	828	11	52	81		10189
POL	SGYIEAEVIPA	833	11	52	81		10190
POL	GIPHPAGLKKK	282	11	53	84		10191
POL	IGGFIKVR	137	8	53	83		10192
POL	GFIKVRQY	139	8	53	83		10193
POL	PIETVPVK	190	8	53	83	0.0049	10194
POL	ETVPVKLK	192	8	53	83		10195
POL	ELEAENR	489	8	53	83		10196
POL	QLKGEAMHI	796	8	53	83		10197
POL	ESMNKELK	904	8	53	83		10198
POL	SMNKELK	905	8	53	83		10199
POL	GIGGFIKVR	136	9	53	83	0.0008	10200
POL	GFIKVRQY	138	9	53	83	0.0004	10201
POL	YIEAEVIPA	835	9	53	83	0.0003	10202
POL	ESMNKELK	904	9	53	83	0.0004	10203
POL	GGIGGFIKVR	135	10	53	83	0.0004	10204
POL	IGGFIKVRQY	137	10	53	83	0.0004	10205
POL	ISPIETVPVK	188	10	53	83	0.0003	10206
POL	PIETVPVKLK	190	10	53	83	0.0002	10207
POL	EAELEAENR	487	10	53	83		10208
POL	LVAVHVASGY	826	10	53	83		10209
POL	GIGGFIKVRQY	136	11	53	83		10210
POL	PIETVPVK	187	11	53	83		10211
POL	ILVAVHVASGY	825	11	53	83		10212
POL	FVNTPLVK	608	9	54	86	0.0120	10213
POL	GIPHPAGLKK	282	10	54	86	0.0110	10214
POL	LGIPHPAGLKK	281	11	54	86		10215
POL	ILVAVIIVA	825	8	54	84		10216
POL	PTPVNIIGR	166	9	54	84	0.0008	10217
POL	PLTEEKIKA	212	9	54	84		10218
POL	LAENREILK	492	9	54	84	0.0002	10219
POL	EVOLGIPHPA	278	10	54	84		10220
POL	ELAENREILK	491	10	54	84		10221
POL	EFVNTPLVK	607	10	54	84	0.0002	10222
POL	PLTEEKIK	212	8	55	86		10223
POL	ETFYVDGA	630	8	55	86		10224
POL	LFLDGIDK	752	8	55	86		10225
POL	FLDGIDKA	753	8	55	86		10226
POL	LFLDGIDKA	752	9	55	86		10227
POL	QLGIPHPA	280	8	56	89		10228
POL	GIPHPAGLK	282	9	56	89	0.2300	10229
POL	KGIGGYSYA	940	9	56	89		10230
POL	LGIPHPAGLK	281	10	56	89	0.0370	10231

Table XVI
HIV X03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	QLGIPIAGLK	280	11	56	89		10232
POL	LTEEKIA	213	8	56	88		10233
POL	VTVLDVGDAY	295	10	56	88	0.0001	10234
POL	ELKKIIGQVR	909	10	56	88		10235
POL	DFWEVOLGIPHI	275	11	56	88		10236
POL	SVTVLDVGDA	294	11	56	88		10237
POL	VTVLDVGDAY	295	11	56	88		10238
POL	PAETGQETAY	842	11	56	88		10239
POL	KTAVQMAVFI	925	11	56	88		10240
POL	TGQETAYF	845	8	57	89	0.0017	10241
POL	AIKKKDKTK	251	9	57	89		10242
POL	ELNKRITQDF	268	9	57	89		10243
POL	VTVLDVGDA	295	9	57	89		10244
POL	TVLDVGDAY	296	9	57	89	0.0002	10245
POL	TPDKKIIQK	404	9	57	89	0.0002	10246
POL	ETGQETAYF	844	9	57	89		10247
POL	HLKTAVQMA	923	9	57	89	0.0003	10248
POL	KTAVQMAVF	925	9	57	89	0.0003	10249
POL	FAIKKDKSTK	250	10	57	89	0.0004	10250
POL	SVTVLDVGDA	294	10	57	89		10251
POL	TVLDVGDAYF	296	10	57	89	0.0004	10252
POL	NTPLVLKLY	610	10	57	89	0.0002	10253
POL	AIKKKDKTKW	251	11	57	89		10254
POL	HLKTAVQMAV	923	11	57	89		10255
POL	MAVFIHFKR	930	11	57	89		10256
POL	GGIGYSAGER	941	11	57	89		10257
POL	NLKTGKYA	540	8	58	92		10258
POL	VLPQGWKQSP	337	11	58	92		10259
POL	KDSTKWRK	255	8	58	91		10260
POL	EVQLGIPHI	278	8	58	91		10261
POL	TVLDVGDA	296	8	58	91		10262
POL	YALGIQA	693	8	58	91		10263
POL	GGNEQVDK	735	8	58	91		10264
POL	FIHFKRK	933	8	58	91		10265
POL	GGYSAGER	944	8	58	91		10266
POL	RVYRDSR	976	8	58	91	0.0004	10267
POL	IGNEQVDK	734	9	58	91		10268
POL	PAETGQETA	842	9	58	91		10269
POL	VFIHFKRK	932	9	58	91	0.0004	10270
POL	IGYSAGER	943	9	58	91	0.0003	10271
POL	STKWRKLVDF	257	10	58	91	0.0005	10272
POL	GIGNEQVDK	733	10	58	91		10273
POL	PAETGQETAY	842	10	58	91	0.6600	10274
POL	AVFIHFKRK	931	10	58	91	0.0003	10275
POL	GIGYSAGER	942	10	58	91		10276
POL	DSTKWRKLVDF	256	11	58	91		10277
POL	STKWRKLVDF	257	11	58	91		10278
POL	DSQYALGIQA	690	11	58	91		10279
POL	KGIGNEQVDK	732	11	58	91		10280
POL	VIPAETGQETA	840	11	58	91		10281

Table XVI
HIV-1 A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	QGWKGSFA	340	8	59	92		10282
POL	AVHVASGY	828	8	59	92		10283
POL	ETQETAY	844	8	59	92		10284
POL	QAEHLKTA	920	8	59	92		10285
POL	GGIGGYS	941	8	59	92		10286
POL	GIWQDCTH	811	9	59	92		10287
POL	VAVHVASGY	827	9	59	92		10288
POL	KGPAKLLWK	988	9	59	92	0.0004	10289
POL	QGWKGSFAIF	340	9	59	92	0.0021	10290
POL	EVNIVTDSQY	684	10	59	92	0.0004	10291
POL	PGIWQLDCTH	810	10	59	92		10292
POL	TAVQMAVFIH	926	10	59	92	0.0004	10293
POL	VGKLNWASQI	450	11	59	92		10294
POL	EVNIVTDSQYA	684	11	59	92		10295
POL	NFKRKGIGGY	936	11	59	92		10296
POL	PAKLLWKGGEG	990	11	59	92		10297
POL	QLDCTHLECK	814	10	60	95	0.0010	10298
POL	DFRELNR	265	8	60	94		10299
POL	VLDVGDAY	297	8	60	94		10300
POL	MAVFIHNF	930	8	60	94		10301
POL	VDFRELNR	264	9	60	94		10302
POL	VLDVGDAYF	297	9	60	94		10303
POL	MGYELHPDK	419	9	60	94	0.0640	10304
POL	KLWASQIY	452	9	60	94	0.1200	10305
POL	AVQMAVFIH	927	9	60	94		10306
POL	QMAVFIHNF	929	9	60	94	0.0010	10307
POL	MAVFIHNF	930	9	60	94	0.0170	10308
POL	KLLWKGEA	992	9	60	94	0.0003	10309
POL	LVDFRELNR	263	10	60	94	0.0005	10310
POL	WMGYELHPDK	418	10	60	94	0.6100	10311
POL	QMAVFIHNF	929	10	60	94	0.0068	10312
POL	MAVFIHNF	930	10	60	94		10313
POL	KLVDRELNR	262	11	60	94		10314
POL	PDKKHQKEPPF	406	11	60	94		10315
POL	AVQMAVFIH	927	11	60	94		10316
POL	QMAVFIHNF	929	11	60	94		10317
POL	EALLDTGA	108	8	61	95		10318
POL	LDVGDAYF	298	8	61	95		10319
POL	LVGKLNWA	449	8	61	95		10320
POL	IVTDSQYA	687	8	61	95		10321
POL	TAVQMAVF	926	8	61	95		10322
POL	NDIQLVKG	444	9	61	95	0.0003	10323
POL	KLVGKLNWA	448	9	61	95		10324
POL	NIVTDSQYA	686	9	61	95		10325
POL	LDCIHLECK	815	9	61	95		10326
POL	TVNDIQLVKG	442	11	61	95	0.0400	10327
POL	MIGGIGF	133	8	62	97		10328
POL	VDFRELNR	264	8	62	97		10329
POL	WTVNDIQL	441	8	62	97	0.0003	10330
POL	DIQLVKG	445	8	62	97		10331

Table XVI
HIV-1 CR1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
POL	NIVTDSQY	686	8	62	97		10332
POL	DCTHLEGG	816	8	62	97		10333
POL	AVEHNFK	931	8	62	97	0.0280	10334
POL	VFIHNFK	932	8	62	97		10335
POL	LLWKGEGA	993	8	62	97		10336
POL	KMIGGIGGF	132	9	62	97	0.0004	10337
POL	LVDRELNK	263	9	62	97	0.0110	10338
POL	AVEHNFK	931	9	62	97	0.1700	10339
POL	MIGGIGGF	133	10	62	97	0.0099	10340
POL	KLVDFELNK	262	10	62	97	0.5100	10341
POL	KMIGGIGGF	132	11	62	97	2.3000	10342
POL	NVLPGGWK	336	8	63	100	0.0003	10343
POL	IGGIGGF	134	9	63	98	0.0004	10344
POL	GGIGGF	135	8	64	100		10345
POL	FLWMGYELH	416	9	64	100		10346
POL	PFLWMGYELH	415	10	64	100		10347
REV	GTRQTRKNR	37	9	01	50		10348
REV	TTRQARRNR	37	9	01	50		10349
REV	GTRQTRKNR	37	10	01	50		10350
REV	TTRQARRNR	37	10	01	50		10351
REV	GTRQTRKNR	37	11	01	50		10352
REV	TTRQARRNR	37	11	01	50		10353
REV	GTRQARRNR	103	8	06	19		10354
REV	GTETGVGR	102	9	06	19		10355
REV	OGTETGVGR	12	9	10	16		10356
REV	LLKTURLK	6	9	11	17		10357
REV	GDSDELLK	76	9	11	17		10358
REV	PLQLPIER	5	10	11	17		10359
REV	SGDSDELLK	4	11	11	17		10360
REV	RSGDSDELLK	74	11	11	17		10361
REV	PVPLQLPIER	50	8	12	19		10362
REV	RARQRIH	7	8	12	19		10363
REV	DSDELLK	63	8	12	19		10364
REV	ILSTCLGR	62	9	12	19		10365
REV	RILSTCLGR	17	9	13	20		10366
REV	AVRIKILY	31	9	13	20		10367
REV	PSPEGTROA	78	9	13	20		10368
REV	QLPLERLH	31	10	13	20		10369
REV	PSPEGTROAR	31	11	13	20		10370
REV	PSPEGTROAR	76	11	13	20		10371
REV	PLQLPLERLH	36	11	14	22		10372
REV	GTRQARKNRR	50	8	15	24		10373
REV	RARQRIH	36	9	15	23		10374
REV	GTRQARKNR	36	10	15	23		10375
REV	GTRQARKNRR	40	9	16	25		10376
REV	QARKNRRR	40	11	16	25		10377
REV	QARKNRRR	40	8	17	27		10378
REV	QARKNRRR	20	11	18	28		10379
REV	IKILYQSNPY	22	9	26	41		10380
REV	KILYQSNPY	23	8	27	42		10381
REV	ILYQSNPY						

Table XVI
HIV A03 Model Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
REV	EGTROARR	35	8	27	42		10382
REV	EGTROARRNR	35	10	27	42		10383
REV	EGTROARRNR	35	11	27	42		10384
REV	GTRQARRNR	36	9	34	53		10385
REV	GTRQARRNR	36	10	34	53		10386
REV	GTRQARRNR	36	11	34	53		10387
REV	PVQLPPLER	74	11	34	53		10388
REV	PLQLPPLER	76	9	35	55		10389
REV	QARRNR	40	11	37	58		10390
REV	QARRNR	40	8	38	59		10391
REV	QARRNR	40	9	38	59		10392
TAT	PGGYPRK	104	8	01	50		10393
TAT	AGPGGYPR	102	9	01	50		10394
TAT	TGPSQPC	102	10	01	50		10395
TAT	ETGPSQPC	101	10	01	50		10396
TAT	KAGPGGYPR	101	10	01	50		10397
TAT	AGPGGYPRK	102	11	01	50		10398
TAT	KAGPGGYPR	101	11	01	50		10399
TAT	GGYPRK	105	11	01	50		10400
TAT	PGSQPRTA	17	8	10	16		10401
TAT	ACTNCYCK	24	8	10	16		10402
TAT	TACTNCYCK	23	9	10	16		10403
TAT	YCKKCCFH	29	8	11	17		10404
TAT	YCKKCCYH	29	8	11	17		10405
TAT	CFHCQVCF	34	8	11	17		10406
TAT	VDPRLEPWK	4	9	11	17		10407
TAT	ACNNCYCK	24	9	11	17		10408
TAT	CFHCQVCF	33	9	11	17		10409
TAT	PVDRLEPWK	3	10	11	17	0.0005	10410
TAT	VDPRLEPWKH	4	10	11	17		10411
TAT	TACNNCYCK	23	10	11	17		10412
TAT	PVDRLEPWK	3	11	11	17		10413
TAT	RGDPTGPKES	84	11	11	17		10414
TAT	GDPTGPKES	85	11	11	17		10415
TAT	ESKKKVESK	93	9	12	19		10416
TAT	GDPTGPKES	85	10	12	19		10417
TAT	PTGPKESKK	88	10	12	19		10418
TAT	TGPKESKK	89	9	13	20		10419
TAT	FLNKGGLISY	41	10	14	22		10420
TAT	PVDNLEPWN	3	11	14	22		10421
TAT	CFLNKGGLISY	40	11	14	22		10422
TAT	RGDPTGPK	84	8	16	25		10423
TAT	VDPNLEPWNH	4	10	16	25		10424
TAT	ACNNCYCK	24	8	17	27		10425
TAT	TACNNCYCK	23	9	17	27		10426
TAT	PTGPKESKK	88	9	18	28		10427
TAT	TGPKESKK	89	8	19	30		10428
TAT	PTGPKESK	88	8	20	31		10429
TAT	YGRKKRRQR	50	11	22	34		10430
TAT	PGSQPKTA	17	8	26	41		10431

Table XVI
HIV-1 A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
TAT	YGRKKRRQR	50	10	38	59		10432
TAT	ISYGRKKRRQR	48	11	39	61		10433
TAT	YGRKKRRQR	50	9	41	64		10434
TAT	GISYGRKKRR	47	10	45	70	0.0003	10435
TAT	LGISYGRKKRR	46	11	45	70		10436
TAT	ISYGRKKRR	48	9	46	72	0.0008	10437
TAT	GLGISYGRKKR	45	11	54	86		10438
TAT	GLGISYGR	45	8	55	87		10439
TAT	GLGISYGRK	45	9	55	87	0.0340	10440
TAT	GLGISYGRKK	45	10	55	87		10441
TAT	KGLGISYGR	44	9	55	86	0.0006	10442
TAT	KGLGISYGRK	44	10	55	86	0.0100	10443
TAT	KGLGISYGRKK	44	11	55	86		10444
TAT	GISYGRKKR	47	9	57	89	0.0008	10445
TAT	LGISYGRKKR	46	10	57	89		10446
TAT	LGISYGRK	46	8	58	91		10447
TAT	GISYGRKK	47	8	58	91		10448
TAT	ISYGRKKR	48	8	58	91		10449
TAT	LGISYGRKK	46	9	58	91	0.0004	10450
VIF	LIVWQVDR	8	8	10	16		10451
VIF	RMINTWK	15	8	10	16		10452
VIF	LKPKKIK	158	8	10	16		10453
VIF	KGWFYRIIHY	36	9	10	16		10454
VIF	ALIKPKKIK	157	9	10	16		10455
VIF	VDRMRINTWK	13	10	10	16		10456
VIF	GVSEWRLLR	87	10	10	16		10457
VIF	QVDRMRINTW	12	11	10	16		10458
VIF	RLVITYWGL	65	11	10	16		10459
VIF	QTGERDWILG	75	11	10	16		10460
VIF	GVSEWRLLR	87	11	10	16		10461
VIF	IDPDLADQLIH	103	11	10	16		10462
VIF	LVEDRWKPKQ	178	11	10	16		10463
VIF	YSTQIDPLA	99	10	11	17		10464
VIF	YSTQIDPGLA	99	10	11	17		10465
VIF	SIEWRLRR	89	8	11	17		10466
VIF	TALIKPKK	156	8	11	17		10467
VIF	LVEDRWK	178	8	11	17		10468
VIF	VSIEWRLRR	88	9	11	17		10469
VIF	SIEWRLRRY	89	9	11	17		10470
VIF	STQVDIPLA	100	9	11	17		10471
VIF	SLQYLAKA	149	9	11	17		10472
VIF	LTALIKPKK	155	9	11	17		10473
VIF	KLVEDRWK	177	9	11	17		10474
VIF	VSIEWRLRRY	88	10	11	17		10475
VIF	GLADQLIHMH	106	10	11	17		10476
VIF	IVSPRCEYQA	133	10	11	17		10477
VIF	GSQYLAKA	148	10	11	17		10478
VIF	ALTALIKPKK	154	10	11	17		10479
VIF	PGLADQLIHMH	105	11	11	17		10480
VIF	GLADQLIHMH	106	11	11	17		10481

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
VIF	VGSLQYLALK	147	11	11	17		10482
VIF	LALTALIKPKK	153	11	11	17		10483
VIF	WYRIHHYESR	38	11	12	19		10484
VIF	KGWFYRIHH	36	8	12	19		10485
VIF	WGLOTGER	72	8	12	19		10486
VIF	QTGERDWH	75	8	12	19		10487
VIF	SDSAIRKA	121	8	12	19		10488
VIF	SLQYLALA	149	8	12	19		10489
VIF	IVWQVDRMK	9	9	12	19		10490
VIF	STQIDPDLA	100	9	12	19		10491
VIF	FSDSAIRKA	120	9	12	19		10492
VIF	FSES AIRNA	120	9	12	19		10493
VIF	GSQYLALA	148	9	12	19		10494
VIF	SLQYLALAA	149	9	12	19		10495
VIF	KIRTWNSLVK	17	10	12	19		10496
VIF	LVKHHIMYVSK	24	10	12	19		10497
VIF	GLQTGERDWII	73	10	12	19		10498
VIF	TGERDWIILGHI	77	10	12	19		10499
VIF	HGVSEWRRLR	86	10	12	19		10500
VIF	CFSDSAIRKA	119	10	12	19		10501
VIF	CFSES AIRNA	119	10	12	19		10502
VIF	VGSLQYLALA	147	10	12	19		10503
VIF	GSQYLALALAA	148	10	12	19		10504
VIF	IVWQVDRMKI	9	11	12	19		10505
VIF	KIRTWNSLVK	17	11	12	19		10506
VIF	SLVKHHIMYVS	23	11	12	19		10507
VIF	LVKHHIMYVSK	24	11	12	19		10508
VIF	WGLQTGERD	72	11	12	19		10509
VIF	DCFESAIRKA	118	11	12	19		10510
VIF	DCFES AIRNA	118	11	12	19		10511
VIF	KVGSQYLAL	146	11	12	19		10512
VIF	VGSLQYLALA	147	11	12	19		10513
VIF	WYRIHHYESR	38	10	13	21		10514
VIF	QVDRMKIR	12	8	13	20		10515
VIF	IMYVSKKA	28	8	13	20		10516
VIF	HIPLGDAR	56	8	13	20		10517
VIF	ADQLIHMH	108	8	13	20		10518
VIF	CFSDSAIR	119	8	13	20		10519
VIF	FSDSAIRK	120	8	13	20		10520
VIF	SLQYLALK	149	8	13	20		10521
VIF	LTALIKPK	155	8	13	20		10522
VIF	LADQLIHMH	107	9	13	20		10523
VIF	ADQLIHMHY	108	9	13	20		10524
VIF	CFSDSAIRK	119	9	13	20		10525
VIF	FSES AIRKA	120	9	13	20		10526
VIF	GSLOYLALK	148	9	13	20		10527
VIF	ALTALIKPK	154	9	13	20		10528
VIF	SVKKLTEDR	174	9	13	20		10529
VIF	EVHPLGDAR	54	10	13	20		10530
VIF	LADQLIHMHY	107	10	13	20		10531

Table XVI
HIV-1 A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
VIF	ADQLHMHYF	108	10	13	20		10532
VIF	DCFSAIRK	118	10	13	20		10533
VIF	CFSESARK	119	10	13	20		10534
VIF	VGSLOYLALK	147	10	13	20		10535
VIF	LALTALIKPK	153	10	13	20		10536
VIF	PSVKKLTEDR	173	10	13	20		10537
VIF	LADQLHMHYF	107	11	13	20		10538
VIF	QLIHLYYFDCF	110	11	13	20		10539
VIF	FDCFSAIRK	117	11	13	20		10540
VIF	YLALTALIKPK	152	11	13	20		10541
VIF	QLIHLYYF	110	8	14	22		10542
VIF	QLIHMHYF	110	8	14	22		10543
VIF	FSESARK	120	8	14	22		10544
VIF	IVSPREY	133	8	14	22		10545
VIF	GVSEWRRLR	87	9	14	22		10546
VIF	ADQLIHLYY	108	9	14	22		10547
VIF	CFSESARK	108	9	14	22		10548
VIF	VDRMRRTWK	119	9	14	22		10549
VIF	LADQLIHLYY	13	10	14	22		10550
VIF	ADQLIHLYYF	107	10	14	22		10551
VIF	RCDYQAGHNK	137	10	14	22		10552
VIF	QVDRMRRTW	12	11	14	22		10553
VIF	RRTWNSLVK	17	11	14	22		10554
VIF	LADQLIHLYYF	107	11	14	22		10555
VIF	QLIHMHYFDCF	110	11	14	22		10556
VIF	RMRTWK	15	8	15	23		10557
VIF	RTWKS LVK	19	8	15	23		10558
VIF	VSIEWRLR	88	8	15	23		10559
VIF	ADQLIHLY	108	8	15	23		10560
VIF	HMIIYFDCF	113	8	15	23		10561
VIF	RTWKS LVKH	19	9	15	23		10562
VIF	QGVSEWRK	86	9	15	23		10563
VIF	LADQLIHLY	107	9	15	23		10564
VIF	AIRKAILGH	124	9	15	23		10565
VIF	CDYQAGHNK	138	9	15	23		10566
VIF	RRTWKS LVK	17	10	15	23		10567
VIF	RRTWKS LVK	17	10	15	23		10568
VIF	RTWKS LVKHH	19	10	15	23		10569
VIF	LIIMHLYFDCF	111	10	15	23		10570
VIF	SAIRKAILGH	123	10	15	23		10571
VIF	RRTWKS LVK	17	11	15	23		10572
VIF	LQGVSEWR	84	11	15	23		10573
VIF	VDPGLADQLIH	103	11	15	23		10574
VIF	ITTYWGLH	68	8	16	25		10575
VIF	GVSEWRK	87	8	16	25		10576
VIF	HLIYFDCF	113	8	16	25		10577
VIF	RCDYQAGH	137	8	16	25		10578
VIF	LALTALIK	153	8	16	25		10579
VIF	VITTYWGLH	67	9	16	25		10580
VIF	YLALTALIK	152	9	16	25		10581

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
VIF	KTKGHRGSH	188	9	16	25	0.0004	10582
VIF	LVITYWGLH	66	10	16	25		10583
VIF	LHLYYDFCF	111	10	16	25		10584
VIF	EDRWKPKQIT	180	11	17	27		10585
VIF	KSLVKHHMY	22	9	18	28		10586
VIF	EDRWKPKQIT	180	11	18	28		10587
VIF	RCEYOAGHINK	137	10	19	30		10588
VIF	HIPLGEAR	56	8	20	31		10589
VIF	EVHPLGEAR	54	10	20	31		10590
VIF	HTGERDWH	75	8	21	33		10591
VIF	DLADQLIH	106	8	21	33		10592
VIF	PDLADQLIH	105	9	21	33		10593
VIF	VSPRCEYQA	134	9	21	33		10594
VIF	GLHTGERDWH	73	10	21	33		10595
VIF	WGLITGERD	72	11	21	33		10596
VIF	VSPRCEYQAG	134	11	21	33		10597
VIF	LTEDRWKPKQ	178	11	21	33		10598
VIF	GSHTMNGH	194	8	22	34	0.0390	10599
VIF	RGSHMTMNGH	193	9	22	34		10600
VIF	TTYWGLTGE	69	11	22	34		10601
VIF	HLGHGVSEW	83	11	22	34		10602
VIF	SSEVHIPLGDA	52	11	23	36		10603
VIF	NSLVKHHMY	22	9	24	38		10604
VIF	EVHPLGDA	54	9	24	38		10605
VIF	QGVSEWR	86	8	25	39		10606
VIF	EVHPLGEA	54	9	25	39		10607
VIF	LGQGVSEWR	84	10	25	39		10608
VIF	SSEVHIPLGEA	52	11	25	39		10609
VIF	HLQGVSEW	83	11	25	39		10610
VIF	RCEYOAGH	137	8	26	41		10611
VIF	RTWNSLVKH	19	9	26	41		10612
VIF	RTWNSLVKHH	19	10	26	41		10613
VIF	RTWNSLVK	19	8	27	42		10614
VIF	HGVSEWR	86	8	27	42		10615
VIF	GLADQLIH	106	8	27	42		10616
VIF	PGLADQLIH	105	9	27	42		10617
VIF	LGHGVSEWR	84	10	27	42		10618
VIF	YDFCFESAIR	116	11	27	42		10619
VIF	WGLHTGER	72	8	28	44		10620
VIF	YDFCFESA	116	9	28	44		10621
VIF	DCFSESAIR	118	9	28	44		10622
VIF	DCFSESAIR	117	10	28	44		10623
VIF	DCFSESA	117	8	29	45		10624
VIF	CFSESAR	119	8	29	45		10625
VIF	KLTEDRWNK	177	9	29	45	0.0130	10626
VIF	VGSLQYLALT	147	11	30	47		10627
VIF	LTEDRWNK	178	8	31	48	0.0003	10628
VIF	SLQYLALTA	149	9	31	48		10629
VIF	GSLQYLALTA	148	10	31	48		10630
VIF	IVWQVDRMRI	9	11	33	52		10631

Table XVI
HIV A03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
VIF	QVDRMRIR	12	8	34	53		10632
VIF	EDRWNRPK	180	9	39	61		10633
VIF	VMIVWQVDR	7	11	41	64		10634
VIF	QVMIVWQVDR	6	10	43	67	0.0062	10635
VIF	MIVWQVDRM	8	10	43	67		10636
VIF	AGINKVGSQ	142	11	43	67		10637
VIF	SLVKHHMY	23	8	44	69	0.0034	10638
VIF	VMIVWQVDR	7	9	44	69		10639
VIF	MIVWQVDR	8	8	46	72		10640
VIF	IVWQVDRMR	9	9	47	73	0.0008	10641
VIF	KVGSLOYLA	146	9	52	81	0.0036	10642
VIF	VGSLOYLA	147	8	58	91		10643
VIF	#LPGRGR	85	8	01	50		10644
VPR	NIRGRVR	85	8	01	50		10645
VPR	#LPGRGRNG	85	11	01	50		10646
VPR	WALELEELK	18	10	09	15		10647
VPR	QLLFVIFR	66	8	10	16		10648
VPR	HSRIGIR	79	8	10	16		10649
VPR	RIGTRQR	81	8	10	16		10650
VPR	IGITRQR	82	8	10	16		10651
VPR	ALELEELK	19	9	10	16		10652
VPR	RIGTRQR	81	9	10	16		10653
VPR	HSRIGITRQR	79	10	10	16		10654
VPR	HSRIGITRQR	79	11	10	16		10655
VPR	WLHGLGQY	38	8	11	17		10656
VPR	HFRIGCRH	71	8	11	17		10657
VPR	HSRIGITR	79	8	11	17		10658
VPR	FIHFRIGCR	69	9	11	17		10659
VPR	FIHFRIGCR	68	10	11	17		10660
VPR	FIHFRIGCR	69	10	11	17		10661
VPR	FVHFRIGCOH	69	10	11	17		10662
VPR	HFRIGCRHSR	71	10	11	17		10663
VPR	LLFIHFRIGCR	67	11	11	17		10664
VPR	LLFIHFRIGCRH	68	11	11	17		10665
VPR	LFVHFRIGCQH	68	11	11	17		10666
VPR	RIGCRHSR	74	8	12	19		10667
VPR	LQGHYNTY	42	9	13	20		10668
VPR	LGQYIYETY	42	9	13	20		10669
VPR	HFPRIVLH	33	8	14	22		10670
VPR	KSEAVRHFP	27	10	14	22		10671
VPR	AVRHFPRIWL	30	11	14	22		10672
VPR	KSEAVRHF	27	8	15	23		10673
VPR	ELKSEAVRHF	25	10	15	23		10674
VPR	ELKSEAVR	25	8	16	25		10675
VPR	ETYGDTWA	48	8	16	25		10676
VPR	DTWAGVEA	52	8	16	25		10677
VPR	AGVEAIR	55	8	16	25		10678
VPR	LLEELKSEA	22	9	16	25		10679
VPR	ELKSEAVRH	25	9	16	25		10680
VPR	GDTWAGVEA	51	9	16	25		10681

Table XVI
HIV-1 03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
VPR	WAGVEAIR	54	9	16	25		10682
VPR	ELLELKNEA	21	10	16	25		10683
VPR	ELLELKSEA	21	10	16	25		10684
VPR	YGDWAGVEA	50	10	16	25		10685
VPR	LEELKSEAVR	22	11	16	25		10686
VPR	DTWAGVEAIR	52	11	16	25		10687
VPR	ELKNEAVR	25	8	17	27		10688
VPR	LEELKNEA	22	9	17	27		10689
VPR	ELKNEAVRH	25	9	17	27		10690
VPR	LGQHYYET	42	9	17	27		10691
VPR	ELKNEAVRHF	25	10	17	27		10692
VPR	LEELKNEAVR	22	11	17	27		10693
VPR	EGVEAIR	55	8	18	28		10694
VPR	DTWEGVEAIR	52	11	18	28		10695
VPR	RARNGASR	93	8	19	30		10696
VPR	WLHGLGQH	38	8	20	31		10697
VPR	HGLGQHYY	40	8	20	31		10698
VPR	WLHGLGQHYY	38	10	20	31		10699
VPR	DTWEGVEA	52	8	23	36		10700
VPR	GDTWEGVEA	51	9	23	36		10701
VPR	YGDWAGVEA	50	10	23	36		10702
VPR	LFHFRIGCOH	68	11	29	45		10703
VPR	FHFRIGCOH	69	10	30	47		10704
VPR	HFRPWLH	33	8	31	49		10705
VPR	AVRHFRPWL	30	11	31	48		10706
VPR	RILQQLFHF	62	11	34	53		10707
VPR	ILQQLFHF	63	10	35	55	0.0130	10708
VPR	ILQQLFHF	63	11	35	55		10709
VPR	RILQQLFHF	62	10	36	56		10710
VPR	ILQQLFHF	63	9	37	58		10711
VPR	EDQGPQREPY	6	10	37	58		10712
VPR	AHRLQQLF	59	11	38	59		10713
VPR	QAPEDQGPQR	3	10	39	62		10714
VPR	IRILQQLF	60	10	41	64		10715
VPR	WTLLEELK	18	10	42	69		10716
VPR	QGPQREPY	8	8	43	68		10717
VPR	QLLFHF	66	8	44	69		10718
VPR	HFRIGCOH	71	8	44	69		10719
VPR	TLEELK	19	9	44	69		10720
VPR	HFRIGCOHSR	71	10	44	69		10721
VPR	RILQQLF	62	8	45	70		10722
VPR	RIGCOHSR	74	8	47	73		10723
VPR	EAVRHFR	29	8	59	92		10724
VPU	IDYRLGVGA	9	9	01	33		10725
VPU	VDYRIVIVA	9	9	01	33		10726
VPU	VDYRLGVGA	9	9	01	33		10727
VPU	KVDYRIVIVA	7	10	01	33		10728
VPU	KVDYRLGVGA	7	10	01	33		10729
VPU	RIDYRLGVGA	7	10	01	33		10730
VPU	VDYRIVIVAF	9	10	01	33		10731

Table XVI
HIV X03 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*0301	SEQ ID NO.
VPU	KVDYRIVIVAF	7	11	01	33		10732
VPU	LVQRKQDR	43	8	01	50		10733
VPU	GVEMGHHA	91	8	01	50		10734
VPU	VTLLSSK	94	8	01	50		10735
VPU	LVQRKQDRR	43	9	01	50		10736
VPU	LVTLSSSK	91	9	01	50		10737
VPU	RIKEIRDDSDY	64	11	01	50		10738
VPU	RIRERDDSDY	64	11	01	50		10739
VPU	LAIVALLVVA	13	9	09	15		10740
VPU	WTIVFIEYR	34	9	10	16		10741
VPU	TIVFIEYR	35	8	10	16		10742
VPU	IDRLIDRIR	54	9	10	16		10743
VPU	RLIDRIRER	56	9	10	16		10744
VPU	KIDRLIDRIR	52	10	10	16		10745
VPU	VVWTVFIEYR	31	11	10	16		10746
VPU	ESGDQEELSA	77	11	11	17		10747
VPU	EGDQEELSA	77	9	12	19		10748
VPU	WTIVFIEY	34	8	12	19		10749
VPU	AIVALLVVA	14	8	12	19		10750
VPU	IVFIEYRK	36	8	12	19		10751
VPU	IDRIRERA	59	8	12	19		10752
VPU	LIDRIRERA	58	9	12	19		10753
VPU	VVWTVFIEY	31	10	12	19		10754
VPU	IVVWTVFIEY	30	11	12	19		10755
VPU	GDQEELSA	78	8	14	22		10756
VPU	LIDRIRER	58	8	14	22		10757
VPU	AIVVWTVF	29	9	14	22		10758
VPU	IVVWTVF	30	8	15	23		10759
VPU	KIDRLIDR	52	8	15	23		10760
VPU	ILQRKIDR	46	9	15	23		10761
VPU	KILQRKIDR	45	10	15	23	0.0039	10762

Table XVII
HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
ENV	IGPGQTFY	361	8	01	25		10763
ENV	IGSGQAFY	361	8	01	25		10764
ENV	GTAGNSSR	375	8	01	33		10765
ENV	NNTPSR	375	8	01	33		10766
ENV	ADNLWTVY	42	9	01	33		10767
ENV	GIGPGQTFY	360	9	01	33		10768
ENV	SIGSGQAFY	360	9	01	33		10769
ENV	ADNLWTVVY	42	10	01	33		10770
ENV	EGKNEINDY	217	10	01	33		10771
ENV	NTSPRSRVAY	376	10	01	33		10772
ENV	TAGNSSRAAY	376	10	01	33		10773
ENV	GTAGNSSRAA	375	11	01	33		10774
ENV	NNTPSRSRVA	375	11	01	33		10775
ENV	KLREIQFENK	405	11	01	25		10776
ENV	KNNTETNK	535	8	01	50		10777
ENV	IIHIITP11	584	8	01	50		10778
ENV	VISTRTHR	584	8	01	50		10779
ENV	IIHIPTHR	585	8	01	50		10780
ENV	STRTHREK	586	8	01	50		10781
ENV	NNTPSR	374	9	01	50		10782
ENV	NANITPCR	478	9	01	50		10783
ENV	IIHIPTHR	584	9	01	50		10784
ENV	ISTRTHREK	585	9	01	50		10785
ENV	NIHTPHREK	586	9	01	50		10786
ENV	STRTHREKR	586	9	01	50		10787
ENV	VISTRTHREK	584	10	01	50		10788
ENV	IIHIPTHREK	585	10	01	50		10789
ENV	ISTRTHREKR	585	10	01	50		10790
ENV	NIHTPHREKR	586	10	01	50		10791
ENV	ITEGNITLQCR	478	11	01	50		10792
ENV	NANITPCRIK	478	11	01	50		10793
ENV	GNSTNGTETF	535	11	01	50		10794
ENV	IIHIPTHREK	584	11	01	50		10795
ENV	VISTRTHREKR	584	11	01	50		10796
ENV	IIHIPTHREKR	585	11	01	50		10797
ENV	DSSNSTGNY	218	9	01	20		10798
ENV	STNGTETFR	537	9	01	17		10799
ENV	TNSSTNDY	537	10	01	17		10800
ENV	NDTENNTETFR	537	11	01	17		10801
ENV	NTEKNTETFR	537	11	01	17		10802
ENV	NTGNTTETFR	537	11	01	17		10803
ENV	NGSENGTETF	537	11	02	33		10804
ENV	GSENGTETFR	538	10	02	18		10805
ENV	NDITLPCR	477	9	03	20		10806
ENV	NDITLPCR	477	11	03	20		10807
ENV	RGWEALKY	895	8	06	19		10808
ENV	KGRLGWGL	891	11	08	27		10809
ENV	LGWEGLKY	895	8	09	29		10810
ENV	RLGWGLKY	894	9	09	29		10811
ENV	GLRLGWGLK	892	11	09	29		10812

Table XVII
HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
ENV	LGRRGWEALK	883	10	09	15		10813
ENV	LLGRRGWEAL	882	11	09	15		10814
ENV	RLGWGLK	894	8	10	32		10815
ENV	GLRGWEGLK	892	10	10	32		10816
ENV	ENLWVTY	43	8	10	17		10817
ENV	ENLWVTY	43	9	10	17		10818
ENV	DIIGDIRQAH	372	10	10	16		10819
ENV	NNTRKSIR	350	8	10	16		10820
ENV	PLGVAPTR	571	8	10	16		10821
ENV	DIINLWLY	769	8	10	16		10822
ENV	DFILIAAR	870	8	10	16		10823
ENV	STITQACPK	243	9	10	16		10824
ENV	FDITNWLWY	768	9	10	16		10825
ENV	DFILIAAR	869	9	10	16		10826
ENV	FAILKCNCKK	269	10	10	16		10827
ENV	MLQLTVWGIK	651	10	10	16		10828
ENV	RVLAVERYLR	665	10	10	16		10829
ENV	WFDITNWLW	767	10	10	16		10830
ENV	EGIEEGGER	828	10	10	16		10831
ENV	GFAILKCNCKK	268	11	10	16		10832
ENV	GDIIGDIRQAH	371	11	10	16		10833
ENV	NVPWNSSWSN	693	11	10	16		10834
ENV	WMEWEREIDN	723	11	10	16		10835
ENV	IAIAVAEGTDR	925	11	10	16		10836
ENV	RGWEALKY	886	8	11	18		10837
ENV	KLWVTY	44	8	11	17		10838
ENV	WNSSWSNR	696	8	11	17		10839
ENV	TITQACPK	244	8	11	17		10840
ENV	IGPGQTFY	358	8	11	17		10841
ENV	LAVERYLR	667	8	11	17		10842
ENV	SNLWYIK	771	8	11	17		10843
ENV	NLCFSYH	859	8	11	17		10844
ENV	RIGPGQTFY	357	9	11	17		10845
ENV	ITHSFNCR	431	9	11	17		10846
ENV	NITLPCRIK	482	9	11	17		10847
ENV	VLAVERYLR	666	9	11	17		10848
ENV	ISNLWYIK	770	9	11	17		10849
ENV	RNLCFSYH	858	9	11	17		10850
ENV	NLCFSYHR	859	9	11	17		10851
ENV	EITHSFNCR	430	10	11	17		10852
ENV	RNLCFSYHR	858	10	11	17		10853
ENV	YATGDIGDIR	368	11	11	17		10854
ENV	DLRNLCFSYH	856	11	11	17		10855
ENV	NLCFSYHRLR	859	11	11	17		10856
ENV	GNLWVTY	43	8	12	20		10857
ENV	GNLWVTY	43	9	12	20		10858
ENV	TGDIIGDIR	370	9	12	19		10859
ENV	EAQOILLK	646	8	12	19		10860
ENV	ILKCNCKK	271	8	12	19		10861
ENV	TTHSFNCR	432	8	12	19		10862

Table XVII
HIV A1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
ENV	MTWMEWER	721	8	12	19		10863
ENV	GGERDRDR	834	8	12	19		10864
ENV	AILKCNDKK	270	9	12	19		10865
ENV	LAEEVVIR	312	9	12	19	0.0002	10866
ENV	INMWQEVGK	493	9	12	19		10867
ENV	NMTWMEWER	720	9	12	19		10868
ENV	GIEEGGER	829	9	12	19		10869
ENV	EGGERDRDR	833	9	12	19		10870
ENV	SLAEVVIR	311	10	12	19		10871
ENV	ATGDIIGDIR	369	10	12	19		10872
ENV	INMWQEVGK	492	10	12	19		10873
ENV	AIEAQHLLK	644	10	12	19		10874
ENV	LLOYWSQELK	906	10	12	19		10875
ENV	AILHIPRRIR	946	10	12	19		10876
ENV	PTRIQGLER	951	10	12	19		10877
ENV	KTLFCASDA	60	11	12	19		10878
ENV	GSLAEVVIR	310	11	12	19		10879
ENV	QINMWQEVG	491	11	12	19		10880
ENV	KNEQELLELDK	750	11	12	19		10881
ENV	GIEEGGERDR	829	11	12	19		10882
ENV	NLLQYWSQEL	905	11	12	19		10883
ENV	RAILHIPRRIR	945	11	12	19		10884
ENV	SVEINCTR	340	8	13	20		10885
ENV	GDIIGDIR	371	8	13	20		10886
ENV	KLTWVGIK	653	8	13	20		10887
ENV	RAILHIPR	945	8	13	20		10888
ENV	AILHIPRR	946	8	13	20		10889
ENV	KAKRRVVQR	579	9	13	20	0.0002	10890
ENV	RAILHIPRR	945	9	13	20		10891
ENV	ILHIPRRIR	947	9	13	20		10892
ENV	TNVSTVQCTH	286	10	13	20		10893
ENV	SGGDPEIVMH	425	10	13	20		10894
ENV	LLKLTWVGIK	651	10	13	20		10895
ENV	NTSVITQACPK	241	11	13	20		10896
ENV	CTNVSTVQCT	285	11	13	20		10897
ENV	SSGGDLITTH	424	11	13	20		10898
ENV	SSGGDPEIVMH	424	11	13	20		10899
ENV	PTKAKRRVVQ	576	11	13	20		10900
ENV	KAKRRVVQRE	579	11	13	20		10901
ENV	HLLKLTWVGI	650	11	13	20		10902
ENV	KNEQDLALD	750	11	13	20		10903
ENV	TGEIGDIR	370	9	14	23		10904
ENV	AITQACPK	244	8	14	22		10905
ENV	GDPEIVMH	427	8	14	22		10906
ENV	QDLALDK	753	8	14	22		10907
ENV	SAITQACPK	243	9	14	22		10908
ENV	FAILKCNDK	269	9	14	22	0.0002	10909
ENV	GGDPEIVMH	426	9	14	22		10910
ENV	TITLPCRIK	482	9	14	22		10911
ENV	TSAITQACPK	242	10	14	22		10912

Table XVII
HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
ENV	TSVITOACPK	242	10	14	22		10913
ENV	GFAILKCNDK	268	10	14	22		10914
ENV	IFAVLSIVNR	793	10	14	22		10915
ENV	NTSAITQACPK	241	11	14	22		10916
ENV	AGFAILKCNDK	267	11	14	22		10917
ENV	IIFAVLSIVNR	792	11	14	22		10918
ENV	KIEPLGVAPTK	568	11	15	24		10919
ENV	FDPIPIHY	255	8	15	23		10920
ENV	PAGYAILK	266	8	15	23		10921
ENV	NMWQEVGK	494	8	15	23		10922
ENV	TNWLWYIK	771	8	15	23		10923
ENV	ITNWLWYIK	770	9	15	23		10924
ENV	SGDLEITTH	425	10	15	23		10925
ENV	IFRPGGDMR	545	10	15	23		10926
ENV	NMWQEVGKA	494	11	15	23		10927
ENV	EIERPGGDMR	544	11	15	23		10928
ENV	DDLRLCLFSY	855	11	15	23		10929
ENV	FNGTGPCK	279	8	16	25		10930
ENV	RNLCLFSY	858	8	16	25		10931
ENV	ITKWLWYIK	770	9	16	25		10932
ENV	SFNCRGEFFY	437	10	16	25		10933
ENV	DLRLCLFSY	836	10	16	25		10934
ENV	ISFNCRGEFFY	434	11	16	25		10935
ENV	WNASWSNK	696	8	17	27		10936
ENV	KAYDTEVII	72	8	17	27		10937
ENV	VITOACPK	244	8	17	27	0.0001	10938
ENV	RVVQREKR	587	8	17	27		10939
ENV	SVITOACPK	243	9	17	27	0.0002	10940
ENV	VAPTKAKRR	574	9	17	27		10941
ENV	DAKAYDTEVH	70	10	17	27		10942
ENV	GVAPTKAKRR	573	10	17	27		10943
ENV	VFAVLSIVNR	793	10	17	27		10944
ENV	SDAKAYDTEV	69	11	17	27		10945
ENV	DTEVINVVAT	75	11	17	27		10946
ENV	NCTRPNNTR	344	11	17	27		10947
ENV	LGVAPTKAKR	572	11	17	27		10948
ENV	IVFAVLSIVNR	792	11	17	27		10949
ENV	WNSSWSNK	696	8	18	29		10950
ENV	ENVTFNFMW	100	11	18	29		10951
ENV	VLAVERYLK	666	9	18	28		10952
ENV	RVLAVERYLK	665	10	18	28		10954
ENV	NCRGEFFY	439	8	19	30		10955
ENV	GVAPTKAK	573	8	19	30		10956
ENV	VAPTKAKR	574	8	19	30		10957
ENV	FNCRGEFFY	438	9	19	30		10958
ENV	LGVAPTKAK	572	9	19	30		10959
ENV	GVAPTKAKR	573	9	19	30		10960
ENV	PLGVAPTKAK	571	10	19	30		10961
ENV	LGVAPTKAKR	572	10	19	30		10962
ENV	SSNITGLLLTR	516	11	19	30		

Table XVII
HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
ENV	PLGVAPTAK	571	11	19	30		10963
ENV	AIKCNCK	270	8	20	31		10964
ENV	ETFRPGGDM	544	11	20	31		10965
ENV	LIEESNQEK	740	11	20	31		10966
ENV	GDLEITH	427	8	21	33		10967
ENV	GGDLEITH	426	9	21	33		10968
ENV	TAIAVAEGTDR	925	11	21	33		10969
ENV	RIVELLGR	878	8	22	34		10970
ENV	IVELLGRR	879	8	22	34		10971
ENV	RIVELLGRR	878	9	22	34	0.0100	10972
ENV	NCTRPNNTR	344	10	22	34		10973
ENV	CTRPNNTRK	345	10	22	34		10974
ENV	TTTLFCASDA	60	11	22	34		10975
ENV	INCTRPNNTR	343	11	22	34		10976
ENV	TVQCTHIGR	290	9	23	36	0.0008	10977
ENV	STVQCTHIGR	289	10	23	36		10978
ENV	VSTVQCTHIGR	288	11	23	36		10979
ENV	TRPFGGDMR	545	10	24	38		10980
ENV	ALAWDDL	851	8	25	39		10981
ENV	LALAWDDL	850	9	25	39		10982
ENV	KNVSTVQCTH	286	10	25	39		10983
ENV	IVQQNNLLR	634	10	25	39	0.0190	10984
ENV	FLALAWDDL	849	10	25	39		10985
ENV	GIVQQNNLLR	633	11	25	39		10986
ENV	GFLALAWDDL	848	11	25	39		10987
ENV	ITLPCRIK	483	8	26	41		10988
ENV	PLGVAPT	571	8	26	41		10989
ENV	LAVERYLK	667	8	26	41		10990
ENV	KNMVEQMH	110	9	26	41		10991
ENV	IVQQSNLLR	634	10	26	41		10992
ENV	GIVQQSNLLR	633	11	26	41		10993
ENV	IGDIRQAH	377	9	27	44		10994
ENV	ESONQKEK	743	8	27	42		10995
ENV	IGDIRQAH	378	8	28	44		10996
ENV	NNMVEQMH	111	8	28	44		10997
ENV	TVQCTHIGK	290	9	28	44	0.0460	10998
ENV	CTRPNNTR	345	9	28	44		10999
ENV	VSFEPPIHY	253	10	28	44		11000
ENV	STVQCTHIGK	289	10	28	44		11001
ENV	ASITLTVQAR	619	10	28	44		11002
ENV	KVSFEPPIHY	252	11	28	44		11003
ENV	YCAPAGFAILK	263	11	28	44		11004
ENV	VSTVQCTHIGK	288	11	28	44		11005
ENV	AASITLTVQAR	618	11	28	44		11006
ENV	VSFEPPIH	253	9	29	45		11007
ENV	KVSFEPPIH	252	10	29	45		11008
ENV	CAPAGFAILK	264	10	29	45		11009
ENV	RSELYKYKV	558	11	29	45		11010
ENV	AVLSVNR	795	8	31	48		11011
ENV	AVAEGTDR	928	8	31	48		11012

Table XVII
HIV-1 MHC Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
ENV	VTENFNMWK	102	9	31	48		11013
ENV	SPEPIPIH	254	9	31	48		11014
ENV	FAVLSIVNR	794	9	31	48		11015
ENV	SLCLFSYHR	859	9	31	48	0.0003	11016
ENV	IAVAEGTDR	927	9	31	48		11017
ENV	NVTENFNMW	101	10	31	48		11018
ENV	AVLSIVNRVR	795	10	31	48		11019
ENV	RSCLFSYHR	858	10	31	48		11020
ENV	AIVAEGTDR	926	10	31	48		11021
ENV	FAVLSIVNRVR	794	11	31	48		11022
ENV	DDLRSCLFSY	855	11	31	48		11023
ENV	SLCLFSYHRLR	859	11	31	48		11024
ENV	ELYKYKVK	560	9	32	51		11025
ENV	RVVEREKR	587	8	32	50		11026
ENV	ITLTQAR	621	8	32	50		11027
ENV	SLCLFSYH	859	8	32	50		11028
ENV	SHLTQAR	620	9	32	50		11029
ENV	RSCLFSYH	858	9	32	50		11030
ENV	DLRSCLFSYH	856	11	32	52		11031
ENV	SPEPIPIH	254	8	33	52		11032
ENV	RVLAVERY	665	8	33	52	0.0003	11033
ENV	QARVLAVER	663	9	33	52		11034
ENV	QARVLAVERY	663	10	33	52		11035
ENV	QLQARVLAVER	661	11	33	52		11036
ENV	IMIVGGLIGLR	781	11	34	54		11037
ENV	LLQLTVWGIK	651	10	34	53	0.0110	11038
ENV	HLQLTVWGI	650	11	34	53		11039
ENV	LSIVNRVRQGY	797	11	34	53		11040
ENV	NLWVTVYY	44	8	35	56		11041
ENV	NCGGEFF	439	8	35	55		11042
ENV	RSCLFSY	858	8	35	55		11043
ENV	EVHNVWATH	77	9	35	55		11044
ENV	FNCGGEFF	438	9	35	55	0.0001	11045
ENV	NITGLLLTR	519	9	35	55		11046
ENV	SFNCGGEFF	437	10	35	55	0.0014	11047
ENV	SNITGLLLTR	517	10	35	55		11048
ENV	DLRSCLFSY	856	10	35	55		11049
ENV	HSFNCGGEFF	434	11	35	55		11050
ENV	GGDMRDNRW	549	10	36	56		11051
ENV	MIVGGLIGLR	782	10	36	56		11052
ENV	SIVNRVRQGY	798	10	36	56		11053
ENV	PGGDMRDNR	548	11	36	56	0.0008	11054
ENV	ITGLLLTR	520	8	37	58		11055
ENV	DMRDNRWSEL	552	11	37	58		11056
ENV	PAGFAIK	266	8	38	59		11057
ENV	LSIVNRVR	797	8	38	59		11058
ENV	VLIVNRVR	796	9	38	59		11059
ENV	IVNRVRQGY	799	9	38	59		11060
ENV	ISLWDQSLK	121	10	38	59	0.0540	11061
ENV	DIISLWDQSLK	120	11	38	59		11062

Table XVII
HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*1101	SEQ ID NO.
ENV	GDMRDNR	551	8	39	61		11063
ENV	GGDMRDNR	550	9	39	61		11064
ENV	RDNWRSELY	554	9	40	63	0.0001	11065
ENV	RDNWRSELYK	554	10	40	63	0.0028	11066
ENV	TLFCASDAKA	64	11	40	63		11067
ENV	RDNWRSELYK	554	11	40	63		11068
ENV	TVYGVVWK	48	10	41	64	7.8000	11069
ENV	VTYYGVVW	47	11	41	64	4.1000	11070
ENV	CASDAKAY	67	8	42	66		11071
ENV	LCLFSYHR	860	8	42	66		11072
ENV	FCASDAKAY	66	9	42	66		11073
ENV	IVGLIGLR	783	9	42	66		11074
ENV	CLFSYHRLR	861	9	42	66	0.0002	11075
ENV	LFCASDAKAY	65	10	42	66		11076
ENV	LCLFSYHRLR	860	10	42	66		11077
ENV	VGLIGLR	784	8	43	67		11078
ENV	QLTVWGIK	653	8	44	69		11079
ENV	LFSYHRLR	862	8	44	69		11080
ENV	RIRQGLR	953	8	44	69		11081
ENV	VNRVRQGY	800	8	45	71		11082
ENV	SLWDQSLK	123	8	47	75		11083
ENV	ISLWDQSLK	122	9	47	73	0.0890	11084
ENV	WDQSLKPCVK	125	10	47	73		11085
ENV	QSLKPCVK	127	8	48	75		11086
ENV	TVWGIKQLQA	655	11	48	75		11087
ENV	DNWRSELY	555	8	49	77		11088
ENV	GIKQLQAR	658	8	49	77		11089
ENV	DNWRSELYK	555	9	49	77	0.0014	11090
ENV	WGKQLQAR	657	9	49	77	0.0001	11091
ENV	DNWRSELYKY	555	10	49	77	0.0001	11092
ENV	DNWRSELYKY	555	11	49	77		11093
ENV	LGIWGCCK	679	9	50	78	0.0023	11094
ENV	TTLFCASDAK	61	10	50	78	0.2200	11095
ENV	LLGIWGCCK	678	10	50	78	0.0120	11096
ENV	NLLRAIEAQH	640	11	50	78		11097
ENV	QLLGIWGCCK	677	11	50	78		11098
ENV	VSTVQCTH	288	8	51	80		11099
ENV	RAIEAQH	643	8	51	80		11100
ENV	NVSTVQCTH	287	9	51	80		11101
ENV	LLRAIEAQH	641	10	51	80		11102
ENV	GIWGCCK	680	8	52	81		11103
ENV	TLFCASDAK	64	9	52	81	0.5300	11104
ENV	RSELYKYK	558	8	54	84		11105
ENV	LFCASDAK	65	8	57	89		11106
ENV	AAAIMQK	405	8	01	25		11107
GAG	SATIMMQR	405	8	01	25		11108
GAG	KDKDKELY	535	8	01	25		11109
GAG	ETIDKELY	537	8	01	25		11110
GAG	NSATIMMQR	404	9	01	33		11111
GAG	TAPPESFR	508	9	01	33		11112

Table XVII
HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
GAG	NGKQANFLGK	461	10	01	25		11113
GAG	NGRQANFLGK	461	10	01	25		11114
GAG	PTAPPESFR	507	10	01	33		11115
GAG	NGKQANFLGK	461	11	01	25		11116
GAG	NGRQANFLGK	461	11	01	25		11117
GAG	PAAADKEK	123	8	01	50		11118
GAG	ASAQQDLK	392	8	01	50		11119
GAG	ATAQQDLK	392	8	01	50		11120
GAG	AADKGVSNY	130	10	01	50		11121
GAG	SAQDCLKGGY	393	10	01	50		11122
GAG	TAQDCLKGGY	393	10	01	50		11123
GAG	GTRPGNYVQK	480	10	01	50		11124
GAG	GTRPGNYVQR	480	10	01	50		11125
GAG	ITSLPKQEOK	526	10	01	50		11126
GAG	PAAADKEKDS	123	11	01	50		11127
GAG	GANSIPVGDY	276	11	01	50		11128
GAG	PNQPIPVGDY	276	11	01	50		11129
GAG	ASAQDCLKGG	392	11	01	50		11130
GAG	ATAQDCLKGG	392	11	01	50		11131
GAG	EITSLPKQEOK	525	11	01	50		11132
GAG	YTA VFMQR	405	8	02	50		11133
GAG	TAPPESFR	508	9	02	67		11134
GAG	PTAPPESFR	507	10	02	67		11135
GAG	EGRQANFLGK	462	10	02	100		11136
GAG	AADKGVSNY	129	11	02	18		11137
GAG	EADKGVSNY	129	11	04	36		11138
GAG	AAAIMMOK	400	8	04	19		11139
GAG	AAIMMOKSNF	406	11	06	15		11140
GAG	KTVKCFNCGK	421	10	08	16		11141
GAG	GARASILR	2	8	10	16		11142
GAG	PGNFPQSR	483	8	10	16		11143
GAG	MGARASILR	1	9	10	16		11144
GAG	KIWPSSKGR	472	9	10	16		11145
GAG	TGNSSQVSN	139	11	10	16		11146
GAG	NFLGKIWPSSK	468	11	10	16		11147
GAG	PVAPGQMR	243	8	10	16		11148
GAG	MMQKSNEK	409	8	10	16		11149
GAG	MMQRGNFK	409	8	10	16		11150
GAG	KLDKWEKIR	12	9	10	16	0.0001	11151
GAG	GKKKKYKLG	24	9	10	16		11152
GAG	RDTEALDK	97	9	10	16		11153
GAG	IMMQKSNEK	408	9	10	16		11154
GAG	LGIKWPSSK	470	9	10	16		11155
GAG	PGGKKYKLG	23	10	10	16		11156
GAG	GKKKKYKLG	24	10	10	16		11157
GAG	AGPVAPGQMR	241	10	10	16		11158
GAG	FLGKIWPSSK	469	10	10	16		11159
GAG	KLDKWEKIRL	12	11	10	16		11160
GAG	PGGKKYKLG	23	11	10	16		11161
GAG	LGIKWPSSKGR	470	11	10	16		11162

Table XVII
HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
GAG	ATIMQRGNF	406	11	11	28		11163
GAG	PSQOEPIDK	528	10	11	18		11164
GAG	PIPVGDIY	279	8	11	17		11165
GAG	TIKCFNCGK	422	9	11	17		11166
GAG	TVKCFNCGK	422	9	11	17		11167
GAG	GNSSQVSQNY	140	10	12	23		11168
GAG	TIMQRGNFR	407	10	12	21		11169
GAG	QTGSEELR	71	8	12	19		11170
GAG	FNCGKEGHAR	426	11	12	19		11171
GAG	PGGKKYK	23	8	12	19		11172
GAG	TLKCVHQK	86	8	12	19		11173
GAG	DTKEALEK	98	8	12	19		11174
GAG	MLNIVGGH	208	8	12	19		11175
GAG	PTSILDIR	303	8	12	19		11176
GAG	GSEELRSY	73	9	12	19		11177
GAG	ATLYCVHQK	85	9	12	19		11178
GAG	KDTKEALEK	97	9	12	19		11179
GAG	MMLNIVGGH	207	9	12	19		11180
GAG	TGSEELRSY	72	10	12	19		11181
GAG	VATLYCVHQK	84	10	12	19		11182
GAG	NMMLNIVGGH	206	10	12	19		11183
GAG	YSPTSILDIR	301	10	12	19		11184
GAG	RAEQASOEVK	329	10	12	19		11185
GAG	RLRPGGKKY	20	11	12	19		11186
GAG	TVATLYCVHQ	83	11	12	19		11187
GAG	LNMLNIVGG	205	11	12	19		11188
GAG	SNPPVPGEIY	273	11	12	19		11189
GAG	TSILDIRQGP	304	11	12	19		11190
GAG	PGNFLQR	483	8	13	21		11191
GAG	IARNCRAPR	434	9	13	21		11192
GAG	KIWPSTNKR	472	9	13	21		11193
GAG	NCGKEGHAR	427	10	13	21		11194
GAG	IARNCRAPRK	434	10	13	21		11195
GAG	IARNCRAPRK	434	11	13	21		11196
GAG	NFLGKIWPSNK	468	11	13	21		11197
GAG	KGRPGNFLQN	478	11	13	21		11198
GAG	RIEVKDTK	93	8	13	20		11199
GAG	IVKCFNCGK	422	9	13	20		11200
GAG	CGKEGHAR	428	9	13	20		11201
GAG	EGHIARNCR	431	9	13	20		11202
GAG	LGIWPSNK	470	9	13	20		11203
GAG	KLKHIWASR	31	10	13	20		11204
GAG	HIARNCRAPR	433	10	13	20		11205
GAG	FLGKIWPSNK	469	10	13	20		11206
GAG	EVKDTKEALD	95	11	13	20		11207
GAG	AAEWDRVHPV	230	11	13	20		11208
GAG	HIARNCRAPRK	433	11	13	20		11209
GAG	LGIWPSNKG	470	11	13	20		11210
GAG	NSQVSQNY	144	9	14	31		11211
GAG	NCGKEGHAR	427	10	14	22		11212

Table XVII
HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
GAG	FNCGKEGIIAK	426	11	14	22		11213
GAG	IAKNCRAPRK	434	11	14	22		11214
GAG	QNAQGMVH	157	9	14	22		11215
GAG	RGNFRNQR	412	9	14	22		11216
GAG	CGKEGIIAK	428	9	14	22		11217
GAG	EGHIAKNCR	431	9	14	22		11218
GAG	FNTVATLYCV	81	11	14	22		11219
GAG	TVATLYCVIIQ	83	11	14	22		11220
GAG	IVQNAQGMV	155	11	14	22		11221
GAG	SSQVSONY	145	8	15	31		11222
GAG	RSLYNTVATL	78	11	15	24		11223
GAG	FNTVATLY	81	8	15	23		11224
GAG	TLYCVIIQR	86	8	15	23		11225
GAG	AAEWDVRH	230	8	15	23		11226
GAG	WDRVHPVH	233	8	15	23		11227
GAG	RGNFRNQR	412	8	15	23		11228
GAG	LFNTVATLY	80	9	15	23		11229
GAG	ATLYCVIIQR	85	9	15	23	0.7100	11230
GAG	EAAEWDVRH	229	9	15	23		11231
GAG	TAPPEESFR	496	9	15	23		11232
GAG	SGGKLDWEK	9	10	15	23		11233
GAG	SLFNTVATLY	79	10	15	23		11234
GAG	VATLYCVIIQR	84	10	15	23		11235
GAG	KIEEQNKSK	105	10	15	23		11236
GAG	RAEQATQDVK	329	10	15	23		11237
GAG	PTAPPEESFR	495	10	15	23		11238
GAG	LSGGKLDWE	8	11	15	23		11239
GAG	PGILLETSEGR	50	11	15	23		11240
GAG	KIEEQNKSKK	105	11	15	23		11241
GAG	MMQRGNFRN	409	11	15	23		11242
GAG	IAKNCRAPRK	434	10	16	25		11243
GAG	LDWEKIR	13	8	16	25		11244
GAG	NAQGMVH	158	8	16	25		11245
GAG	PVSILDIK	303	8	16	25		11246
GAG	GNFRNQRK	413	8	16	25		11247
GAG	KLDWEKIR	12	9	16	25		11248
GAG	GGKKKYRLK	24	9	16	25		11249
GAG	LDWEKIRL	13	10	16	25		11250
GAG	PGKKKYRLK	23	10	16	25		11251
GAG	GGKKKYRLKH	24	10	16	25		11252
GAG	GLLETSEGR	51	10	16	25		11253
GAG	YSPVSILDIK	301	10	16	25		11254
GAG	GGKLDWEKI	10	11	16	25		11255
GAG	KLDWEKIRL	12	11	16	25		11256
GAG	PGKKKYRLK	23	11	16	25		11257
GAG	VSILDIKQPK	304	11	16	25		11258
GAG	HIANKNCRAPRK	433	11	16	25		11259
GAG	PIPPQMR	243	8	17	27		11260
GAG	GGKLDWEK	10	9	17	27		11261
GAG	DAWEKIRL	14	9	17	27		11262

Table XVII
HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
GAG	LLETSEGR	52	9	17	27		11263
GAG	RLKHLVWASR	31	10	17	27		11264
GAG	LDKIEEQNK	103	10	17	27		11265
GAG	AGPIPPGQMR	241	10	17	27		11266
GAG	ALDKIEEQNK	102	11	17	27		11267
GAG	LSPRTLNAWV	168	11	17	27		11268
GAG	HAGPIPPGQMR	240	11	17	27		11269
GAG	PIPPGQMR	243	11	17	27		11270
GAG	IAKNCRAPR	434	9	18	29	0.0003	11271
GAG	LDKWEKIR	13	8	18	28		11272
GAG	PVGDIYKR	281	8	18	28		11273
GAG	PDCKTILR	352	8	18	28		11274
GAG	LDKWEKIRL	13	10	18	28		11275
GAG	SILDIKQGP	305	10	18	28		11276
GAG	ANPCKTILR	350	10	18	28		11277
GAG	IIAKNCRAPR	433	10	18	28		11278
GAG	IIAGPIAPGOM	240	11	18	28		11279
GAG	NNPIPVGEY	273	11	18	28		11280
GAG	NANPDKTILR	349	11	19	30		11281
GAG	LARNCRAPRK	434	11	19	30		11282
GAG	PIAPGQMR	243	8	19	30		11283
GAG	LDIKQGP	307	8	19	30		11284
GAG	ILDIKQGP	306	9	19	30		11285
GAG	AGPIAPGQMR	241	10	19	30		11286
GAG	IAPGOMREPR	244	10	19	30		11287
GAG	RLRPGGKKY	20	11	19	30		11288
GAG	PIAPGQMR	243	11	19	30		11289
GAG	DIKQGPKEPR	308	11	19	30		11290
GAG	LARNCRAPR	434	9	20	32		11291
GAG	LARNCRAPRK	434	10	20	32		11292
GAG	PGGKKYR	23	8	20	31		11293
GAG	IMMQRGNFR	408	9	20	31		11294
GAG	KNCRAPRK	436	9	20	31	0.0066	11295
GAG	IVWASRELER	35	10	20	31		11296
GAG	HLARNCRAPR	433	10	20	31		11297
GAG	HIVWASRELER	34	11	20	31		11298
GAG	HLARNCRAPR	433	11	20	31		11299
GAG	EGHLARNCR	431	9	21	33	0.0005	11300
GAG	KIWPISHGR	472	9	22	35		11301
GAG	GGPSHKAR	378	8	22	34		11302
GAG	KNCRAPRK	436	8	22	34		11303
GAG	VGGPSHKAR	377	9	22	34		11304
GAG	SLYNTVATLY	79	10	22	34		11305
GAG	GVGGPSHKAR	376	10	22	34		11306
GAG	QVGGPSHKA	375	11	22	34		11307
GAG	LGIWPSHKG	470	11	22	34		11308
GAG	NFLGKIWPCHK	468	11	23	37		11309
GAG	YNTVATLY	81	8	23	36		11310
GAG	KIEEQNK	105	8	23	36		11311
GAG	QVGGPSH	375	8	23	36		11312

Table XVII
HIV-1 CR1 Mediator Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
GAG	GVGGPSHK	376	8	23	36		11313
GAG	MMORGNER	409	8	23	36		11314
GAG	QGVGGPSHK	375	9	23	36		11315
GAG	LGKIWPESH	470	9	23	36		11316
GAG	ACQVGGPSH	373	10	23	36		11317
GAG	FLGKIWPESH	469	10	23	36	0.0013	11318
GAG	YNTVATLYCV	81	11	23	36		11319
GAG	TACQVGGPS	372	11	23	36		11320
GAG	ACQVGGPSH	373	11	23	36		11321
GAG	ACQVGGPSH	373	11	24	38		11322
GAG	ACQVGGPSH	427	10	24	38		11323
GAG	NCGKEGHLAR	426	11	24	38		11324
GAG	FNCGKEGHLA	428	9	24	38		11325
GAG	CGKEGHLAR	301	10	24	38		11326
GAG	YSPVILDIR	468	10	25	40		11327
GAG	NFLGKIWPESH	303	8	25	39		11328
GAG	PVSILDIR	470	8	25	39		11329
GAG	LGKIWPESH	97	9	25	39		11330
GAG	KDTKEALDK	469	9	25	39		11331
GAG	FLGKIWPESH	304	11	25	39		11332
GAG	VSILDIRQPK	467	11	25	39		11333
GAG	ANFLGKIWPESH	35	10	26	41		11334
GAG	LVWASRELER	34	11	26	42	0.0670	11335
GAG	HLVWASRELE	163	9	27	42		11336
GAG	MVHQISPR	321	9	27	42	0.0010	11337
GAG	VDRFKTLR	162	10	27	42		11338
GAG	QMVHQISPR	320	10	27	42		11339
GAG	YVDRFKTLR	329	10	27	42	0.0002	11340
GAG	RAEQATQEVK	350	10	27	42		11341
GAG	ANPCKTILK	349	11	28	44		11342
GAG	KGRPGNFLOS	478	8	28	44		11343
GAG	PDCKTILK	352	8	28	44		11344
GAG	VDRFKTLR	321	9	28	44		11345
GAG	PFRDYVDREY	316	10	28	44	0.0006	11346
GAG	YVDRFKTLR	320	10	28	44		11347
GAG	PFRDYVDREY	316	11	28	44		11348
GAG	GARASVLSGG	2	11	29	46		11349
GAG	ASVLSGGK	5	8	29	45		11350
GAG	NLQGMVH	158	8	29	45		11351
GAG	WVKVIEK	176	8	29	45		11352
GAG	WDRHPVH	233	8	29	45		11353
GAG	RDYVDREY	318	8	29	45		11354
GAG	RASVLSGGK	4	9	29	45		11355
GAG	QNLQGMVH	157	9	29	45	0.0400	11356
GAG	RDYVDREYK	318	9	29	45		11357
GAG	NAWVKVIEK	174	10	29	45		11358
GAG	IVQNLQGMV	155	11	29	45		11359
GAG	LNAWVKVIEE	173	11	29	45		11360
GAG	AAEWDRLIIPV	230	11	29	45		11361
GAG	PGNFLOS	483	8	30	48	0.0002	11362
GAG	NAWVKVIEK	174	10	30	47		

Table XVII
HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
GAG	KIRLRPGKKK	18	11	30	47		11363
GAG	LNAWVKVVEE	173	11	30	47		11364
GAG	WVKVVEEK	176	8	31	48	0.0001	11365
GAG	RDYVDRFFK	318	9	33	52		11366
GAG	RNCRAPRKK	436	9	33	52		11367
GAG	PFRDYVDRFF	316	11	33	52		11368
GAG	RNCRAPRKK	436	8	34	53		11369
GAG	RLRPGGKKK	20	9	34	53		11370
GAG	RLRPGGKKKY	20	10	34	53	0.0001	11371
GAG	PIPVGEIYKR	279	10	34	53		11372
GAG	PIPVGEIY	279	8	35	55	0.0012	11373
GAG	PIPVGEIYK	279	9	35	55	0.0001	11374
GAG	DTKEALDK	98	8	36	56	0.0001	11375
GAG	QVGGPGHK	375	8	36	56		11376
GAG	QVGGPGHK	375	9	36	56		11377
GAG	ACQGVGGPGH	373	10	36	56		11378
GAG	ISPTLNAWV	168	11	36	56	0.0001	11379
GAG	TACQGVGGPG	372	11	36	56		11380
GAG	ACQGVGGPGH	373	11	36	56		11381
GAG	QVGGPGHKA	375	11	36	56	0.0018	11382
GAG	GVGGPGHK	376	8	37	58		11383
GAG	GGPGHKAR	378	8	37	58		11384
GAG	VGGPGHKAR	377	9	37	58	0.0001	11385
GAG	GVGGPGHKAR	376	10	37	58		11386
GAG	AAEWDRLLH	230	8	39	61		11387
GAG	AAEWDRLLH	229	9	39	61	0.0001	11388
GAG	AAEWDRLLH	281	8	40	63		11389
GAG	PVGEIYKR	83	8	40	63		11390
GAG	TVATLYCVH	82	9	40	63		11391
GAG	NTVATLYCVH	305	10	40	63	0.7100	11392
GAG	SILDIRQGP	308	11	41	64		11393
GAG	DIRQGPKEPR	84	8	42	66		11394
GAG	VATLYCVH	307	8	42	66		11395
GAG	LDIROGPK	306	9	42	66	0.0048	11396
GAG	NTMLNTVGGH	206	10	42	66		11397
GAG	LNTMLNTVGG	205	11	42	66		11398
GAG	TMLNTVGGH	207	9	43	67		11399
GAG	KGCWKCGK	444	8	44	69		11400
GAG	KIRLRPGKK	18	9	44	69		11401
GAG	KIRLRPGKK	18	10	44	69	0.0010	11402
GAG	KGCWKCGREG	444	11	44	69		11403
GAG	PGQREPR	246	8	45	70		11404
GAG	CGKEGHQMK	449	9	45	70		11405
GAG	KGCKEGHQMK	448	10	45	70		11406
GAG	MLNTVGGH	208	8	47	73		11407
GAG	WASRELER	37	8	48	75		11408
GAG	GCWKCGKEGH	445	10	48	75		11409
GAG	RLRPGKK	20	8	49	77		11410
GAG	QMKDCTER	455	8	49	77		11411
GAG	EGHQMKDCTE	452	11	49	77		11412

Table XVII
HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
GAG	RAPRKKGCKWK	439	10	51	80		11413
GAG	CTERQANFLG	459	11	52	83		11414
GAG	NCRAPRKK	437	8	53	84		11415
GAG	TINEEAAEWD	225	11	53	83		11416
GAG	INEEAAEWD	226	10	55	86		11417
GAG	FNCGKEGH	426	8	57	90		11418
GAG	WILGLNK	289	8	57	89		11419
GAG	CFNCGKEGH	425	9	57	89	0.0006	11420
GAG	ILGLNKIVR	290	10	57	89		11421
GAG	KCFNCGKEGH	424	10	57	89		11422
GAG	WILGLNKIVR	289	11	57	89		11423
GAG	ILGLNKIVRMY	291	11	57	89		11424
GAG	ILGLNKIVR	291	9	58	91	0.0001	11425
GAG	LGLNKIVRMY	292	10	58	91	0.0002	11426
GAG	LLVQANPDC	345	11	58	91		11427
GAG	LGLNKIVR	292	8	59	92		11428
GAG	LVQANPDC	292	10	59	92	0.0110	11429
GAG	LNKIVRMY	294	8	60	94		11430
GAG	GLNKIVRMY	293	9	60	94	0.0002	11431
GAG	QAAMQMLK	216	8	61	95		11432
GAG	QNANPDC	348	8	61	95		11433
GAG	GGHQAAQM	213	11	61	95		11434
GAG	RTLNAWVK	171	8	63	98	0.0560	11435
GAG	QGPKEPR	311	8	63	98		11436
GAG	PERDYVDR	316	8	63	98		11437
GAG	QGPKEPRDY	311	10	63	98	0.0002	11438
NEF	AADGVGAVSR	42	10	09	15		11439
NEF	ANEGENSLH	249	11	09	15		11440
NEF	VGWTAIRER	11	9	10	17		11441
NEF	FDSRLAFH	310	8	10	16		11442
NEF	FDSRLAFIH	310	9	10	16		11443
NEF	DSRLAFIH	311	8	10	16		11444
NEF	AVSQDLK	48	8	10	16		11445
NEF	PLRPMTEK	102	8	10	16		11446
NEF	GAVSQDLK	47	9	10	16		11447
NEF	GLEGLYSK	125	9	10	16		11448
NEF	MARELHPEY	321	9	10	16		11449
NEF	VGAVSQDLK	46	10	10	16		11450
NEF	QVPLRPMTEK	100	10	10	16		11451
NEF	GAFDLSFLLK	110	10	10	16		11452
NEF	GLEGLYSK	124	10	10	16		11453
NEF	CFKLVDPDR	226	10	10	16		11454
NEF	HMARELHPEY	320	10	10	16		11455
NEF	MARELHPEY	321	10	10	16		11456
NEF	GVGAVSQDLK	45	11	10	16		11457
NEF	KGAFDLSFLLK	109	11	10	16		11458
NEF	KGLEGLYSK	122	11	10	16		11459
NEF	WCFKLVDPDR	225	11	10	16		11460
NEF	NNSLLHPICQH	254	11	10	16		11461
NEF	HMARELHPEY	320	11	10	16		11462

Table XVII
HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
NEF	MARELHPEYY	321	11	10	16		11463
NEF	ANEENNCCLL	249	11	11	18		11464
NEF	AVSRDLEK	48	8	11	17		11465
NEF	VSRDLEKH	49	8	11	17		11466
NEF	KLVPVDPR	228	8	11	17		11467
NEF	GAVSRDLEK	47	9	11	17	0.0009	11468
NEF	AVSRDLEKH	48	9	11	17		11469
NEF	VGA VSRDLEK	46	10	11	17		11470
NEF	GA VSRDLEKH	47	10	11	17		11471
NEF	QNYTPGPGVR	205	10	11	17		11472
NEF	NSLLHPICQH	255	10	11	17		11473
NEF	GVGA VSRDLE	45	11	11	17		11474
NEF	VGA VSRDLEK	46	11	11	17		11475
NEF	EGENNCCLH	251	9	12	19		11476
NEF	YTPGPGVR	207	8	12	19		11477
NEF	DILDWVYH	185	9	12	19		11478
NEF	QDILDWVYH	184	10	12	19		11479
NEF	EGENNSLLH	251	9	13	21		11480
NEF	VDLSHFLKEK	112	10	13	20		11481
NEF	AVDLSHFLKEK	111	11	13	22		11482
NEF	VDLSHFLK	112	8	14	22		11483
NEF	DGLYSKK	172	8	14	22		11484
NEF	ELHPEFYK	324	8	14	22	1.1000	11485
NEF	AVDLSHFLK	111	9	14	22		11486
NEF	LDGLYSKK	171	9	14	22		11487
NEF	DGLYSKKR	172	9	14	22		11488
NEF	SLHPCQH	256	9	14	22		11489
NEF	GLDGLYSKK	125	10	14	22		11490
NEF	LDGLYSKKR	171	10	14	22		11491
NEF	GGLDGLYSKK	124	11	14	22		11492
NEF	GLDGLYSKKR	125	11	14	22		11493
NEF	NNCLLIIPMSQ	254	11	14	22		11494
NEF	CLLHPMSQH	255	9	15	23		11495
NEF	NCLLHPMSQH	255	10	15	23		11496
NEF	QNYTPGPGIRY	205	11	15	23		11497
NEF	LDGLYSK	171	8	16	25		11498
NEF	GLDGLYSK	125	9	16	25		11499
NEF	GGLDGLYSK	124	10	16	25		11500
NEF	KGGLDGLYSK	122	11	16	25		11501
NEF	RFPLTFGWCF	216	11	17	27		11502
NEF	FPDWQNY	199	8	17	27		11503
NEF	LLHPMSQH	257	8	17	27		11504
NEF	GFPDWQNY	198	9	17	27		11505
NEF	YTPGPGIRY	207	9	17	27		11506
NEF	FDLSFFLEK	112	10	17	27		11507
NEF	QGFPPDWQNY	196	10	17	27		11508
NEF	AFDLSFFLEK	111	11	17	27		11509
NEF	FDLSFFLK	112	8	18	28		11510
NEF	LLHPICQH	257	8	18	28		11511
NEF	AFDLSFFLK	111	9	18	28		11512

Table XVII
 HIV-1 X1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
NEF	QNYTPGPIR	205	10	18	28		11513
NEF	GGLEGLY	124	8	19	30		11514
NEF	KGGLEGLY	122	9	19	30		11515
NEF	DILDWVY	185	8	20	31		11516
NEF	YTPGPGR	207	8	20	31		11517
NEF	QDILDWVY	184	9	20	31		11518
NEF	QNYTPGPIR	205	10	20	31		11519
NEF	GGLDGLY	124	8	21	33		11520
NEF	WVYHTQY	191	8	21	33		11521
NEF	YTPGPGR	207	8	21	33		11522
NEF	KGGLDGLY	122	9	21	33		11523
NEF	DLWVYHTQY	188	10	21	33		11524
NEF	LDLWVYHTQY	187	11	21	33		11525
NEF	LSFELKEK	114	8	22	34		11526
NEF	ELIPEYK	324	8	22	34		11527
NEF	DLSFELKEK	113	9	22	34		11528
NEF	EILDWVYH	185	9	22	34		11529
NEF	GLYSKKR	173	8	23	36		11530
NEF	LSHFLKEK	114	8	27	42		11531
NEF	DLSHFLKEK	113	9	27	42		11532
NEF	EILDWVYH	186	8	33	52		11533
NEF	YFPDWQNY	199	8	34	53		11534
NEF	QGYFPDWQNY	196	10	36	56	0.0017	11535
NEF	LTFGWCFK	221	8	36	56		11536
NEF	PLTFGWCFK	219	9	39	61		11537
NEF	QVPLRPMTY	100	9	39	61		11538
NEF	PVRPQVPLR	95	10	46	72	0.6300	11539
NEF	GFPVRPQVPLR	93	9	46	75		11540
NEF	PLRPMTYK	102	11	48	75		11541
POL	STNSPTSR	32	8	49	77	0.0003	11542
POL	RANSPSSR	35	8	01	33		11543
POL	NTNSPTSR	31	9	01	33		11544
POL	PTSRELQVR	36	9	01	33		11545
POL	QTRANSPTSR	33	10	01	33		11546
POL	QTRANSPTTR	35	10	01	33		11547
POL	NSPTSRELQVR	34	11	01	33		11548
POL	RANSPTR	37	8	01	50		11549
POL	PSSRELQVR	39	9	01	50		11550
POL	PSRANSPTR	24	10	01	50		11551
POL	NSPSSRELQVR	37	11	01	50		11552
POL	NSPTTRELQV	39	11	01	50		11553
POL	NNSLSEAGAD	55	11	05	25		11554
POL	NLAFFQGEAR	5	10	10	16		11555
POL	ILIEICGH	149	8	10	16		11556
POL	LIEICGHK	150	8	10	16		11557
POL	YAKMRTAH	546	8	10	16		11558
POL	RSANINDVK	550	9	10	16		11559
POL	ETWETWTD	588	10	10	16		11560
							11561
							11562

Table XVII
HIV-1 Nucleotide Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
POL	ETWETWTE	588	10	10	16		11563
POL	VSLDTTNQK	659	10	10	16		11564
POL	ENLAFQGEAR	4	11	10	16		11565
POL	TGKYAKMRTA	543	11	10	16		11566
POL	VVSLDTTNQ	658	11	10	16		11567
POL	QTKELQKQIK	961	11	10	16		11568
POL	QTRANSPTRR	21	10	11	18		11569
POL	TNNETPGIR	324	9	11	17		11570
POL	TNNETPGIRY	324	10	11	17		11571
POL	LDGDKAQEDH	754	11	11	17		11572
POL	IGGFIKVK	137	8	11	17		11573
POL	RIGPENPY	238	8	11	17		11575
POL	TAHTNDVK	551	8	11	17		11576
POL	QLTEVVQK	559	8	11	17		11577
POL	IDKAAQEDH	757	8	11	17		11578
POL	VVPRRKVK	1012	8	11	17		11579
POL	KIKDYGK	1019	8	11	17		11580
POL	GIGGFIKVK	136	9	11	17		11581
POL	SLDTTNQK	660	9	11	17		11582
POL	GIDKAAQEDH	756	9	11	17		11583
POL	SNFTSTTVK	871	9	11	17		11584
POL	KVPRRKVK	1011	9	11	17		11585
POL	GGIGGFIKVK	135	10	11	17		11586
POL	ISRIGPENPY	236	10	11	17		11587
POL	STNNETPGIR	323	10	11	17		11588
POL	ESWTVDIOK	439	10	11	17		11589
POL	ETNQKTELH	663	10	11	17		11590
POL	DGIDKAAQEDH	755	10	11	17		11591
POL	GSNFTSTTVK	870	10	11	17		11592
POL	GIOQEFIPY	886	10	11	17		11593
POL	SDIQTKELQK	958	10	11	17		11594
POL	FNFPQITLWOR	85	11	11	17		11595
POL	IGGIGGFIKVK	134	11	11	17		11596
POL	KISRIGPENPY	235	11	11	17		11597
POL	PSTNNETPGIR	322	11	11	17		11598
POL	STNNETPGIRY	323	11	11	17		11599
POL	VVSLTETTNQ	658	11	11	17		11600
POL	NGSNFTSTTV	869	11	11	17		11601
POL	AGIQQEFIPY	885	11	11	17		11602
POL	IDIASDIQTK	953	11	11	17		11603
POL	VDIATDIQTK	953	11	11	17		11604
POL	957		11	11	17		11605
POL	ASDIQTKELQK	957	11	11	17		11606
POL	NSEIKVPRRK	1007	11	11	17		11607
POL	QTRANSPTSR	21	10	12	19		11608
POL	IKIQNFR	969	8	12	19		11609
POL	QIYPGKVK	458	9	12	19		11610
POL	QDQWTYQIY	526	9	12	19		11611
POL	IKIQNFRVY	969	10	12	19		11612
POL	ASQIYPGKVK	456	11	12	19		11613
POL	IKIQNFRVY	969	11	12	19		11614

Table XVII
HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
POL	AFPOGEAR	7	8	12	19		11613
POL	TNQTTELH	665	8	12	19		11614
POL	KTELQAIY	668	8	12	19		11615
POL	LAFPOGEAR	6	9	12	19		11616
POL	EINLPKWK	122	9	12	19		11617
POL	TTNQTTELH	664	9	12	19		11618
POL	QIKIQNFR	968	9	12	19		11619
POL	VIQDNSEIK	1003	9	12	19		11620
POL	NSEIKVVPR	1007	9	12	19		11621
POL	VLEEINLPK	119	10	12	19		11622
POL	VVIQDNSEIK	1002	10	12	19		11623
POL	DNSEIKVVPR	1006	10	12	19		11624
POL	NSEIKVVPRR	1007	10	12	19		11625
POL	TVLEEINLPK	118	11	12	19		11626
POL	EINLPKWKPK	122	11	12	19		11627
POL	QGDDQWTYQI	524	11	12	19		11628
POL	RMRGAHTNDV	548	11	12	19		11629
POL	TNQTTELQAIY	665	11	12	19		11630
POL	QIKIQNFRVY	968	11	12	19		11631
POL	AVVIQDNSEIK	1000	11	12	19		11632
POL	QDNSEIKVVPR	1005	11	12	19		11633
POL	DNSEIKVVPRR	1006	11	12	19		11634
POL	ELQKQIK	964	8	13	21		11635
POL	KTGKYARMR	542	9	13	21		11636
POL	NLKTGKYARM	540	11	13	21		11637
POL	EDINLPK	121	8	13	20		11638
POL	TGKYARMR	543	8	13	20		11639
POL	YARMRGH	546	8	13	20		11640
POL	QVREQAEH	916	8	13	20		11641
POL	DINLPKWK	122	9	13	20		11642
POL	VLEDINLPK	119	10	13	20		11643
POL	EDINLPKWK	121	10	13	20		11644
POL	RAKIELREH	388	10	13	20		11645
POL	TVQPIVLPEK	429	10	13	20		11646
POL	AGRWPVKTIH	857	10	13	20	5.6000	11647
POL	IGQVREQAEH	914	10	13	20		11648
POL	QVREQAEHLK	916	10	13	20		11649
POL	TLWQRPLTV	91	11	13	20		11650
POL	LVTIKGGQK	97	11	13	20		11651
POL	TVLEDINLPK	118	11	13	20		11652
POL	DINLPKWK	122	11	13	20		11653
POL	KIEELREHLK	390	11	13	20		11654
POL	WTQPIVLPEK	428	11	13	20		11655
POL	TGKYARMRGA	543	11	13	20	0.0510	11656
POL	LAGRWPVKTI	856	11	13	20		11657
POL	IIGQVREQAEH	913	11	13	20		11658
POL	EIKVVPRRKAK	1009	11	13	20		11659
POL	EFSEQTR	16	8	14	22		11660
POL	QIYPGKVR	458	9	14	22		11661
POL	ASQIYTGKVR	456	11	14	22		11662

Table XVII
HIV-1 A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
POL	IATESIWIWVK	567	11	14	22		11663
POL	ILIEICGK	149	8	14	22		11664
POL	LIEICGKK	150	8	14	22		11665
POL	QNPDIVY	363	8	14	22		11666
POL	NFTSTTVK	372	8	14	22		11667
POL	IASDIQTK	956	8	14	22		11668
POL	DSRDPLWK	981	8	14	22		11669
POL	QILIEICGK	148	9	14	22		11670
POL	ILIEICGKK	149	9	14	22		11671
POL	IASDIQTK	955	9	14	22		11672
POL	RDSRDPLWK	980	9	14	22		11673
POL	QILIEICGK	148	10	14	22		11674
POL	QNPDIVYQY	363	10	14	22		11675
POL	RTKIEELRQIH	388	10	14	22		11676
POL	PGIKVRQLCK	461	10	14	22		11677
POL	DIASDIQTK	954	10	14	22		11678
POL	RDPLWKGPAK	983	10	14	22		11679
POL	FSFPQITLWQR	85	11	14	22		11680
POL	YDQILIEICGK	146	11	14	22		11681
POL	KTPKFKLPIQK	577	11	14	22		11682
POL	GIDKAQEEHER	756	11	14	22		11683
POL	QTRANSPTIR	21	9	15	24		11684
POL	LVEICTEMEK	221	10	15	24	0.0120	11685
POL	ELRQIILLR	393	8	15	23		11686
POL	QGQDQWTY	524	8	15	23		11687
POL	KTELOAIH	668	8	15	23		11688
POL	EIKVVPKPK	1009	9	15	23		11689
POL	LGIIQAQPDPR	695	10	15	23		11690
POL	VDKLVSAQIR	740	10	15	23		11691
POL	IDKAQEEHER	757	10	15	23		11692
POL	ALVEICTEMEK	220	11	15	23		11693
POL	KIEELRQHLLR	390	11	15	23		11694
POL	TNQTTELQAIH	665	11	15	23		11695
POL	ALGIIQAQPDPR	694	11	15	23		11696
POL	LVNQHIEQLIK	709	11	15	23		11697
POL	QVDKLVSAQIR	739	11	15	23		11698
POL	VDKLVSAQIRK	740	11	15	23		11699
POL	IDKAQEEHERY	757	11	15	23		11700
POL	KAQEEHER	759	8	16	25		11701
POL	KAQEEHERY	759	9	16	25		11702
POL	NLAFQQGEAR	5	10	16	25		11703
POL	KAQEEHERYH	759	10	16	25		11704
POL	AFQQGEAR	7	8	16	25		11705
POL	RANSPTIR	26	8	16	25		11706
POL	SAHTNDVK	551	8	16	25		11707
POL	IIGAQPDPR	697	8	16	25		11708
POL	KLVSAQIR	742	8	16	25		11709
POL	LVSAGIRK	743	8	16	25		11710
POL	EIKVVPKPK	1009	8	16	25	0.0054	11711
POL	LAFQQGEAR	6	9	16	25		11712

Table XVII
HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
POL	GIHQAPDR	696	9	16	25		11713
POL	KLVSAGIRK	742	9	16	25	0.0770	11714
POL	ENLAFQGEA	4	11	16	25		11715
POL	RANSPTSR	26	8	17	27		11716
POL	KIEELROH	390	8	17	27		11717
POL	ELREHLK	393	8	17	27		11718
POL	WGKTPKFK	575	8	17	27		11719
POL	TIKIGGQLK	99	9	17	27	0.0330	11720
POL	VTIKIGGQLK	98	10	17	27	0.2100	11721
POL	TVQPIQLPEK	429	10	17	27		11722
POL	VIWGRPLVTI	573	10	17	27		11723
POL	TLWQRPLVTI	91	11	17	27		11724
POL	WTVQIQLPEK	428	11	17	27		11725
POL	IVIWGKTPKFK	572	11	17	27		11726
POL	YFSVPLDKDFR	304	11	18	29		11727
POL	NLKTGKYAKM	540	11	18	29		11728
POL	PDIVIVQY	365	8	18	28		11729
POL	SVPLDKDFR	306	9	18	28		11730
POL	FSVPLDKDFR	305	10	18	28		11731
POL	SVPLDKDFR	306	10	18	28		11732
POL	AGIKVKQLCK	461	10	18	28		11733
POL	VNQHIEQLIK	710	10	18	28		11734
POL	FSVPLDKDFR	305	11	18	28		11735
POL	SVPLDKDFR	306	11	18	28		11736
POL	YAGIKVKQLCK	460	11	18	28		11737
POL	LVSQIEQLIK	709	11	18	28		11738
POL	VNQHIEQLIK	710	11	18	28		11739
POL	PLDKDFR	308	8	19	30		11740
POL	PLDKDFRKY	308	9	19	30		11741
POL	KTGKYAKMR	542	9	19	30		11742
POL	LDKDFRKY	309	8	19	30		11743
POL	KIEELREH	390	8	19	30		11744
POL	TKGYAKMR	543	8	19	30		11745
POL	GAHTNDVK	551	8	19	30		11746
POL	LTDTTNQK	661	8	19	30		11747
POL	PLWGPAPK	985	8	19	30		11748
POL	GKVRQLCK	462	9	19	30		11749
POL	RGHTNDVK	550	9	19	30		11750
POL	KVRQLCKLLR	464	10	19	30		11751
POL	ATESIVIWGK	568	10	19	30		11752
POL	VSQIEQLIK	710	10	19	30	0.0370	11753
POL	MAGDDCVASR	1028	10	19	30		11754
POL	VSQIEQLIK	710	11	19	30		11755
POL	QMAGDGCVAS	1027	11	19	30		11756
POL	QIYAGIKVK	458	9	20	32	0.0036	11757
POL	KVYLAWVPAH	722	10	20	32	0.0740	11758
POL	KAACWVAGIK	879	10	20	32		11759
POL	ASQIYAGIKVK	456	11	20	32		11760
POL	KVYLAWVPAH	722	11	20	32	2.3000	11761
POL	KFKLPIQK	580	8	20	31		11762

Table XVII
HIV-1 α_1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*1101	SEQ ID NO.
POL	GDDCVASR	1030	8	20	31		11763
POL	AGDDCVASR	1029	9	20	31		11764
POL	VSLTETNQK	659	10	20	31		11765
POL	LLKLAGRWPV	853	11	20	31		11766
POL	YFSVPLDK	304	8	21	33		11767
POL	ACWWAGIK	881	8	21	33		11768
POL	SLTETNQK	660	9	21	33		11769
POL	AACWWAGIK	880	9	21	33	0.0470	11770
POL	DAYFSVPLDK	302	10	21	33		11771
POL	DLEIGQHRTK	381	10	21	33		11772
POL	QLCKLLRGTK	467	10	21	33		11773
POL	IFAIKKDKSTK	249	11	21	33		11774
POL	GDAYFSVPLD	301	11	21	33		11775
POL	SDLEIGQHRTK	380	11	21	33		11776
POL	SDFNLPTIVAK	776	11	21	33		11777
POL	AGIKQEFGIPY	885	11	21	33		11778
POL	EIGQHRTK	383	8	22	34		11779
POL	RTKIEELR	388	8	22	34		11780
POL	YLAWVPAH	724	8	22	34		11781
POL	LAWVPAHK	725	8	22	34		11782
POL	YLAWVPAHK	724	9	22	34	0.0570	11783
POL	NFPQITLWQR	86	10	22	34		11784
POL	MTKILEPFRK	353	10	22	34	0.0380	11785
POL	AGRWPKVVIH	857	10	22	34		11786
POL	GIKQEFGIPY	886	10	22	34	0.0002	11787
POL	SMTKILEPFRK	352	11	22	34		11788
POL	KTPKFLPLQK	577	11	22	34		11789
POL	LAGRWPKVI	856	11	22	34		11790
POL	KVYLSWVPAH	722	10	23	37		11791
POL	KVYLSWVPAH	722	11	23	37		11792
POL	KILEPFRK	355	8	23	36		11793
POL	KVILVAVH	823	8	23	36		11794
POL	SFPQITLWQR	86	10	23	36		11795
POL	DFNLPIVAK	777	10	23	36		11796
POL	EGKVILVAVH	821	10	23	36		11797
POL	LLKWGFTTPD	398	11	23	36		11798
POL	LLRWGFTTPD	398	11	23	36		11799
POL	IDHATDIQTK	953	11	23	36		11800
POL	NTPIFAIK	246	8	24	38		11801
POL	GDDCVAGR	1030	8	24	38		11802
POL	YNTPIFAIK	245	9	24	38		11803
POL	NTPIFAIKK	246	9	24	38	0.0001	11804
POL	LCKLLRGTK	468	9	24	38		11805
POL	AGDDCVAGR	1029	9	24	38		11806
POL	YNTPIFAIKK	245	10	24	38		11807
POL	YNTPIFAIKK	246	10	24	38		11808
POL	YNTPIFAIKK	1028	10	24	38		11809
POL	MAGDDCVAGR	245	11	24	38		11810
POL	YNTPIFAIKK	524	11	24	38		11811
POL	QGGQWITYQI	643	11	24	38		11812
POL	KLKAGYVTD						

Table XVII
HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
POL	TAYFLKLAG	849	11	24	38		11813
POL	QMAQDDCVAG	1027	11	24	38		11814
POL	QGWTYQIY	526	9	25	40	0.0001	11815
POL	PIFAIKK	248	8	25	39		11816
POL	QGGQWTY	524	8	25	39		11817
POL	FLKLAGR	852	8	25	39		11818
POL	YFLKLAGR	851	9	25	39		11819
POL	QLCKLLRGAK	467	10	25	39		11820
POL	LGKAGYVTR	644	10	25	39		11821
POL	IDKAEHEHEK	757	10	25	39		11822
POL	PSKDLIAEIQK	513	11	25	39		11823
POL	GIDKAEHEHEK	756	11	25	39		11824
POL	IDKAEHEHEK	757	11	25	39		11825
POL	SDFNLPVAVK	776	11	25	39		11826
POL	RAKIEELR	388	8	26	41		11827
POL	KFRLPIQK	580	8	26	41		11828
POL	NLPPVAVK	779	8	26	41		11829
POL	LCKLLRGAK	468	9	26	41		11830
POL	FNLPIVAVK	778	9	26	41		11831
POL	SNFTSAVVK	871	9	26	41		11832
POL	DFNLPPVAVK	777	10	26	41		11833
POL	GSNFTSAVVK	870	10	26	41		11834
POL	TGOETAYFLL	845	11	26	41		11835
POL	NGSNFTSAV	869	11	26	41		11836
POL	KAQEEHEK	759	8	27	43	0.3400	11837
POL	ASQIYAGIK	456	9	27	43		11838
POL	KAQEEHEKY	759	9	27	43		11839
POL	KAQEEHEKYH	759	10	27	43		11840
POL	INLPGKWK	123	8	27	42		11841
POL	EICTEMEK	223	8	27	42		11842
POL	EIQHRAK	383	8	27	42		11843
POL	LVSSGIRK	743	8	27	42		11844
POL	NLPPVAVK	779	8	27	42		11845
POL	ETAYFLLK	848	8	27	42	0.0430	11846
POL	KLVSIGIRK	742	9	27	42		11847
POL	FNLPPVAVK	778	9	27	42		11848
POL	INLPGKWKPK	123	10	27	42		11849
POL	DLEIGQIRAK	381	10	27	42		11850
POL	WASQIYAGIK	455	10	27	42		11851
POL	KVQLCKLLR	464	10	27	42		11852
POL	EICTEMEKEGK	223	11	27	42		11853
POL	SDLEIGQIRAK	380	11	27	42		11854
POL	VDKLVSIGIRK	740	11	27	42		11855
POL	ASQIYPGIK	456	9	28	44		11856
POL	KDLIAEIQK	515	9	28	44		11857
POL	NLTKGYAK	540	9	28	44		11858
POL	DLIAEIQK	516	8	28	44		11859
POL	IVGAETFY	626	8	28	44		11860
POL	NFTSAVVK	872	8	28	44		11861
POL	CTEMEKEGK	225	9	28	44	0.0001	11862

Table XVII
HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
POL	GIKVKQLCK	462	9	28	44		11863
POL	PIVGAETFY	625	9	28	44		11864
POL	QLIKKEKVV	716	9	28	44		11865
POL	ICTEMEKEGK	224	10	28	44		11866
POL	WASQIYPGK	455	10	28	44		11867
POL	KNLKTGKYAK	539	10	28	44		11868
POL	NLKTGKYAR	540	9	29	46	0.0001	11869
POL	KLVSIGIR	742	8	29	45		11870
POL	KNLKTGKYAR	539	10	29	45		11871
POL	VIWGTKPKFR	573	10	29	45		11872
POL	VDKLVSSGIR	740	10	29	45		11873
POL	IVIWGKTPKFR	572	11	29	45		11874
POL	QVDKLVSSGIR	739	11	29	45		11875
POL	WGKTPKFR	575	8	30	47		11876
POL	LTETTNOK	661	8	30	47		11877
POL	ANRETKLGG	638	9	30	47	0.0001	11878
POL	AANRETKLGG	637	10	30	47	0.0016	11879
POL	IEQLIKKEK	713	10	30	47	0.0003	11880
POL	GAANRETKLG	636	11	30	47		11881
POL	QIEQLIKKEK	712	11	30	47		11882
POL	ILKLAGRWTV	853	11	30	47		11883
POL	KILVAVII	823	8	31	48		11884
POL	ETAYFILK	848	8	31	48		11885
POL	YFILKLAGR	851	9	31	48		11886
POL	EGKILVAVII	821	10	31	48		11887
POL	PSINNETPGIR	322	11	31	48		11888
POL	TGQETAYFILK	845	11	31	48		11889
POL	TAYFILKLAGR	849	11	31	48		11890
POL	INNETPGIR	324	9	32	51		11891
POL	INNETPGIRY	324	10	32	51		11892
POL	FILKLAGR	852	8	32	50		11893
POL	SINNETPGIR	323	10	32	50		11894
POL	SINNETPGIRY	323	11	32	50		11895
POL	SSMTKILEPFR	351	11	32	50	0.0100	11896
POL	QTKELQKQITK	961	11	32	50	0.0001	11897
POL	EMEKEGKISK	229	10	33	52	0.0240	11898
POL	DVKQLTEAVQ	556	11	33	52		11899
POL	DIATDIQTK	954	10	34	53	0.0130	11900
POL	ELOKQITK	964	8	35	56		11901
POL	LIKKEKVV	717	8	35	55		11902
POL	DSRDPWK	981	8	35	55		11903
POL	ETKLKAGY	641	9	35	55		11904
POL	IATDIQTK	955	9	35	55	0.0980	11905
POL	QITKIQNFR	968	9	35	55	0.0045	11906
POL	RDSRDPWK	980	9	35	55		11907
POL	TDIQTKELOK	958	10	35	55	0.0001	11908
POL	RDPWKGPAK	983	10	35	55		11909
POL	ATDIQTKELOK	957	11	35	55	0.1800	11910
POL	QITKIQNFRVY	968	11	35	55		11911
POL	ITKIQNFR	969	8	36	57		11912

Table XVII
HEX A11 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
POL	ITKIQNFRVY	969	10	36	57	0.0012	11913
POL	ITKIQNFRVYY	969	11	36	57		11914
POL	IATDIQTK	956	8	36	56		11915
POL	PIWKGPAK	985	8	36	56		11916
POL	NLPKGWKPK	124	9	36	56		11917
POL	AIQSSMTK	347	9	36	56	0.9600	11918
POL	PAIQSSMTK	346	10	36	56	0.0830	11919
POL	VFAIKKKDSTK	249	11	36	56		11920
POL	NTPVFAIK	246	8	37	58	0.0003	11921
POL	PVFAIKKK	248	8	37	58	0.0001	11922
POL	QLTEAVQK	559	8	37	58		11923
POL	QIEQLIK	712	8	37	58		11924
POL	IEQLIKK	713	8	37	58		11925
POL	YLSWVPAH	724	8	37	58		11926
POL	LSWVPAHK	725	8	37	58		11927
POL	YNTVFAIK	245	9	37	58	0.0002	11928
POL	NTPVFAIKK	246	9	37	58	0.0600	11929
POL	QIEQLIKK	712	9	37	58	0.1600	11930
POL	YLSWVPAHK	724	9	37	58		11931
POL	VIQDNSDIK	1003	9	37	58	0.0068	11932
POL	YNTVFAIKK	245	10	37	58		11933
POL	NTPVFAIKK	246	10	37	58	0.0046	11934
POL	VVIQDNSDIK	1002	10	37	58	0.0210	11935
POL	YNTVFAIKK	245	11	37	58		11936
POL	AVVIQDNSDIK	1000	11	37	58	0.0150	11937
POL	IFOSSMTK	348	8	38	59	0.0073	11938
POL	ILKEPVHGVY	498	11	38	59		11939
POL	LDGIDKAQEEH	754	11	39	62		11940
POL	AGYVTDGR	647	9	39	61	0.0010	11941
POL	YVTDGRQK	649	9	39	61		11942
POL	KAGYVTDGR	646	10	39	61		11943
POL	LGIIQAQPK	695	10	39	61	0.0001	11944
POL	DGIDKAQEEH	755	10	39	61		11945
POL	PVHGVYDPS	505	11	39	61		11946
POL	AGYVTDGRQ	647	11	39	61		11947
POL	ALGIIQAQPK	694	11	39	61		11948
POL	DIKVVPRKAK	1009	11	39	61		11949
POL	VTDGRQK	650	8	40	63	0.0065	11950
POL	IIQAQPK	697	8	40	63		11951
POL	GIIQAQPK	696	9	40	63	0.0400	11952
POL	GIDKAQEEH	756	9	40	63		11953
POL	NSDIKVVPR	1007	9	40	63		11954
POL	ILKEPVHGVY	498	10	40	63		11955
POL	DNSDIKVVPR	1006	10	40	63	0.0001	11956
POL	NSDIKVVPRR	1007	10	40	63		11957
POL	ELKEPVHGVY	497	11	40	63		11958
POL	WTYQIQEPF	529	11	40	63	0.0540	11959
POL	QIQEPFNK	532	11	40	63	0.2900	11960
POL	QDSDIKVVPR	1005	11	40	63		11961
POL	DNSDIKVVPRR	1006	11	40	63		11962

Table XVII
HIV-1 Mediator Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*1101	SEQ ID NO.
POL	NSDIKVVPRK	1007	11	40	63		11963
POL	ESIVWGTKPK	570	11	41	65		11964
POL	QIYQEPFK	532	8	41	64	0.0013	11965
POL	IDKAQEEH	757	8	41	64		11966
POL	KAKIRDY	1017	8	41	64		11967
POL	KAKIRDYDK	1017	10	41	64	0.0018	11968
POL	KISKIGPENPY	235	11	41	64		11969
POL	KAGYVTDK	646	8	42	66		11970
POL	ISKIGPENPY	236	10	42	66		11971
POL	SMTKILEPFR	352	10	42	66	0.0004	11972
POL	SIVWGTKPK	571	10	42	66		11973
POL	IVIYQYMDLY	367	11	42	66		11974
POL	VPRKKAKIIR	1012	11	42	66		11975
POL	GVYDPSK	508	8	43	67		11976
POL	SCDKCQLK	791	8	43	67		11977
POL	MTKILEPFR	353	9	43	67	0.0160	11978
POL	HGVYDPSK	507	9	43	67	0.0001	11979
POL	ASCDKCOLK	790	9	43	67	0.0140	11980
POL	DSWTVNDIQ	439	10	43	67	0.0002	11981
POL	TFYVDGAANR	631	10	43	67	0.0008	11982
POL	VASCDKCOLK	789	10	43	67	0.0004	11983
POL	KDSWTVNDIQ	438	11	43	67		11984
POL	ETFYVDGAAN	630	11	43	67		11985
POL	IVASCDKCOLK	788	11	43	67	0.1000	11986
POL	SDIKVVPR	1008	8	44	69		11987
POL	SDIKVVPRR	1008	9	44	69	0.0001	11988
POL	VDGAANRET	634	10	44	69		11989
POL	IGQVRDQAEH	914	10	44	69		11990
POL	QVRDQAEHLK	916	10	44	69	0.0093	11991
POL	SDIKVVPRK	1008	10	44	69	0.0001	11992
POL	ENREILKEPVH	494	11	44	69		11993
POL	YVDGAANRET	633	11	44	69		11994
POL	IIGQVRDQAEH	913	11	44	69		11995
POL	VAKEIVASCDK	784	11	45	71		11996
POL	GAANRET	636	8	45	70		11997
POL	EIVASCDK	787	8	45	70		11998
POL	DGAANRET	635	9	45	70		11999
POL	PFKNLKTGKY	537	10	45	70	0.0002	12000
POL	PLVKLWYQLE	613	11	45	70		12001
POL	EILKEPVH	497	8	46	72		12002
POL	KLWYQLEK	616	8	46	72		12003
POL	RDQAEHLK	918	8	46	72		12004
POL	PFKNLKTGK	537	9	46	72		12005
POL	DIQTKELQK	959	9	46	72	0.0006	12006
POL	LVKLWYQLEK	614	10	46	72	0.0820	12007
POL	KVKQWPLTEE	207	11	46	72	0.0330	12008
POL	VIWGTKPK	573	8	48	75		12009
POL	QVRDQAEH	916	8	48	75		12010
POL	DIKVVPRR	1009	8	48	75		12011
POL	IVIWGTKPK	572	9	48	75	0.3700	12012

Table XVII
HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
POL	DIKVVPRRK	1009	9	48	75	0.0001	12013
POL	KVLFLDGIDK	750	10	48	75	0.7800	12014
POL	KCQLKGEAMH	794	10	48	75		12015
POL	VVESMNKELK	902	10	48	75		12016
POL	GVVESMNKEL	901	11	48	75		12017
POL	VVESMNKELK	902	11	48	75		12018
POL	GVVESMNK	901	8	49	77		12019
POL	QGVVESMNK	900	9	49	77	0.0760	12020
POL	KLKFGMDGPK	197	10	49	77		12021
POL	QSQGVVESMN	898	11	49	77		12022
POL	ESVIWQK	570	8	50	79	0.0001	12023
POL	YVDGAANR	633	8	50	78		12024
POL	LAGRWPVK	856	8	50	78		12025
POL	KIIRDYQK	1019	8	50	78		12026
POL	KLGRWPVK	855	9	50	78	0.0690	12027
POL	QNFVYYRDS	973	11	50	78		12028
POL	GMDGPKVK	201	8	51	80	0.0004	12029
POL	KIGPENPY	238	8	51	80		12030
POL	NNETGIR	325	8	51	80		12031
POL	FTTPDKKH	403	8	51	80	0.0001	12032
POL	PGMDGPKVK	200	9	51	80		12033
POL	NNETGIRY	325	9	51	80		12034
POL	GFTTPDKKH	402	9	51	80	0.0320	12035
POL	VFLDGDIDK	751	9	51	80	0.0090	12036
POL	VVQYMDLY	368	10	51	80		12037
POL	WGFTTPDKKH	401	10	51	80	0.0150	12038
POL	FTTPDKKHQ	403	10	51	80		12039
POL	NNETGIRYQY	325	11	51	80		12040
POL	GFTTPDKKHQ	402	11	51	80		12041
POL	PAGLKKKK	286	8	52	81		12042
POL	SDLEIGH	380	8	52	81		12043
POL	DLEIGHQIR	381	8	52	81		12044
POL	WGFTTPDK	401	8	52	81		12045
POL	GFTTPDKK	402	8	52	81		12046
POL	KIQNFVY	971	8	52	81		12047
POL	VVPRRKAK	1012	8	52	81	0.0001	12048
POL	ETPGIRYQY	327	9	52	81		12049
POL	GSDLEIGHQ	379	9	52	81	0.0001	12050
POL	SDLEIGHQIR	380	9	52	81	0.0039	12051
POL	WGFTTPDKK	401	9	52	81	0.1400	12052
POL	KIQNFVY	971	9	52	81	0.0039	12053
POL	KVPRRKAK	1011	9	52	81		12054
POL	VGSDLEIGHQ	378	10	52	81		12055
POL	GSDLEIGHQIR	379	10	52	81	0.2100	12056
POL	KIQNFVYR	971	10	52	81		12057
POL	NFRVYYRDSR	974	10	52	81		12058
POL	IGGIGGFIKVR	134	11	52	81		12059
POL	VGTPVNIIR	164	11	52	81		12060
POL	YVGSDEIGHQ	377	11	52	81		12061
POL	VGSDLEIGHQIR	378	11	52	81		12062

Table XVII
HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*1101	SEQ ID NO.
POL	GIPHPAGLKKK	282	11	53	84		12063
POL	IGGFIKVR	137	8	53	83		12064
POL	GFIKVRQY	139	8	53	83		12065
POL	PIETVPVK	190	8	53	83		12066
POL	ETVPVKLK	192	8	53	83	0.0001	12067
POL	ELELAENR	489	8	53	83		12068
POL	QLKGEAMH	796	8	53	83		12069
POL	ESMNKELK	904	8	53	83		12070
POL	SMNKELKK	905	8	53	83		12071
POL	GIGGFIKVR	136	9	53	83	0.0005	12072
POL	GIGGFIKVRQY	138	9	53	83	0.0001	12073
POL	GIGGFIKVRQY	135	10	53	83	0.0002	12074
POL	IGGFIKVRQY	137	10	53	83	0.0002	12075
POL	ISPIETVPVK	188	10	53	83	0.0310	12076
POL	PIETVPVKLK	190	10	53	83	0.0001	12077
POL	EAELELAENR	487	10	53	83		12078
POL	LVAVIIVASGY	826	10	53	83		12079
POL	GIGGFIKVRQY	136	11	53	83		12080
POL	PIETVPVK	187	11	53	83		12081
POL	ILVAVIIVASGY	825	11	53	83		12082
POL	FVNTPLVK	608	9	54	86	0.0660	12083
POL	GIPHPAGLKK	282	10	54	86	0.1700	12084
POL	QNFVVYR	973	8	54	84		12085
POL	PIPVNIIGR	166	9	54	84	0.0001	12086
POL	LAENREILK	492	9	54	84	0.0003	12087
POL	ELAENREILK	491	10	54	84		12088
POL	EFVNTPLVK	607	10	54	84		12089
POL	PLTEEKIK	212	8	55	86	0.0003	12090
POL	LFLDGIDK	752	8	55	86		12091
POL	GIPHPAGLKK	282	9	56	86		12092
POL	LGIPHPAGLKK	281	10	56	89	0.0650	12093
POL	QLGIPHPAGLKK	280	11	56	89	0.0150	12094
POL	VTVLDVGDAY	295	10	56	89		12095
POL	ELKKIIGQVR	909	10	56	88	0.0004	12096
POL	DFWEVQLGIPH	275	11	56	88		12097
POL	SVTVLDVGDA	294	11	56	88		12098
POL	KTAVQMAVFI	925	11	56	88		12099
POL	VNTPLVK	609	8	57	88		12100
POL	AIKKKDKTK	251	9	57	89		12101
POL	TVLDVGDAY	296	9	57	89	0.0086	12102
POL	TPDKKHQK	404	9	57	89	0.0056	12103
POL	FAIKKKDKTK	250	10	57	89	0.0042	12104
POL	NTPLVKLWY	610	10	57	89	0.0002	12105
POL	AIKKKDKTKW	251	11	57	89	0.0002	12106
POL	VNTPLVKLW	609	11	57	89		12107
POL	MAVFIHFKR	930	11	57	89		12108
POL	GGIGYSAGER	941	11	57	89		12109
POL	KDSTKWRK	255	8	58	91		12110
							12111
							12112

Table XVII
HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
POL	EVOLGIPH	278	8	58	91		12113
POL	GGNEQVDK	735	8	58	91		12114
POL	FIHNFRRK	933	8	58	91		12115
POL	GGYSAGER	944	8	58	91		12116
POL	RVYRDSR	976	8	58	91		12117
POL	IGGNEQVDK	734	9	58	91		12118
POL	VFIHNFRRK	932	9	58	91	0.0001	12119
POL	IGGYSAGER	943	9	58	91	0.0003	12120
POL	GIGGNEQVDK	733	10	58	91	0.0001	12121
POL	PAETGOETAY	842	10	58	91		12122
POL	AVFIHNFRRK	931	10	58	91	0.8500	12123
POL	GIGGYSAGER	942	10	58	91	0.0001	12124
POL	STKWRKLVDK	257	11	58	91		12125
POL	KIGGNEQVDK	732	11	58	91		12126
POL	AVHVASGY	828	8	59	92		12127
POL	ETGOETAY	844	8	59	92		12128
POL	GIWQLDCTH	811	9	59	92		12129
POL	VAVIIVASGY	827	9	59	92	0.0001	12130
POL	KGPALLWK	988	9	59	92	0.0007	12131
POL	EVNIVDSQY	684	10	59	92		12132
POL	PGIWLDCSTH	810	10	59	92		12133
POL	TAVQMAVFIH	926	10	59	92	0.0110	12134
POL	VGKLNWASQI	450	11	59	92		12135
POL	NFKRKGIGGY	936	11	59	92		12136
POL	QLDCTHLEGG	814	10	60	95	0.0003	12137
POL	DFRELNR	265	8	60	94		12138
POL	VLDVGDAY	297	8	60	94		12139
POL	KNLKTGKY	539	8	60	94		12140
POL	VDFRELNR	264	9	60	94		12141
POL	MGYELHPDK	419	9	60	94		12142
POL	KLNWASQIY	452	9	60	94	0.0960	12143
POL	AVQMAVFIH	927	9	60	94	0.0006	12144
POL	MAVFIHFK	930	9	60	94		12145
POL	LVDRELNR	263	10	60	94	0.3000	12146
POL	WMGYELHPDK	418	10	60	94		12147
POL	QMAVFIHFK	929	10	60	94	0.0004	12148
POL	MAVFIHFKR	930	10	60	94	0.6400	12149
POL	KLVDRELNR	262	11	60	94	0.0083	12150
POL	QMAVFIHFK	929	11	60	94		12151
POL	LNWASQIY	453	8	61	95		12152
POL	NDIQKLVGK	444	9	61	95		12153
POL	LDCTHLEGG	815	9	61	95		12154
POL	VNDIQKLVGK	443	10	61	95		12155
POL	TVNDIQKLVGK	442	11	61	95	0.1700	12156
POL	VDFRELNR	264	8	62	97		12157
POL	WTVNDIQK	441	8	62	97	0.0001	12158
POL	DIQKLVGK	445	8	62	97		12159
POL	NIVTDSQY	686	8	62	97		12160
POL	DCTHLEGG	816	8	62	97		12161
POL	AVFIHFK	931	8	62	97	0.0380	12162

Table XVII
HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SFQ ID NO.
POL	VFIHFKR	932	8	62	97		12163
POL	LVDRELNK	263	9	62	97	0.0300	12164
POL	VNIVTDSQY	685	9	62	97		12165
POL	AVFIHFKR	931	9	62	97	1.8000	12166
POL	MIGGIGGFIK	133	10	62	97	0.0550	12167
POL	KLVDRELNK	262	10	62	97	0.0900	12168
POL	KMIGGIGGFIK	132	11	62	97	0.7000	12169
POL	NVLPGQWK	336	8	63	100	0.0012	12170
POL	IGGIGGFIK	134	9	63	98	0.0037	12171
POL	YNVLPQGWK	335	9	63	98	0.0001	12172
POL	GGIGGFIK	135	8	64	100		12173
POL	FLWMGYELH	416	9	64	100		12174
POL	PFLWMGYELH	415	10	64	100		12175
REV	GTQTRKNR	37	9	01	50		12176
REV	TTRQARRNR	37	9	01	50		12177
REV	GTQTRKNRR	37	10	01	50		12178
REV	TTRQARRNR	37	10	01	50		12179
REV	GTQTRKNRR	37	11	01	50		12180
REV	TTRQARRNR	37	11	01	50		12181
REV	GTETGVGR	103	8	06	19		12182
REV	QGTETGVGR	102	9	06	19		12183
REV	LLKTVRLIK	12	9	10	16		12184
REV	GDSDELLK	6	9	11	17		12185
REV	PLQLPIER	76	9	11	17		12186
REV	SGDSDELLK	5	10	11	17		12187
REV	RSQDSDELLK	4	11	11	17		12188
REV	PVPLQPIER	74	11	11	17		12189
REV	RARQRIK	50	8	12	19		12190
REV	DSDELLK	7	8	12	19		12191
REV	ILSTCLGR	63	8	12	19		12192
REV	RILSTCLGR	62	9	12	19		12193
REV	SNPTSPETGR	27	11	12	19		12194
REV	AVRIKILY	17	9	13	20		12195
REV	QLPPLERLH	78	9	13	20		12196
REV	PSPEGRQAR	31	10	13	20		12197
REV	KNRRRRWRER	43	10	13	20		12198
REV	PSPECTROAR	31	11	13	20		12199
REV	PLQLPPLERLH	76	11	13	20		12200
REV	GTQARKNRR	36	11	14	22		12201
REV	RARQRIH	50	8	15	24		12202
REV	GTQARKNRR	36	9	15	23		12203
REV	GTQARKNRR	36	10	15	25		12204
REV	QARKNRRRR	40	9	16	25		12205
REV	QARKNRRRR	40	11	16	27		12206
REV	QARKNRRRR	40	8	17	28		12207
REV	IKILYQSNPY	20	11	18	30		12208
REV	KNRRRRWRA	43	10	19	33		12209
REV	KNRRRRWR	43	8	21	36		12210
REV	RNRRRRWRA	43	10	23	41		12211
REV	KILYQSNPY	22	9	26			12212

Table XVII
HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
REV	ILYQSNPY	23	8	27	42		12213
REV	EGTRQARR	35	8	27	42		12214
REV	EGTRQARRNR	35	10	27	42		12215
REV	EGTRQARRNR	35	11	27	42		12216
REV	GTRQARRNR	36	9	34	53		12217
REV	GTRQARRNR	36	10	34	53		12218
REV	GTRQARRNR	36	11	34	53		12219
REV	PVPLQLPPLER	74	11	34	53		12220
REV	PLQLPPLER	76	9	35	55		12221
REV	QARRNRNR	40	11	37	58		12222
REV	QARRNRNR	40	8	38	59		12223
REV	QARRNRNR	40	9	38	59		12224
REV	RNRNRNR	43	8	40	63		12225
TAT	PGGYPRRK	104	8	01	50		12226
TAT	AGPGGYPRR	102	9	01	50		12227
TAT	TGPGGQPC	102	9	01	50		12228
TAT	ETGPGQPC	101	10	01	50		12229
TAT	KAGPGGYPRR	101	10	01	50		12230
TAT	AGPGGYPRRK	102	10	01	50		12231
TAT	KAGPGGYPRR	101	11	01	50		12232
TAT	GGYPRRGSC	105	11	01	50		12233
TAT	ACTNICYK	24	8	10	16		12234
TAT	TACTNICYK	23	9	10	16		12235
TAT	CNNICYCK	25	8	11	17		12236
TAT	YCKKCCFH	29	8	11	17		12237
TAT	YCKKCCYH	29	8	11	17		12238
TAT	VDPRLEPWK	4	9	11	17		12239
TAT	ACNNICYCK	24	9	11	17		12240
TAT	PVDPRLEPWK	3	10	11	17	0.0001	12241
TAT	VDPRLEPWKH	4	10	11	17		12242
TAT	TACNNICYCK	23	10	11	17		12243
TAT	PVDPRLEPWK	3	11	11	17		12244
TAT	RGDPTGPKES	84	11	11	17		12245
TAT	GDPTGPKESK	85	11	11	17		12246
TAT	ESKKKVESK	93	9	12	19		12247
TAT	GDPTGPKESK	85	10	12	19		12248
TAT	PTGPKESKKK	88	10	12	19		12249
TAT	TGPKESKKK	89	9	13	20		12250
TAT	LNKGLGISY	42	9	14	22		12251
TAT	FLNKGLGISY	41	10	14	22		12252
TAT	PVDNLEPWN	3	11	14	22		12253
TAT	CFLNKGLGISY	40	11	14	22		12254
TAT	LNKGLGISYGR	42	11	14	22		12255
TAT	WNHPSQPK	14	9	15	23		12256
TAT	RGDPTGPK	84	8	16	25		12257
TAT	VDNLEPWNH	4	10	16	25		12258
TAT	PNLEPWNH	9	8	17	27		12259
TAT	ACNNICYCK	24	8	17	27		12260
TAT	TACNNICYCK	23	9	17	27		12261
TAT	PTGPKESKK	88	9	18	28		12262

Table XVII
HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
TAT	TGPKESKK	89	8	19	30		12263
TAT	PTGPKESK	88	8	20	31		12264
TAT	YGRKKRRQR	50	11	22	34		12265
TAT	YGRKKRRQR	50	10	38	59		12266
TAT	ISYGRKKRRQR	48	11	39	61		12267
TAT	YGRKKRRQR	50	9	41	64		12268
TAT	GISYGRKKRR	47	10	45	70	0.0001	12269
TAT	LGISYGRKKRR	46	11	45	70	0.0005	12270
TAT	ISYGRKKRR	48	9	46	72		12271
TAT	GLGISYGRKKR	45	11	54	86		12272
TAT	GLGISYGR	45	8	55	87		12273
TAT	GLGISYGRK	45	9	55	87	0.0006	12274
TAT	GLGISYGRK	45	10	55	87		12275
TAT	KGLGISYGR	44	9	55	86	0.0180	12276
TAT	KGLGISYGRK	44	10	55	86	0.0007	12277
TAT	KGLGISYGRKK	44	11	55	86		12278
TAT	GISYGRKKR	47	9	57	89	0.0005	12279
TAT	LGISYGRKKR	46	10	57	89		12280
TAT	LGISYGRK	46	8	58	91		12281
TAT	GISYGRKK	47	8	58	91		12282
TAT	ISYGRKKR	48	8	58	91		12283
TAT	LGISYGRKK	46	9	58	91	0.0005	12284
VIF	LIVWQVDR	8	8	10	16		12285
VIF	RMRLNTWK	15	8	10	16		12286
VIF	LKPKKIK	158	8	10	16		12287
VIF	KGWYFRHHY	36	9	10	16		12288
VIF	ALIKPKKIK	157	9	10	16		12289
VIF	VDRMLNTWK	13	10	10	16		12290
VIF	GVSEWRLRR	87	10	10	16		12291
VIF	QVDRMLNTW	12	11	10	16		12292
VIF	RLVTTYWGL	65	11	10	16		12293
VIF	QTGERDWHLG	75	11	10	16		12294
VIF	GVSEWRLRR	87	11	10	16		12295
VIF	IDPDLADQLIH	103	11	10	16		12296
VIF	LVEDRWKPKQ	178	11	10	16		12297
VIF	SIEWRLRR	89	8	11	17		12298
VIF	TALIKPKK	156	8	11	17		12299
VIF	LVEDRWK	178	8	11	17		12300
VIF	VSIEWRLRR	88	9	11	17		12301
VIF	SIEWRLRRY	89	9	11	17		12302
VIF	LTALIKPKK	155	9	11	17		12303
VIF	KLVEDRWK	177	9	11	17		12304
VIF	VSIEWRLRRY	88	10	11	17		12305
VIF	GLADQLIHMH	106	10	11	17		12306
VIF	ALTALIKPKK	154	10	11	17		12307
VIF	WNKPQKTRGH	183	10	11	17		12308
VIF	PGLADQLIHMH	105	11	11	17		12309
VIF	GLADQLIHMH	106	11	11	17		12310
VIF	LALTALIKPKK	153	11	11	17		12311
VIF	WNKPQKTRGH	183	11	11	17		12312

Table XVII
HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*101	SEQ ID NO.
VIF	WFYRIHYESR	38	11	12	19		12313
VIF	KGWYFRHH	36	8	12	19		12314
VIF	WGLQTGER	72	8	12	19		12315
VIF	QTGERDWH	75	8	12	19		12316
VIF	IVWQVDRMK	9	9	12	19		12317
VIF	KRTWNSLVK	17	10	12	19		12318
VIF	LVKHHMYVSK	24	10	12	19		12319
VIF	GLQTGERDWH	73	10	12	19		12320
VIF	TGERDWHLGH	77	10	12	19		12321
VIF	HGVSEWRRLR	86	10	12	19		12322
VIF	IVWQVDRMKI	9	11	12	19		12323
VIF	KRTWNSLVK	17	11	12	19		12324
VIF	SLVKHHMYVS	23	11	12	19		12325
VIF	LVKHHMYVSK	24	11	12	19		12326
VIF	WGLQTGERD	72	11	12	19		12327
VIF	WFYRIHYESR	38	10	13	21		12328
VIF	QVDRMKIR	12	8	13	20		12329
VIF	HIPLGDAR	56	8	13	20		12330
VIF	ADQLIHMH	108	8	13	20		12331
VIF	CFDSAIR	119	8	13	20		12332
VIF	FSDSAIRK	120	8	13	20		12333
VIF	SLOYLALK	149	8	13	20		12334
VIF	LALIKPK	155	8	13	20		12335
VIF	LADQLIHMH	107	9	13	20		12336
VIF	ADQLIHMHY	108	9	13	20		12337
VIF	CFDSAIRK	119	9	13	20		12338
VIF	GSLOYLALK	148	9	13	20		12339
VIF	ALTALIKPK	154	9	13	20		12340
VIF	SVKKLTEDR	174	9	13	20		12341
VIF	EVHPLGDAR	54	10	13	20		12342
VIF	LADQLIHMHY	107	10	13	20		12343
VIF	DCFESAIRK	118	10	13	20		12344
VIF	VGSLOYLALK	147	10	13	20		12345
VIF	LALTALIKPK	153	10	13	20		12346
VIF	PSYKKLTEDR	173	10	13	20		12347
VIF	FDCFESAIRK	117	11	13	20		12348
VIF	YLALTALIKPK	152	11	13	20		12349
VIF	FSESARK	120	8	14	22		12350
VIF	IVSPRCEY	133	8	14	22		12351
VIF	GVSEWRRLR	87	9	14	22		12352
VIF	ADQLIHLYY	108	9	14	22		12353
VIF	CFESAIRK	119	9	14	22		12354
VIF	VDRMRIRTWK	13	10	14	22		12355
VIF	LADQLIHLYY	107	10	14	22		12356
VIF	RCDYQAGHINK	137	10	14	22		12357
VIF	QVDRMRIRTW	12	11	14	22		12358
VIF	RRTWNSLVK	17	11	14	22		12359
VIF	RMIRITWK	15	8	15	23		12360
VIF	RTWKSIVK	19	8	15	23		12361
VIF	VSIEWRLR	88	8	15	23		12362

Table XVII
HLV A11E Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
VIF	ADQLIHLY	108	8	15	23		12363
VIF	RTWKSIVKH	19	9	15	23		12364
VIF	QGVSEWRK	86	9	15	23		12365
VIF	LADQLIHLY	107	9	15	23		12366
VIF	AIRKAILGH	124	9	15	23		12367
VIF	CDYQAGHNK	138	9	15	23		12368
VIF	RRTWKSIVK	17	10	15	23		12369
VIF	RRTWNSLVK	17	10	15	23		12370
VIF	RTWKSIVKHH	19	10	15	23		12371
VIF	SAIRKAILGH	123	10	15	23		12372
VIF	RRTWKSIVK	17	11	15	23		12373
VIF	LQQGVSEWR	84	11	15	23		12374
VIF	VDPLGLADQLIH	103	11	15	23		12375
VIF	ITTYWGLH	68	8	16	25		12376
VIF	GVSEWRK	87	8	16	25		12377
VIF	RCDYQAGHI	137	8	16	25		12378
VIF	LALTALIK	153	8	16	25		12379
VIF	VITYWGLH	67	9	16	25		12380
VIF	YLALTALIK	152	9	16	25		12381
VIF	KTKGHRGSH	188	9	16	25	0.0001	12382
VIF	LVITYWGLH	66	10	16	25		12383
VIF	WNPQKTKGHI	183	10	16	25		12384
VIF	WNPQKTKGH	183	11	16	25		12385
VIF	EDRWNPQKT	180	11	17	27		12386
VIF	WNPQKTK	183	8	18	28		12387
VIF	KSLVKHHMY	22	9	18	28		12388
VIF	EDRWNPQKT	180	11	18	28		12389
VIF	RCEYQAGHKN	137	10	19	30		12390
VIF	HIPLGEAR	56	8	20	31		12391
VIF	WNPQKTR	183	8	20	31		12392
VIF	EVHPLGEAR	54	10	20	31		12393
VIF	ITGERDWH	75	8	21	33		12394
VIF	DLADQLIH	106	8	21	33		12395
VIF	PDLADQLIH	105	9	21	33		12396
VIF	GLHTGERDWH	73	10	21	33		12397
VIF	WGLHTGERD	72	11	21	33		12398
VIF	VSPRCEYQAG	134	11	21	33		12399
VIF	LTEDRWNPQ	178	11	21	33	0.0130	12400
VIF	GSHTMNGH	194	8	22	34		12401
VIF	RGSHTMNGH	193	9	22	34		12402
VIF	TTYWGLHTGE	69	11	22	34		12403
VIF	HLGHGVSEW	83	11	22	34		12404
VIF	NSLVKHHMY	22	9	24	38		12405
VIF	WNSLVKHHM	21	10	24	38		12406
VIF	QGVSEWR	86	8	25	39		12407
VIF	LQQGVSEWR	84	10	25	39		12408
VIF	HLQQGVSEW	83	11	25	39		12409
VIF	RCEYQAGH	137	8	26	41		12410
VIF	RTWNSLVKH	19	9	26	41		12411
VIF	RTWNSLVKHH	19	10	26	41		12412

Table XVII
HIV-1 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*1101	SEQ ID NO.
VIF	RTWNSLVK	19	8	27	42		12413
VIF	HGVSEWR	86	8	27	42		12414
VIF	GLADQLH	106	8	27	42		12415
VIF	PGLADQLH	105	9	27	42		12416
VIF	LGHGVSEWR	84	10	27	42		12417
VIF	YFDCFSASIR	116	11	27	42		12418
VIF	WGLHTGR	72	8	28	44		12419
VIF	DCFSASIR	118	9	28	44		12420
VIF	FDCFSASIR	117	10	28	44		12421
VIF	WNSLVKHH	21	8	29	45		12422
VIF	CFSESAR	119	8	29	45		12423
VIF	KLTEDRWNK	177	9	29	45	0.2700	12424
VIF	LTEDRWNK	178	8	31	48	0.0045	12425
VIF	IVWQVDRMRI	9	11	33	52		12426
VIF	QVDRMRIR	12	8	34	53		12427
VIF	EDRWNKPOK	180	9	39	61		12428
VIF	VMIVWQVDR	7	11	41	64		12429
VIF	QVMIVWQVDR	6	10	43	67		12430
VIF	MIVWQVDRM	8	10	43	67	0.0001	12431
VIF	AGHINKVGSLO	142	11	43	67		12432
VIF	SLVKHHMY	23	8	44	69		12433
VIF	VMIVWQVDR	7	9	44	69	0.0220	12434
VIF	MIVWQVDR	8	8	46	72		12435
VIF	IVWQVDRMR	9	9	47	73	0.0007	12436
VIF	HNKVGSLQY	144	9	47	73		12437
VPR	#LPGRGR	85	8	01	50		12438
VPR	NIRGRVR	85	8	01	50		12439
VPR	WALELLEELK	18	10	09	15		12440
VPR	QLLFVHFR	66	8	10	16		12441
VPR	HSRIGIR	79	8	10	16		12442
VPR	RIGTROR	81	8	10	16		12443
VPR	IGTRQRR	82	8	10	16		12444
VPR	ALELLEELK	19	9	10	16		12445
VPR	RIGTRQRR	81	9	10	16		12446
VPR	HSRIGTRQRR	79	10	10	16		12447
VPR	HSRIGTRQRR	79	11	10	16		12448
VPR	WLHGLGQY	38	8	11	17		12449
VPR	HFRIGCRH	71	8	11	17		12450
VPR	HSRIGTR	79	8	11	17		12451
VPR	FHFRIGCR	69	9	11	17		12452
VPR	LFIHFRIGCR	68	10	11	17		12453
VPR	FHFRIGCRH	69	10	11	17		12454
VPR	FVHFRIGCOH	69	10	11	17		12455
VPR	HFRIGCRHSR	71	10	11	17		12456
VPR	LLFIHFRIGCR	67	11	11	17		12457
VPR	LFIHFRIGCRH	68	11	11	17		12458
VPR	LFVHFRIGCOH	68	11	11	17		12459
VPR	RIGCRHSR	74	8	12	19		12460
VPR	LQGHYNTY	42	9	13	20		12461
VPR	LQGYIYET	42	9	13	20		12462

Table XVII
HIV-1 All Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
VPR	HFPRWLII	33	8	14	22		12463
VPR	KSEAVRHFPR	27	10	14	22		12464
VPR	AVRIHFRIWL	30	11	14	22		12465
VPR	ELKSEAVR	25	8	16	25		12466
VPR	AGVEAIR	55	8	16	25		12467
VPR	ELKSEAVRH	25	9	16	25		12468
VPR	WAGVEAIR	54	9	16	25		12469
VPR	LLEBKSEAVR	22	11	16	25		12470
VPR	DTWAGVEAIR	52	11	16	25		12471
VPR	ELKNEAVR	25	8	17	27		12472
VPR	ELKNEAVRH	25	9	17	27		12473
VPR	LQGHYETY	42	9	17	27		12474
VPR	LLELKNEAVR	22	11	17	27		12475
VPR	EGVEAIR	55	8	18	28		12476
VPR	DTWEGVEAIR	52	11	18	28		12477
VPR	RARNGASR	93	8	19	30		12478
VPR	KNEAVRIHFPR	27	10	19	30		12479
VPR	WLHGLQGH	38	8	20	31		12480
VPR	HGLGQHIY	40	8	20	31		12481
VPR	WLHGLGQHIY	38	10	20	31		12482
VPR	LFHFRIQCQH	68	11	29	45		12483
VPR	FHFRIQCQH	69	10	30	47		12484
VPR	HFPRWLII	33	8	31	49		12485
VPR	AVRHFPRPWL	30	11	31	48		12486
VPR	ILQQLFIHF	63	11	35	55		12487
VPR	RILOQLLFH	62	10	36	56		12488
VPR	ILQQLFIH	63	9	37	58		12489
VPR	EDQGPQREPY	6	10	37	58		12490
VPR	QAPEDQGPQR	3	10	39	62		12491
VPR	WTLLEELK	18	10	42	69		12492
VPR	QGPQREPY	8	8	43	68		12493
VPR	QLLFIHF	66	8	44	69		12494
VPR	HFRIGCQH	71	8	44	69		12495
VPR	TLELEELK	19	9	44	69		12496
VPR	HFRIGCQHSR	71	10	44	69		12497
VPR	RIGCQHSR	74	8	47	73		12498
VPR	EAVRIHFPR	29	8	59	92		12499
VPU	LVQRKQDR	43	8	01	50		12500
VPU	VTLLSSSK	94	8	01	50		12501
VPU	LVQRKQDRR	43	9	01	50		12502
VPU	LVTLSSSK	91	9	01	50		12503
VPU	RIKEIRDDSDY	64	11	01	50		12504
VPU	RIKEIRDDSDY	64	11	01	50		12505
VPU	WTIVFIEYR	34	9	10	16		12506
VPU	TIVFIEYR	35	8	10	16		12507
VPU	IDRLDIR	54	9	10	16		12508
VPU	RLDIRIR	56	9	10	16		12509
VPU	KIDRLDIR	52	10	10	16		12510
VPU	VVWTVFIEYR	31	11	10	16		12511
VPU	WTIVFIEY	34	8	12	19		12512

Table XVII
HIV-1 Mod Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*1101	SEQ ID NO.
VP1	IVFIEYRK	36	8	12	19		12513
VP1	VVWTVFIEY	31	10	12	19		12514
VP1	IVVWTVFIEY	30	11	12	19		12515
VP1	LIDRIR	58	8	14	22		12516
VP1	KIDRLIDR	52	8	15	23		12517
VP1	ILRQRKIDR	46	9	15	23		12518
VP1	KILRQRKIDR	45	10	15	23	0.0001	12519

Table XVIII
HIV-1 A24-Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO.
ENV	HMLQTVW	650	8	10	16		12520
ENV	WFDITNW	767	8	10	16		12521
ENV	WFDITNLW	767	9	10	16		12522
ENV	HYCTPAGFAI	262	10	10	16		12523
ENV	IWNNTWME	717	10	10	16		12524
ENV	WFDITNLW	767	11	10	16		12525
ENV	SYHRLRDLLI	864	11	10	16		12526
ENV	HYCTPAGF	262	8	11	17		12527
ENV	FYATGDIIGDI	367	11	11	17		12528
ENV	FYATGDII	367	8	12	19		12529
ENV	WMEWEREI	723	8	12	19		12530
ENV	GWEALKYL	896	8	12	19		12531
ENV	GWEGLKYL	896	8	12	19		12532
ENV	TWMEWEREI	722	9	12	19		12533
ENV	SYHRLRDLLL	864	10	12	19		12534
ENV	NMTWMEWER	720	11	12	19		12535
ENV	YWGQELKNSA	909	11	12	19		12536
ENV	LYKYKVEI	561	9	13	20		12537
ENV	SYHRLRDFI	864	9	13	20		12538
ENV	SYHRLRDFIL	864	10	13	20		12539
ENV	VMIISFNCGGIE	432	11	13	20		12540
ENV	LFSYHRLRDFI	862	11	13	20		12541
ENV	LFSYHRLRDLL	862	11	13	20		12542
ENV	SYHRLRDLL	864	9	14	22		12543
ENV	KYWWNLLQY	901	10	14	22		12544
ENV	WWNLLQYW	903	8	15	23		12545
ENV	YWWNLLQYW	902	9	15	23		12546
ENV	KWASLWNWF	760	11	15	23		12547
ENV	SFNCRGEF	437	8	16	25		12548
ENV	SFNCRGEFF	437	9	16	25		12549
ENV	KWLWYIKIF	772	9	16	25		12550
ENV	KWLWYIKIFI	772	10	16	25		12551
ENV	RYLRDQQLL	671	9	17	27	0.2300	12552
ENV	RYLRDQQLLGI	671	11	17	27		12553
ENV	RYLRDQQL	671	8	18	28		12554
ENV	SYHRLRDF	864	8	18	28		12555
ENV	AYDTEVHNWV	73	10	18	28		12556
ENV	LFSYHRLRDF	862	10	18	28		12557
ENV	KWLWYIKI	772	8	19	30		12558
ENV	AWDDLRLSL	853	8	20	31		12559
ENV	NMVEQMHEDI	112	10	20	31	0.0004	12560
ENV	AWDDLRLSLCL	853	10	20	31		12561
ENV	NMVEQMHEDIH	112	11	20	31		12562
ENV	AWDDLRLSLCL	853	11	20	31		12563
ENV	FYCNTSGL	445	8	21	33		12564
ENV	FFYCNTSGL	444	9	21	33		12565
ENV	FYCNTSGLF	445	9	21	33		12566
ENV	EFFYCNTSGL	443	10	21	33		12567
ENV	FFYCNTSGLF	444	10	21	33		12568
ENV	EFFYCNTSGLF	443	11	21	33		12569

Table XVIII
HIV-A24 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO.
ENV	VWKEATTL	55	9	22	34	0.0300	12570
ENV	VWKEATTLF	55	10	22	34	0.2700	12571
ENV	LSYHRLRDL	862	10	22	34		12572
ENV	SYHRLRDL	864	8	23	36		12573
ENV	NWLWYIKI	772	8	25	39		12574
ENV	NWLWYIKIF	772	9	25	39		12575
ENV	KYKVKIEPL	563	10	25	39		12576
ENV	NWLWYIKIFI	772	10	25	39		12577
ENV	GFLALAWDDL	848	10	25	39		12578
ENV	RYLKDOQLLGI	671	11	25	39		12579
ENV	KWASLWNW	760	8	26	41		12580
ENV	KWASLVNWF	760	9	26	41		12581
ENV	HYCAPAGF	262	8	27	42		12582
ENV	HYCAPAGFAI	262	10	27	42		12583
ENV	HYCAPAGFAIL	262	11	27	42		12584
ENV	QMIEDIISL	116	9	29	45		12585
ENV	LYKYVVKI	561	9	29	45	0.0200	12586
ENV	RYLKDOQLL	671	9	29	45	0.7600	12587
ENV	QMIEDIISLW	116	10	29	45		12588
ENV	GYSPLSFQTL	806	10	29	45		12589
ENV	RYLKDOQL	671	8	30	47		12590
ENV	IFIMIVGGI	779	10	33	52		12591
ENV	IMIVGGI	781	10	34	54		12592
ENV	IMIVGGI	781	8	35	56		12593
ENV	SNCGGEFF	437	9	35	55		12594
ENV	SNCGGEFF	437	8	36	56		12595
ENV	DMRDNRSEL	552	10	37	58		12596
ENV	TMGAASITL	615	9	39	61		12597
ENV	IFIMIVGGL	779	9	41	64		12598
ENV	WYIKIFIMI	775	9	43	67		12599
ENV	WYIKIFIMI	774	10	43	67		12600
ENV	IWGCCKLI	681	8	48	75		12601
ENV	IWGCCKLI	681	9	48	75		12602
ENV	IWGCCKLI	774	8	49	77	0.0270	12603
ENV	WYIKIFI	49	8	55	86		12604
ENV	VYGVVW	49	8	55	86		12605
ENV	LYPLASLKS	544	10	09	17		12606
GAG	LYPLASLKS	544	11	09	17		12607
GAG	KYKLKHIV	29	9	10	16		12608
GAG	GWMTSNPI	269	9	10	16		12609
GAG	IMQKSNF	408	8	11	17		12610
GAG	LYCVHQL	87	8	13	20		12611
GAG	MYSPTSILDI	300	10	13	20		12612
GAG	MYSPTSILDI	299	11	13	20		12613
GAG	RMYSPTSI	299	8	14	22		12614
GAG	MYSPTSIL	300	8	14	22		12615
GAG	RMYSPTSIL	299	9	14	22		12616
GAG	RFVNPGL	45	8	16	25		12617
GAG	LFNTVATL	80	8	16	25		12618
GAG	WMTSNPI	270	8	16	25		12619
GAG	NWMTDTLL	339	8	16	25		12619

Table XVIII
HIV-1 24-Mer Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO.
GAG	KYRLKHLVW	29	9	16	25		12620
GAG	RFVAVNPGLL	45	9	16	25	0.0100	12621
GAG	LYCVHQRI	87	8	18	28		12622
GAG	GWMTNNPPI	269	9	18	28	0.0140	12623
GAG	RFALNPGL	45	8	20	31		12624
GAG	WMTNNPPI	270	8	20	31		12625
GAG	RFALNPGLL	45	9	20	31		12626
GAG	LYNTVATL	80	8	22	34		12627
GAG	AWVKVIEKA	175	11	24	38		12628
GAG	AMQMLKETI	218	9	26	41		12629
GAG	IMMQRGNF	408	8	27	42		12630
GAG	DYVDRFEKTL	319	10	27	42		12631
GAG	CFNCGKEGHI	425	10	27	42		12632
GAG	CFNCGREGHL	425	10	27	42		12633
GAG	DYVDRFYKTL	319	10	28	44		12634
GAG	AWVKVVEKA	175	11	28	44	0.0010	12635
GAG	NYPIVQNL	152	8	31	48		12636
GAG	AMQMLKDTI	218	9	33	52		12637
GAG	PFRDYVDRFF	316	10	35	55		12638
GAG	NWMTETLL	339	8	36	56		12639
GAG	RMSPVSI	299	11	38	59		12640
GAG	RMSPVSILDI	299	8	40	63		12641
GAG	RMSPVSIL	299	9	40	63		12642
GAG	MSPVSILDI	300	10	40	63		12643
GAG	MSPVSIL	300	8	42	66		12644
GAG	QMRPRGSDI	248	10	44	69		12645
GAG	VWASRELERF	36	10	45	70		12646
GAG	AFSPEVPMF	184	10	50	78	0.0078	12647
GAG	IYKRWIIL	285	8	54	84		12648
GAG	IYKRWIILGL	285	10	54	84	0.0140	12649
GAG	RWILGLNKI	288	10	56	88		12650
GAG	PFRDYVDRF	316	9	63	98		12651
NEF	PMYKGAFF	105	8	12	19		12652
NEF	TYKGAFFL	107	8	12	19		12653
NEF	PMYKGAFFL	105	10	12	19		12654
NEF	VYHTQGF	192	8	13	20		12655
NEF	LWVYHTQGF	190	9	13	20		12656
NEF	LWVYHTQGF	190	10	13	20		12657
NEF	NYTPGTRF	206	10	13	20		12658
NEF	VYHTQGF	192	11	13	20		12659
NEF	RFPLTFGWCF	216	10	17	27		12660
NEF	IYSKKRQEI	175	9	18	29		12661
NEF	IYSKKRQEI	175	10	18	29		12662
NEF	AFDLSFLL	111	8	18	28		12663
NEF	DWQNYTPGPG	203	11	18	28		12664
NEF	RFPLTFGW	216	8	20	32		12665
NEF	NYTPGPGI	206	8	20	31		12666
NEF	KWSKSSIVGW	4	10	20	31		12667
NEF	RYPLTFGWCF	216	10	21	33		12668
NEF	VYHTQGYF	192	8	21	33		12669

Table XVIII
 HIV-1 A24 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO.
NEF	LWVYHTQGYF	190	10	21	33		12670
NEF	VYHTQGYFPD	192	11	21	33		12671
NEF	SFELKEKGGI	115	10	22	34		12672
NEF	FFLKEKGGI	116	9	26	41		12673
NEF	RYPLTFGW	216	8	27	43		12674
NEF	HFLKEKGGI	116	9	29	45		12675
NEF	TFGWCFKL	222	8	40	63		12676
NEF	GFPVRPQVPL	93	10	48	75		12677
POL	APQGEAREF	7	10	10	16		12678
POL	NMLTQLGCTL	175	10	10	16		12679
POL	TWETWWTY	589	10	10	16		12680
POL	TWWTYWQA	592	11	10	16		12681
POL	CWWAGIQEFG	882	10	11	17		12682
POL	IWGIKPKF	574	8	11	17		12683
POL	WYQLETEPI	618	9	11	17		12684
POL	WWAGIQEFG	883	9	11	17		12685
POL	IYPIKVKQL	459	10	11	17		12686
POL	LWYQLETEPI	617	10	11	17		12687
POL	WWAGIQEFG	883	11	11	17		12688
POL	QYDQPIEI	145	9	12	19		12689
POL	KWTVQPIVL	427	9	12	19		12690
POL	LWQRLVTVK	92	11	12	19		12691
POL	TWWTYWQA	592	11	12	19		12692
POL	SFSFQITLW	84	10	13	20		12693
POL	SFSFQITL	84	9	14	22		12694
POL	WYQLEKDP	618	9	14	22		12695
POL	YYRDSRDPL	978	9	14	22		12696
POL	WWTDYWQAT	593	10	14	22		12697
POL	LWYQLEKDP	617	10	14	22		12698
POL	VYRDSRDPL	977	10	14	22		12699
POL	YYRDSRDPL	978	10	14	22		12700
POL	LWQRLVTVK	92	11	14	22		12701
POL	PERKQNPDI	359	11	14	22		12702
POL	WWTDYWQAT	593	11	14	22		12703
POL	GYSAGERIVDI	945	11	14	22		12704
POL	VYRDSRDPL	977	11	14	22		12705
POL	FFREDLAF	1	8	15	23		12706
POL	IYPIKVKRQL	459	10	15	23		12707
POL	PERKQNPDI	359	9	16	25		12708
POL	RWKPKMIGGI	128	10	17	27		12709
POL	IWGIKPKFKL	574	10	17	27		12710
POL	YFSVPLDKDF	304	10	18	29		12711
POL	LWKGPAKLL	986	9	18	28		12712
POL	NMLTQIGCTL	175	10	18	28		12713
POL	IYAGIKVKQL	459	10	18	28		12714
POL	LWKGPAKLLW	986	10	18	28		12715
POL	AYFSVPLDKDF	303	11	18	28		12716
POL	AMASDFNLPI	773	11	18	28		12717
POL	LWKGPAKL	986	8	19	30		12718
POL	DYWQATWIPE	596	11	19	30		12719

Table XVIII
HIV-1 A24 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	A*2401	SEQ ID NO.
POL	DYWQATWI	596	8	20	31		12720
POL	KFKLPQKETW	580	11	20	31		12721
POL	CWAGIKQEF	882	10	21	33		12722
POL	LWQRPLVTI	92	9	21	33	0.0190	12723
POL	WWAGIKQEF	883	9	21	33	0.0120	12724
POL	WWAGIKQFEG	883	11	21	33		12725
POL	NFPQITLW	86	8	22	34		12726
POL	AWVPAHKGI	726	9	22	34		12727
POL	SFPQITLW	86	8	23	36		12728
POL	WWTEYWQAT	593	10	23	36		12729
POL	WWTEYWQAT	593	11	23	36		12730
POL	PYNTPIFAI	244	9	24	38		12731
POL	YFLKLAGRW	851	10	25	39		12732
POL	AYFLKLAGR	850	11	25	39		12733
POL	KFLPQKETW	580	11	26	41		12734
POL	QYDQILIEI	145	9	27	42		12735
POL	NWASQIYAGI	454	10	27	42		12736
POL	KWTVQPIQL	427	9	28	44		12737
POL	NWASQIYPGI	454	10	29	45		12738
POL	IWGTKTPKFL	574	10	30	47		12739
POL	WYQLEKEPI	618	9	31	48	0.0001	12740
POL	VYDPSKDLJ	509	10	31	48	0.0150	12741
POL	LYYQLEKEPI	617	10	31	48		12742
POL	YFILKLAGRW	851	10	31	48		12743
POL	AYFILKLAGR	850	11	31	48		12744
POL	EMEKEGKISKI	229	11	32	50		12745
POL	EYWOATWIPE	596	11	33	52		12746
POL	YYRDSRDP	978	9	34	53		12747
POL	VYRDSRDP	977	10	34	53		12748
POL	VYRDSRDP	978	10	34	53		12749
POL	VYRDSRDP	977	11	34	53		12750
POL	YYDPSKDLJ	510	9	35	55		12751
POL	IWKGPAKLL	986	9	35	55		12752
POL	IWKGPAKLLW	986	10	35	55		12753
POL	IWKGPAKL	986	8	36	56		12754
POL	EYWQATWI	596	8	37	58	0.0310	12755
POL	PYNTPIFAI	244	9	37	58		12756
POL	SWVPAHKGI	726	9	37	58		12757
POL	KYTAFTPSI	315	10	37	58		12758
POL	IFQSSMTKI	348	9	38	59	0.0029	12759
POL	IFQSSMTKIL	348	10	38	59	0.0002	12760
POL	VYDPSKDL	509	9	39	61	0.0004	12761
POL	IYQEPFKNL	533	9	40	63	0.0520	12762
POL	GYSAGERIIDI	945	11	40	63		12763
POL	FFRENLA	1	8	41	64		12764
POL	GYSAGERII	945	9	41	64		12765
POL	GFIKVRQYDQI	139	11	41	64		12766
POL	NWRAMASDF	770	11	41	64		12767
POL	EMEKEGKI	229	8	42	66		12768
POL	DFRKYTAF	312	8	42	66		12769

Table XVIII
HIV-A24 Motif-Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Λ^*2401	SEQ ID NO.
POL	TYQIQEPF	530	9	42	66	0.3000	12770
POL	KWKPKMIGGI	128	10	42	66		12771
POL	DERKYTAFTI	312	10	42	66		12772
POL	QWTYQIQEP	528	11	42	66		12773
POL	YYPDSKDL	510	8	43	67		12774
POL	SMTKILEPF	352	9	43	67	0.0110	12775
POL	NWRAMASDF	770	9	43	67	0.0016	12776
POL	AMASDFNL	773	8	45	70		12777
POL	IWGTKTKF	574	8	48	75		12778
POL	EWEFVNTPL	605	10	50	78		12779
POL	GMDGPKVKQ	201	10	51	80		12780
POL	TIPIWEF	601	8	52	81		12781
POL	YWQATWIFE	597	10	52	81	0.0660	12782
POL	SMNKELKKI	905	9	53	83		12783
POL	SMNKELKKII	905	10	53	83		12784
POL	EFVNTPL	607	8	54	84		12785
POL	GYIEAEVI	834	8	54	84		12786
POL	SWTVNDIQKL	440	10	54	84		12787
POL	EFVNTPLVKL	607	11	54	84		12788
POL	QWPLTEEKI	210	9	56	88		12789
POL	DFWEVQLGI	275	9	56	88		12790
POL	FWEVQLGI	276	8	57	89		12791
POL	GYSAGERI	945	8	57	89		12792
POL	LYVGSLEI	376	9	58	91		12793
POL	KWRKLVDF	259	8	59	92		12794
POL	GWKGSPIF	341	8	59	92		12795
POL	GWKGSPIF	341	9	59	92		12796
POL	IWQLDCTHL	812	9	59	92	0.0095	12797
POL	LWKCEGAVVI	994	10	59	92		12798
POL	KWRKLVDFRE	259	11	59	92		12799
POL	NFKRKGGI	936	8	60	94		12800
POL	GVELHPDKW	420	9	60	94	0.0001	12801
POL	QMAVFHNF	929	9	60	94	0.0190	12802
POL	WMGYELHPDK	418	11	60	94		12803
POL	IYQYMDL	369	8	61	95		12804
POL	YMDLYVGS	372	11	61	95		12805
POL	KMIGGIGGF	132	9	62	97	0.0011	12806
POL	KMIGGIGGF	132	10	62	97	0.0001	12807
POL	QYNVLPQGW	334	9	63	98	0.0036	12808
POL	RYQYNVLPQG	332	11	63	98		12809
POL	PFLWMGYEL	415	9	64	100		12810
REV	RWRERQRI	48	9	11	17		12811
REV	RWRARQRI	48	9	35	55		12812
TAT	CYCKKCCF	28	8	11	17		12813
TAT	CFHCQVCF	34	8	11	17		12814
TAT	CFLNKGLGI	40	9	14	22		12815
VIF	RWQVLIVW	4	8	10	16		12816
VIF	RYSTQVDPGL	98	10	10	16		12817
VIF	CFSDSAIRKAI	119	11	10	16		12818
VIF	QYLALKAL	151	8	11	17		12819

Table XVIII
HIV-A24 Motif Peptides with Binding Information

Protein	Sequence	Position	No. of Amino Acids	Sequence Frequency	Conservancy (%)	Δ^*2401	SEQ ID NO.
VIF	QYLALAL	151	8	12	19		12820
VIF	RMKIRTWNSL	15	10	12	19		12821
VIF	YWGLQTGERD	71	11	12	19		12822
VIF	CFSESARKAI	119	11	12	19		12823
VIF	CFSESARKAI	119	11	12	19		12824
VIF	VWQVDRMKI	10	9	13	20		12825
VIF	IMHYFDCF	113	8	15	23		12826
VIF	RMIRITWNSL	15	10	15	23		12827
VIF	RMIRITWNSL	15	10	15	23		12828
VIF	DWHLGGVSI	81	10	18	28		12829
VIF	YYFDFCESAI	115	11	20	31		12830
VIF	DWHLGGVSI	81	10	21	33		12831
VIF	DWHLGGVSI	81	10	22	34		12832
VIF	YWLHTGERD	71	11	28	44		12833
VIF	QYLALAL	151	9	28	44		12834
VIF	YFDFCESAI	116	10	33	52		12835
VIF	QYLALAL	151	8	43	67		12836
VIF	RWQVMIVW	4	8	48	75		12837
VIF	VWQVDRMRI	10	9	10	16		12838
VPR	IFPRIWLHSL	33	10	10	16		12839
VPR	IFPRIGRHSL	71	11	12	19		12840
VPR	PWLHGLGQIII	37	10	14	22		12841
VPR	QYIYTYGDT	44	11	14	22		12842
VPR	TWEGVEIIRI	53	11	15	23		12843
VPR	TWAGVEAI	53	8	16	25		12844
VPR	TWAGVEAI	53	9	16	25		12845
VPR	TYNTYGDW	46	9	18	28		12846
VPR	TWEGVEAI	53	9	19	30		12847
VPR	TWEGVEAI	53	8	20	31		12848
VPR	IFPRPWHLGL	33	10	24	38		12849
VPR	PYNEWTLLEL	14	9	30	47	0.1400	12850
VPR	IFPRPWHLGL	14	10	30	47		12851
VPR	IFPRPWHLGL	14	9	31	48	0.0580	12852
VPR	IFPRPWHLGL	14	9	40	63		12853
VPR	IFPRPWHLGL	14	10	44	69		12854
VPR	IFPRPWHLGL	14	11	01	25		12855
VPU	NYELAVGAL	5	9	01	25		12856
VPU	NYELAVGAL	5	10	01	25		12857
VPU	DYKLGVGAL	10	9	02	29		12858
VPU	DYKLGVGAL	10	10	02	29		12859
VPU	DYKLGVGAL	10	9	03	43		12860
VPU	DYKLGVGAL	10	10	03	43		12861
VPU	EMGHAPW	89	8	11	17		12862
VPU	VFIEYRKI	37	8	12	19		12863
VPU	EYRKILRQKRI	41	11	13	21		12863

HIV DR Super Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)	SEQ ID NO.
ENV	VSTOLLNG	61	95	KPVVSTQLLLNGSLA	299	29	45	12864
ENV	VVSTQLLN	60	94	IKPVVSTQLLLNGSL	298	29	45	12865
ENV	LTWGIKQL	59	92	LLQLTWGIKQLQAR	651	26	41	12866
ENV	LLSGIVQQQ	58	91	ARQLSGIVQQQSNL	627	22	34	12867
ENV	WATHACVPT	56	88	HNWATHACVPTDPN	79	44	69	12868
ENV	LGAAGSTMG	55	86	LGFLGAAGSTMGAAS	605	36	56	12869
ENV	VRQGSPLS	55	86	VNRVQGSPLSFQT	800	36	57	12870
ENV	LLNGSLAE	54	84	STQLLLNGSLABEEV	303	16	25	12871
ENV	VKLTPLCVT	53	83	KPCVKLTPLCVTLNC	130	29	45	12872
ENV	LRAEAQQH	51	80	NNLLRAEAQQHLLQ	639	18	28	12873
ENV	VSTVQCTHG	51	80	CKNVSTVQCTHGKIF	285	14	22	12874
ENV	LGIWGCSCGK	50	78	QQLGIWGCSCGKLC	676	46	72	12875
ENV	LWDQSLKPC	50	78	IISLWDQSLKPCVKL	121	35	55	12876
ENV	LGFLGAGS	49	77	AVFLGFLGAGSTMG	602	19	30	12877
ENV	WATHACVPT	49	77	VHNVWATHACVPTDP	78	34	53	12878
ENV	WGKQLQAR	49	77	LTWGIKQLQARVLA	654	39	61	12879
ENV	WYIKIFIM	43	67	TNWLWYIKIFIMVIG	771	11	17	12880
ENV	FCASDAKAY	42	66	TTLFCASDAKAYDTE	18	22	28	12881
ENV	IVGGLIGLR	42	66	FIMIVGGLIGLRIVF	780	30	47	12882
ENV	IFIMIVGGL	41	64	YIKIFIMIVGGLIGL	776	30	34	12883
ENV	VYGVVWVK	41	64	WYTVYGVVWVWKEAT	46	22	49	12884
ENV	IKQLQARVL	40	63	VWGIKQLQARVLAVE	656	31	49	12885
ENV	IKIFIMIVG	39	61	LWYIKIFIMIVGGLI	774	31	48	12886
ENV	MGAASITLI	39	61	GSTMGAASITLTVQA	613	28	44	12887
ENV	YIKIFIMIV	39	61	WLWYIKIFIMIVGGL	773	38	59	12888
ENV	ITGLLLTRD	37	58	SSNITGLLLTRDGGK	516	21	33	12889
ENV	IFIHYCAPA	36	56	FEPIPIHYCAPAGFA	255	22	34	12890
ENV	MIWGLLGL	36	56	IFIMIVGGLIGLRIV	779	35	55	12891
ENV	VQARQLLSG	35	55	TLTVQARQLLSGIVQ	622	35	55	12892
ENV	FEPIPIHYC	35	55	KVSFEPIPIHYCAPA	252	17	27	12893
ENV	LRSLCLFSY	35	55	WDDLRLSLCLFSYHRL	854	28	44	12894
ENV	MWKNMVEQ	35	55	NFNMWKNMVEQMHIE	105	11	17	12895
ENV	VINWATHA	35	55	DTEVINWATHACVPT	75	17	27	12896
ENV	WKNMVEQM	35	55	FNMWKNMVEQMHED	106	20	31	12897
ENV	YGVVWVKE	35	55	VTYGVVWVWKEATT	47	22	34	12898
ENV	LLQLTVWGI	34	53	QQHLLQLTVWGIKQL	648	34	53	12899
ENV	IEPLGVAPT	33	52	VVKIEPLGVAPTAK	566	12	19	12900
ENV	IKPVVSTQL	33	52	THGIKPVVSTQLLLN	295	32	50	12901
ENV	LQARVLAVE	33	52	IKQLQARVLAVERYL	659	32	50	12902
ENV	WDDLRLSLCL	33	52	ALAWDDLRLSLCLFSY	851	18	28	12903
ENV	INIHTPHR	01	50	SRPINIHTPHREKR	581	01	2	12904
ENV	INIHTPHR	01	50	RPINIHTPHREKRA	582	01	2	12905
ENV	ITQACPKVS	32	50	TSVITQACPKVSFEP	242	08	13	12906
ENV	IVQQSNLL	32	50	LSGIVQQSNLLRAI	631	26	41	12907
ENV	LGNSTNST	01	50	NKTLGNSTNSTLGN	151	01	2	12908
ENV	VISITRTHRE	01	50	ARPVISTRTHREKRA	580	01	2	12909
ENV	WRWGTFLG	01	50	QNLWRWGTFLGMLM	12	01	5	12910
ENV	WRWGTMLG	01	50	QHLWRWGTMLGMLM	12	03	22	12911
ENV	FAVLSIVNR	31	48	RIVEFAVLSIVNRVQ	791	14	22	12912
ENV	LLNGSLAE	31	48	TQLLLNGSLABEEVV	304	14	22	12913

HIV DR Super Motif Peptides

Protein

Table XXa HIV DR Super Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)	SEQ ID NO.
ENV	LLNATAIAV	15	23	AYSLNATAIAVAEG	918	10	16	12964
ENV	LRIFA VLS	15	23	LGLRIIFAVLSIVN	787	11	17	12965
ENV	VITQACPKV	15	23	NTSVITQACPKVSFE	241	08	13	12966
ENV	YWNLLQYW	15	23	VLKYWNLLQYWSQE	899	07	11	12967
ENV	FAIKCNDK	14	22	PAGFAIKCNDKKFN	266	09	14	12968
ENV	IFAVLSIVN	14	22	LRIIFAVLSIVNRVR	790	13	20	12969
ENV	INCNTSAIT	14	22	YRLNCNTSAITQAC	235	14	16	12970
ENV	LNATAIAVA	14	22	VSLNATAIAVAEGT	919	10	5	12971
ENV	WNSSWSNKS	14	22	NVPWNSSWSNKS LDE	693	03	3	12972
ENV	WNASWSNKS	13	21	NVPWNASWSNKS YED	693	02	9	12973
ENV	ICTTTVPWN	13	20	GKLICTTTVPWNASW	686	06	20	12974
ENV	LLKLTWGI	13	20	QQHLKLTWGIKQL	648	13	8	12975
ENV	LYKYKVEI	13	20	RSELYKYKVEIKPL	558	05	11	12976
ENV	MFLGFLGAA	13	20	LGAMFLGFLGAA GST	600	07	20	12977
ENV	MHSFNCGGE	13	20	EIVMHSFNCGGEFFY	430	13	8	12978
ENV	YWSQELKNS	12	20	LIQYWSQELKNSAVS	906	10	16	12979
ENV	IGAVFLGFL	12	19	AVGIGAVFLGFLGAA	595	04	14	12980
ENV	LIAARTVEL	12	19	DFLIAARTVELLGH	870	09	6	12981
ENV	LICTTTVPW	12	19	SGKLICTTTVPWNAS	304	06	9	12982
ENV	LLNGSLAEG	12	19	TQLLNGSLAEGEIL	906	02	5	12983
ENV	YWGQELKNS	12	19	LVWYWGQELKNSAIS	600	03	3	12984
ENV	IAARTVELL	11	17	FILIAARTVELLGH	871	06	5	12985
ENV	LFGLGFLGAA	11	17	IGALFLGFLGAA GST	911	08	9	12986
ENV	LKNSAVSLL	11	17	SOELKNSAVSLLNAT	593	11	13	12987
ENV	VGIGAVFLG	11	17	KRAVGIGAVFLGFLG	916	09	17	12988
ENV	VSLNATAIA	11	17	NSAVSLNATAIAVA	922	04	14	12989
ENV	YATGDIIGD	11	16	QTFYATGDIIGDIRQ	365	02	6	12990
ENV	IAIAVAEGT	10	16	LDIAIAVAEGTDRI	922	08	3	12991
ENV	IHYCTPAGF	10	16	PIPIHYCTPAGFAIL	258	03	13	12992
ENV	ILGLVICS	10	16	GTILGLVICSASN	19	01	5	12993
ENV	IWNMTWME	10	16	VDEIWNMTWMEWER	714	04	2	12994
ENV	LGLVICS	10	16	TLILGLVICSASN	20	06	6	12995
ENV	LRDFILIAA	10	16	YHRLRDFILIAARTV	865	03	9	12996
ENV	LPLCVTLTD	10	16	CVKLTPLCVTLDCN	132	06	5	12997
ENV	MLQLTVWGI	10	16	QQHMLQLTVWGIKQL	648	08	13	12998
ENV	VRQLLSGIV	10	16	NESVEINCTRPNNNT	338	02	3	12999
ENV	LILGLVICS	09	15	WGTLILGLVICSAS	624	08	13	13000
GAG	VGGHQAAMQ	60	94	LNTVGGHQAAMQMLK	18	07	11	13001
GAG	LLVQANPD	59	92	TETLLVQANPDCKT	209	47	73	13002
GAG	VQANPDCK	59	92	TLLVQANPDCKTIL	342	26	41	13003
GAG	LGLNKIVRM	58	91	WILGLNKIVRMYSF	344	44	69	13004
GAG	LSEGATPD	57	89	FSALSEGATPD LNT	289	55	86	13005
GAG	WILGLNKI	56	88	YKRWILGLNKIVRM	193	29	45	13006
GAG	LEEMMTACQ	55	86	GATLEEMMTACQGVG	286	54	84	13007
GAG	YKRWILGL	54	84	GEIKRWILGLNKI	364	37	42	13008
GAG	YKRWILGL	48	83	VGEIKRWILGLNKI	283	37	58	13009
GAG	VSQNYPIVQ	46	78	SSQVSNQNYPIVQNLQ	145	16	19	13010
GAG	WEKIRLRPG	46	72	LDKWEKIRLRPGGKK	13	16	25	13011
GAG	IAGTTSTLQ	46	72	GSDIAGTTSTLQEQI	254	45	70	13012

6550071 6550071 6550071 6550071 6550071
Table XIXa
HIV DR Super Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)	SEQ ID NO.
GAG	WASRELERF	46	72	HLVWASRELERFALN	34	17	27	13014
GAG	IPMFALSE	45	70	PEVIMFALSSEGAT	187	44	69	13015
GAG	MFSALSEGA	45	70	VIPMFALSSEGATPQ	189	43	67	13016
GAG	VIPMFALS	45	70	SPEVIMFALSSEGA	186	40	63	13017
GAG	MYSPVSILD	41	64	IVRMYSVSLDIRQ	297	23	36	13018
GAG	IVRMYSVPS	40	63	LNKIVRMYSVPSILD	294	39	61	13019
GAG	VRMYSVPSI	40	63	NKIVRMYSVPSILDI	295	38	59	13020
GAG	YSPVSILDI	40	63	VRMYSVPSILDIRQG	298	23	36	13021
GAG	MTETLLVQN	38	59	KNWMTETLLVQNANP	338	34	53	13022
GAG	WMTETLLVQ	37	58	VKNWMTETLLVQAN	337	34	53	13023
GAG	ISPRTLNAW	36	56	HOAISPRTLNAWVKV	165	27	42	13024
GAG	VKNWMTETL	36	56	TQEVKNWMTETLLVQ	314	14	22	13025
GAG	IKCFNCCKE	34	53	QKRKICFNCCKEGHL	418	05	8	13026
GAG	IPVGEIYKR	34	53	NPPIPVGEIYKRWII	277	32	51	13027
GAG	YTAVFMQRG	02	50	KGGYTAVFMQRQNP	399	02	3	13028
GAG	VATLYCVHQ	30	47	YNTVATLYCVHQRIE	81	07	11	13029
GAG	WDLRHPVHA	29	45	AAEWDLRHPVHAGPI	230	22	34	13030
GAG	FLQSRPEPT	28	44	PGNFLQSRPEPTAPP	483	27	43	13031
GAG	EKTLRAEQ	27	42	DRFFKTLRAEQATOE	322	16	25	13032
GAG	MYHQAISPR	27	42	QQQMYHQAISPRTLN	160	26	41	13033
GAG	VHQAISPR	27	42	GQMVHQAISPRTLNA	161	27	42	13034
GAG	YKTLRAEQ	27	42	DRFYKTLRAEQASOE	322	12	19	13035
GAG	VSILDIRQ	25	39	YSPVSILDIRQGPKE	301	24	38	13036
GAG	LAEMSQVT	23	37	ARVLAEMSQVTNSA	384	08	13	13037
GAG	LGKIWPSHK	23	36	ANFLGKIWPSHKGRP	467	22	34	13038
GAG	VKCFNCCKE	23	36	RKTVKCFNCCKEGHI	420	07	11	13039
GAG	YNTVATLYC	23	36	RSLYNTVATLYCVHQ	78	11	17	13040
GAG	LHPVHAGPI	22	34	WDLRHPVHAGPIAPG	233	15	23	13041
GAG	LYNTVATLY	22	34	LRSLYNTVATLYCVH	77	13	20	13042
GAG	MTDTLLVQN	22	34	KNWMTDTLLVQNANP	338	16	25	13043
GAG	WMTDTLLVQ	22	34	VKNWMTDTLLVQNAN	337	16	25	13044
GAG	IEVKDTKEA	21	33	HQRIEVDKTEALDK	91	07	11	13045
GAG	LQGMVHQA	21	33	VQNQQGMVHQAISP	156	15	23	13046
GAG	MTNPPIPV	20	31	IGWMTNPPIPVGEI	268	16	25	13047
GAG	WMTNPPIP	20	30	QIGWMTNPPIPVGE	267	16	25	13048
GAG	IAPQMREP	19	30	AGPIAPQMREPGRS	241	19	30	13049
GAG	VHAGPIAPG	19	30	LHPVHAGPIAPGQMR	236	14	22	13050
GAG	LGPATLEE	18	28	LRALGPATLEEMMT	358	09	14	13051
GAG	VHAGPIPG	18	28	VHPVHAGPIPGQMR	236	10	16	13052
GAG	IPPGQMRP	17	27	AGPIPPGQMRPGRS	241	16	25	13053
GAG	LSPRTLNAW	17	27	HQAISPRTLNAWVKV	165	10	20	13054
GAG	YRLKHLVWA	17	27	KKKYRLKHLVWASRE	27	13	25	13055
GAG	LGPATLEE	16	25	LKALGPAATLEEMMT	358	16	25	13056
GAG	LKALGPAAT	16	25	QEQLKALGPAATLEE	355	16	25	13057
GAG	LKDKPEPLA	01	25	QEQLKDKPEPLASLR	532	01	2	13058
GAG	LSGKLDAAW	16	25	ASVLSGKLDAAWEKI	5	14	22	13059
GAG	MTSNPPIPV	16	25	IGWMTSNPPIPVGEI	268	06	9	13060
GAG	VSILDIKOG	16	25	TQDVKNWMTDTLLVQ	334	11	17	13061
GAG	WMTSNPPIP	16	25	YSPVSILDIKQGPKE	301	16	25	13062
GAG	WMTSNPPIP	16	25	QIGWMTSNPPIPVGE	267	06	10	13063

Table XIXa
HIV DR Super Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)	SEQ ID NO.
GAG	FNTVATLYC	15	23	KSLFNTVATLYCVHQ	78	07	11	13064
GAG	IPMFTALSE	15	23	PEVIPMFTALSEGAT	187	13	20	13065
GAG	LASLSKSLFG	15	23	LYPLASLSKSLFGNDP	544	06	11	13066
GAG	LERFAVNP	15	23	SRLEERFAVNPGLLE	39	14	22	13067
GAG	LFRNTVATLY	15	23	LRSLENTVATLYCVH	77	07	11	13068
GAG	MFTALSEGA	15	23	VIPMFTALSEGAIPQ	189	14	22	13069
GAG	WDRVHPVHA	15	23	AAEWDRVHPVHAGPI	230	12	19	13070
GAG	IVRMYSPTS	14	22	LNKIVRMYSPTSILD	294	13	20	13071
GAG	LERFALNPG	14	22	SRELERFALNPGLE	39	14	22	13072
GAG	LOEQIAWMT	14	22	TSTLQEQIAWMTGNP	261	05	8	13073
GAG	VHPVHAGPI	14	22	WDRVHPVHAGPIPG	233	11	17	13074
GAG	VIPMFTALS	14	22	SPEVIPMFTALSEGA	186	13	20	13075
GAG	VRMYSPTSI	14	22	NKIVRMYSPTSILDI	295	13	20	13076
GAG	LGIWPSNK	13	20	ANFLGKIWPSNKGPR	467	13	20	13077
GAG	MTSPTSILD	13	20	LYPLTSLKSLFGNDP	544	04	7	13078
GAG	YKLKHVWA	13	20	IVRMYSPTSILDIRQ	297	12	19	13079
GAG	LTSLSLFG	12	19	KKKYKLKHVWASRE	27	08	13	13080
GAG	MMNLNIVGGH	12	19	VRMYSPTSILDIRQ	297	12	19	13081
GAG	IDVKDTKEA	11	17	LYPLTSLRSLFGNDP	544	04	7	13082
GAG	IGWMTSNPP	11	17	DLNMMNLNIVGGHQA	204	12	19	13083
GAG	IPVGDYKR	11	17	HQRIDVKDTKEALDK	91	03	5	13084
GAG	LYPLASLS	11	17	QEQIGWMTSNPPIPV	265	09	14	13085
GAG	VHQALSPT	11	17	NPPIVGDYKRWII	277	08	13	13086
GAG	VNPGLETS	11	17	DKELYPLASLSLFG	541	06	10	13087
GAG	YPLASLSL	10	16	QGMVHQALSPTLNA	161	07	11	13088
GAG	IMMQSNFK	10	16	RFAVNPGLLESEGC	45	11	17	13089
GAG	LAEAMSVQ	10	16	KELYPLASLSLFGN	483	06	16	13090
GAG	LGIWPSK	10	16	PGNFIQNRPEPTAPP	405	01	25	13091
GAG	LNPGLETA	10	16	AAAIMMQSNFKGPR	384	02	3	13092
GAG	WQNYTPGFG	10	16	ARVLAEMSQQVQSN	467	10	16	13093
GAG	VRPQVPLRP	10	16	ANFLGKIWPSSKGRP	542	08	13	13094
GAG	YPLRMITYK	10	16	RFALNPGLLLEAEGC	45	04	6	13095
NEF	WQNYTPGFG	8	15	KELYPLASLSLFGN	542	08	6	13096
NEF	VRPQVPLRP	8	15	FPDWQNYTPGIRY	200	15	23	13097
NEF	YPLRMITYK	8	15	GFPVRPQVPLRPMTY	93	36	56	13098
NEF	LTFGWCFKL	8	15	RYPLTFGWCFKLVPV	216	07	11	13099
NEF	ILDLWVYHT	8	15	RQELDILWVYHTQGY	182	12	24	13100
NEF	WCFKLVPVD	8	15	TFGWCFKLVPVDPRE	222	07	11	13101
NEF	LWVYHTQGY	8	15	ILDLWVYHTQGYFPD	186	21	33	13102
NEF	WSKSSIVGW	8	15	GGKWSKSSIVGWPAI	2	05	8	13103
NEF	ILDLWVYNT	8	15	RQDILDLWVYNTQGY	182	05	8	13104
NEF	LLHPMSQHG	8	15	NNCLLHPMSQHGMD	254	06	9	13105
NEF	IRYPLTFGW	8	15	NNSLHPICQHGMD	254	04	6	13106
NEF	ITSSNTAAT	8	15	GGIRYPLTFGWCFK	210	06	9	13107
NEF	LEKHGAITS	8	15	HGAITSNTAATNAD	61	10	16	13108
NEF	LWVYHTQGF	8	15	SRDLEKHGAITSNT	50	13	20	13109
NEF	MTYKGAFDL	8	15	ILDLWVYHTQGFDP	186	13	20	13110
NEF	LVPVDPREV	8	15	LRPMTYKGAFDLSEF	103	06	9	13111
NEF		8	15	CFKLVPVDPREVSEA	226	08	13	13112
NEF		8	15					13113

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Table XIXa

HIV DR Super Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)	SEQ ID NO.
NEF	VGWPAIRER	10	17	SSIVGWPAIRERMRR	8	03	5	13114
NEF	WCFKLVPE	11	17	TFGWCFKLVPEPEK	222	04	6	13115
NEF	FDSRLAFHH	10	16	EWRFDLSRLAFHHVAR	307	02	3	13116
NEF	FKLVFVDFR	10	16	GWCFKLVFVDFPREVE	224	10	16	13117
NEF	VPLRPMDFK	10	16	RQVFLRPMDFKGF	98	04	6	13118
NEF	LLDTGADDT	63	98	KEALLDTGADDTVLE	107	37	58	13119
POL	WMGYELHPD	63	98	PFLWMGYELHPDKWT	415	60	94	13120
POL	YOYVLPQ	63	98	GIRYQYVLPQGWKG	330	52	81	13121
POL	FRKYAFT	61	97	KDFRKYAFTPSI	310	10	16	13122
POL	WTYNDIQL	62	97	KDSWTYNDIQLVKG	438	43	67	13123
POL	LDCTHLEK	61	95	IWQLDCTHLEKRIIL	812	29	45	13124
POL	LDVGDAYS	61	95	VTVLDVGDAYSFVPL	295	50	78	13125
POL	MDLYVGS	61	95	YQYMDLYVGSDFEI	370	57	89	13126
POL	VIPAETGQE	61	95	EAEPVIPAETGQETAY	837	57	90	13127
POL	WQGDGAVVI	61	95	KLLWQGDGAVVIQDN	992	53	83	13128
POL	WQDCTHLE	61	95	PGIWQDCTHLEGGKI	810	32	50	13129
POL	VDRELNR	60	94	RKLVDRELNRKTQD	261	57	61	13130
POL	WPKMIGGI	59	94	PGKWPKMIGGIGGF	126	39	88	13131
POL	IWQLDCTHL	59	92	SPGIWQLDCTHLEGG	809	56	41	13132
POL	VAVHVASGY	58	92	IILVAVHVASGYIEA	824	26	66	13133
POL	WKGSAIFQ	58	92	PQGWKGSAIFQSSM	339	42	59	13134
POL	YALGIIQAO	58	91	DSQYALGIIQAOQDK	940	37	61	13135
POL	FWVQLGIP	57	89	TQDFWEVQLGIPHPA	690	39	81	13136
POL	IKKDKSTK	57	89	VFAIKKDKSTKWRKL	249	36	56	13137
POL	LQIIQAQPD	57	89	QYALQIIQAQPDKSE	692	51	61	13138
POL	LGIPHAGL	56	89	EVQLGIPHAGLKKK	278	39	80	13139
POL	VNTPLVKL	57	89	WEFVNTPLVKLWYQ	606	50	79	13140
POL	VTVLDVGD	57	89	KKSVTVLDVGDAYS	292	49	77	13141
POL	FPISPIETV	56	88	TLNFPISPIETVPVK	183	52	83	13142
POL	FNVTPLVK	54	86	NFPISPIETVPVKLK	185	52	81	13143
POL	WFEVNTPL	55	86	WFEVNTPLVKLWY	605	50	78	13144
POL	WFEVNTPL	54	86	GCTLNFPISPIETVP	181	53	83	13145
POL	WFEVNTPL	54	86	IPWFEVNTPLVKL	603	49	77	13146
POL	IQNFRVYR	52	84	ITKIQNFRVYRDSR	969	49	51	13147
POL	LVGTPVNI	54	84	GTVLVGTPTVNIIGR	160	51	80	13148
POL	VQLGIPHPA	54	84	FWVQLGIPHPAGLK	276	53	83	13149
POL	WQATWIPEW	54	84	TEYWQATWIPEWFEV	595	19	30	13150
POL	IVTVPVKLK	53	83	ISPIETVPVKLKPGM	188	51	80	13151
POL	ICVLVGTPT	53	83	KKAIGTVLVGTPTVN	156	22	34	13152
POL	VLVGTPTVN	53	83	KIILVAVHVASGYIE	823	26	41	13153
POL	YVGSLEIG	53	83	IGTVLVGTPTVNIIG	159	45	70	13154
POL	MDGPKVKQW	52	81	ASGYIEAEVIPAETG	832	52	81	13155
POL	VASGYIEAE	52	81	DDLYVGSLEIGQHR	374	47	73	13156
POL	VQWPLTEE	52	81	KPGMDGPKVKQWPLT	199	52	81	13157
POL	VYRDRDP	52	81	AVHVASGYIEAEVIP	828	47	73	13158
POL	WGFTTPDKK	52	81	TVLVGTPTVNIIGRN	161	51	80	13159
POL		52	81	GPKVKQWPLTEEKIK	205	45	70	13160
POL		52	81	NFRVYRDRDPDWK	974	29	45	13161
POL		52	81	LLRWGFTTPDKKHQK	398	23	36	13162
POL		52	81					13163

555001 " 63221460

Table XIXa

HIV DR Super Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)	SEQ ID NO.
POL	VIIQYMDL	51	80	PEIVYQYMDLLVVG	365	23	36	13164
POL	LKKKSVTV	49	78	PAGLKKKSVTVLDV	286	46	72	13165
POL	VPRKAKII	50	78	IKVPRKAKIIRDY	1010	41	64	13166
POL	PPQITLWQR	49	77	SFSPQITLWQPLV	84	09	14	13167
POL	VIWGTTPKF	47	73	ESIVWGTTPKFRLP	570	23	37	13168
POL	YVDGAANRE	46	72	ETFYVDGAANRETKL	630	24	38	13169
POL	FNKLTKGY	45	70	QEPFNKLTKGYAKM	535	15	23	13170
POL	IQTKELQKQ	45	70	ATDIQTKELQKQITK	957	24	38	13171
POL	YGKQMGDD	45	70	IRDYGKQMGDDCVA	1021	41	64	13172
POL	WRAMASDFN	43	67	HSNWRAMASDFNLPP	768	31	48	13173
POL	ISKIGPENP	42	66	EGKISKIGPENPYNT	233	40	63	13174
POL	LTOIGCTLN	41	64	RNLLTQIGCTLNFI	174	21	33	13175
POL	IIQAQPKS	40	63	ALGHQAQPKSESE	694	38	59	13176
POL	LPEKDSWT	40	63	PIVLPEKDSWTNDI	432	13	20	13177
POL	FQSSMTKIL	38	59	PAIFQSSMTKILEPF	346	32	56	13178
POL	FTIPSINNE	38	59	YTAFTIPSINNEIPG	316	36	56	13179
POL	IFQSSMTKI	37	58	SPAFQSSMTKILEP	345	33	30	13180
POL	IIELIKKE	37	58	VSQIEQLIKKEKVV	710	19	37	13181
POL	LSWVPAHKG	37	58	KVYLSWVPAHKGIGG	722	23	37	13182
POL	YLSWVPAHK	37	58	EKVYLSWVPAHKGIG	721	15	24	13183
POL	IIATDIQTK	35	55	*FRKYTAFTIPSINNE	313	37	59	13184
POL	IWKGPALL	35	55	IIIDIIATDIQTKELQ	952	22	34	13185
POL	LKEALIDTG	34	53	RDPWKGPALLWKG	983	34	53	13186
POL	VYLSWVPAH	33	52	TKELQKQTKIQNFR	962	29	46	13187
POL	FLKLAGRW	32	50	GGOLKEALIDTGADD	103	31	48	13188
POL	LEGKILVA	31	48	KEKYLSWVPAHKGIG	720	15	23	13189
POL	YFLKLAGR	31	47	TAYFLKLAGRWPKV	849	27	42	13190
POL	ILVAVHVA	30	47	CTHLEKILVAVHV	817	30	47	13191
POL	IWKGTTPKF	30	47	ETAYFLKLAGRWPV	821	30	47	13192
POL	LAGRWPKV	30	47	EGKILVAVHVASGY	853	19	34	13193
POL	VVAKEIVAS	30	47	SIVIWGTTPKFRPLI	571	22	34	13194
POL	IIIDIIATDIQ	29	45	ILKLAGRWPKVVIHT	780	21	30	13195
POL	IIIDIIATDI	29	45	LPPVVAKEIVASCDK	950	22	34	13196
POL	IIGRNMLTQ	29	45	ERIIDIATDIQTK	949	23	36	13197
POL	IKVKQLCKL	29	45	GERIDIATDIQTK	168	11	17	13198
POL	VDKLVSSGI	28	44	PVNIIGRNMLTQIGC	460	18	28	13199
POL	IVGAETFYV	28	44	YAGIKVKQLCKLRG	737	26	41	13200
POL	LPPVVAKEI	28	44	NEQVDKLVSSGIRKV	623	16	25	13201
POL	WTVPQILP	27	42	KEPIVGAETFYVDGA	777	26	41	13202
POL	FNLPPVAK	27	42	DFNLPPVVAKEIVAS	425	13	20	13203
POL	FTSAAVKAA	27	42	PDKWTVPQILPEKD	775	25	39	13204
POL	LALQDSGLE	27	42	ASDFNLPPVVAKEIV	870	25	39	13205
POL	LPPVVAKEI	27	42	AIHLALQDSGLEVNI	673	15	23	13206
POL	LQDSGLEVN	26	41	DFNLPPVVAKEIVAS	777	20	33	13207
POL	FNLPPIVAK	26	41	HLALQDSGLEVNI	775	21	33	13208
POL	IIQRNLLTQ	26	41	ASDFNLPPVVAKEIV	775	21	33	13209
POL	LEVNIIVTDS	26	41	DLEIGQIRAKIEELR	381	23	36	13210
POL	IIQRNLLTQ	26	41	PVNIIGRNLLTQIGC	168	21	33	13211
POL	LEVNIIVTDS	26	41	DSGLEVNIIVTDSQYA	680	26	41	13212
POL	LEVNIIVTDS	26	41	DSGLEVNIIVTDSQYA	680	26	41	13213

Table XIXa
HIV DR Super Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)	SEQ ID NO.
POL	LRGAKALTD	26	41	CKLLRGAKALTDIVP	469	12	19	13214
POL	LVSSGIRKV	26	41	VDKLVSSGIRKVLFL	740	25	39	13215
POL	FLKLAGRW	25	39	TAYFLKLAGRWPKV	849	19	30	13216
POL	LALQDSGE	25	39	AHLALQDSGSEVNI	673	08	13	13217
POL	LQDSGSEVN	25	39	HLALQDSGSEVNIT	675	08	13	13218
POL	VKVIHTDNG	25	39	RWPVKVIHTDNGSNF	859	21	33	13219
POL	WPVKVIHTD	25	39	AGRPVKVIHTDNGS	857	20	31	13220
POL	YFLKLAGR	25	39	ETAYFLKLAGRWPV	848	24	38	13221
POL	ICGKKAIGT	24	38	LEICGKKAIGTVLV	150	12	19	13222
POL	IVAKEIVAS	24	38	LPPIVAKHIVASCDK	780	22	34	13223
POL	LRWGFTTPD	24	38	QHLLRWGFTTPDKKH	396	12	19	13224
POL	LEGKVLVA	23	36	CTHLEGKVLVAHV	817	23	36	13225
POL	LKWGFTTPD	23	36	EHLKKGFTTPDKKH	396	13	33	13226
POL	VILVAIIVA	23	36	EGKVILVAHVVASGY	821	21	33	13227
POL	LAWVPAHKG	22	34	KVYLAWVPAHKGIGG	722	20	32	13228
POL	YDQILIEC	22	34	VRQYDQILIEICGKK	143	08	13	13229
POL	IGQRTKIE	21	33	EKVYLAWVPAHKGIG	721	20	32	13230
POL	IGRNLITQI	21	33	DLFEGQRTKIEELR	381	19	30	13231
POL	LWQRPVLI	21	33	VNIHGRNLLTQIGCT	169	21	33	13232
POL	VSLTETTPQ	21	33	QITLWQRPVLIKIG	89	11	17	13233
POL	ICGHKAIGT	20	30	QKVSLSLTETTPQKTE	720	10	16	13234
POL	LVNQIEQL	19	30	KEKVYLAWVPAHKGIG	720	20	31	13235
POL	YFVPLDKD	18	28	LIJICGHKAIGTVLV	150	10	16	13236
POL	IKVRQLCKL	18	28	CKLLRGTKALTEVIP	469	11	17	13237
POL	LWQRPVLI	18	28	ESELVNSQIEQLIKK	706	13	20	13238
POL	YAGIKVKQL	18	28	ESELVNSQIEQLIKK	706	18	28	13239
POL	IGRNLITQI	18	28	GDAYFSVPLDKDFRK	301	18	28	13240
POL	IKVRQLCKL	18	28	VNIHGRNMLTQIGCT	169	12	19	13241
POL	LWQRPVLI	18	28	YPGKVRQLCKLLRG	460	13	20	13242
POL	YAGIKVKQL	18	28	RDPLWKGPAKLLWKG	983	13	20	13243
POL	IKVRQLCKL	18	28	QITLWQRPVLIKIG	457	18	28	13244
POL	YAGIKVKQL	18	28	SQIYAGIKVKQLCKL	571	17	27	13245
POL	YAGIKVKQL	18	28	IEELREHLLKWWGFTT	391	17	27	13246
POL	YAGIKVKQL	18	28	KWTVPQIQLPEKDSW	427	11	17	13247
POL	YAGIKVKQL	18	28	ITLWQRPVLIKIG	90	13	20	13248
POL	YAGIKVKQL	18	28	ALGIQAQPDSESE	694	12	19	13249
POL	YAGIKVKQL	18	28	KTELQAIHLALQDSG	668	15	23	13250
POL	YAGIKVKQL	18	28	IKALVEICTEMEKEG	218	15	23	13251
POL	YAGIKVKQL	18	28	IEELRQHLLRWGFTT	391	12	19	13252
POL	YAGIKVKQL	18	28	RNMLTLQGLCTLNPH	174	10	16	13253
POL	YAGIKVKQL	18	28	VDKLVSAKIRKVLFL	740	14	22	13254
POL	YAGIKVKQL	18	28	NEQVDKLVSAKIRKV	737	14	22	13255
POL	YAGIKVKQL	18	28	SOIYPGKVRQLCKL	457	12	19	13256
POL	YAGIKVKQL	18	28	LEFRRQNPDIVYQ	357	14	22	13257
POL	YAGIKVKQL	18	28	TVSFSFQITLWQRP	77	05	10	13258
POL	YAGIKVKQL	18	28	GSNFTSTTVKAAACW	870	11	17	13259
POL	YAGIKVKQL	18	28	IIDIASDIQTKBLQ	952	11	17	13260
POL	YAGIKVKQL	18	28	LLKLAGRWPKVKTHT	853	09	14	13261
POL	YAGIKVKQL	18	28	TEAVQKIATISIVW	561	10	16	13262
POL	YAGIKVKQL	18	28					13263

HIV DR Super Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)	SEQ ID NO.
POL	FTIPSTNNE	13	20	YTAFTIPSTNNETPG	316	13	20	13264
POL	LEDINLPGK	13	20	DTVLEDINLPGKWKP	117	13	20	13265
POL	LTDIVPLTE	13	20	AKALTDIVPLTEAE	475	08	20	13266
POL	LVTKIGGQ	13	20	QRPLVTIKIGGQKE	94	13	20	13267
POL	MARGAHTNDV	13	20	YARMGAHTNDVKQL	546	12	19	13268
POL	VKTHIDNG	13	20	RWPVKTHIDNGSNF	859	09	19	13269
POL	VQPIVPEK	13	20	KWTQPIVPEKDSW	427	12	19	13270
POL	WPKVTHID	13	20	AGRWPVKTHIDNGS	857	09	14	13271
POL	WQPLVTVK	13	20	ITLWQPLVTVKIGG	90	09	14	13272
POL	WTQPIVLP	13	20	PKWTQPIVLPPEKD	425	12	19	13273
POL	YTAFTIPST	13	20	FRKYTAFTIPSTNNE	313	13	21	13274
POL	IDIASDIQ	12	19	ERUIDIASDIQKE	950	11	17	13275
POL	IVDIATDI	12	19	GERIVDIATDIQTK	949	11	17	13276
POL	LEENLPGK	12	19	DTVLEENLPGKWKP	117	11	16	13277
POL	LQAIYLAQ	12	19	KTELOAIYLAQDSG	668	11	17	13278
POL	LQKQIKIQ	12	19	TKELQKQIKIQNFR	962	09	14	13279
POL	VDIATDIQ	12	19	ERIVDIATDIQKE	950	10	16	13280
POL	YDQPIEIC	12	19	VRQYDQPIEICGKK	143	05	8	13281
POL	FNFPQITLW	11	17	VPTFNFPQITLWQRP	79	01	17	13282
POL	IGRNMLTQL	11	17	VNIIGRNMLTQLGCT	169	10	16	13283
POL	ISRGPNP	11	17	EGKISRGPNPNT	233	10	16	13284
POL	LTEVIPLTE	11	17	TKALTEVIPLTEAE	475	10	16	13285
POL	MESIVWKG	11	17	KIAMESIVWKGTPK	566	07	11	13286
POL	VPRKVKII	11	17	IKVPRKVKIIRDY	1010	08	13	13287
POL	VYQLETEPI	11	17	QGTVYQLETEPIVGA	615	05	8	13288
POL	YFGIKVKQL	11	17	SOIYFGIKVKQLCKL	457	04	6	13289
POL	FQGEAREF	10	16	NLAFFQGEAREFPE	5	05	14	13290
POL	LIEALLDTG	10	16	GGQLIEALLDTGADD	103	09	8	13291
POL	VSLTDITNQ	10	16	QKVSLTDITNQKTE	656	09	14	13292
POL	WETWTDYW	10	16	KETWETWTDYWQAT	587	09	14	13293
POL	YAKMRTAHT	10	16	TGKYAKMRTAHTNDV	543	09	14	13294
POL	YKMLTKGY	10	16	QEPYKMLTKGYARM	535	03	5	13295
POL	LQLPPLERL	36	56	PVPLQLPPLERLTD	74	13	20	13296
REV	VPLQLPPLLE	36	56	AEPVPLQLPPLERLT	72	10	16	13297
REV	LYQSNPPPS	18	28	IKFLYQSNPPPSPEG	21	04	6	13298
REV	VRIKILYQ	16	25	LKAVRIKILYQSNP	13	06	9	13299
REV	YQSNPPSP	12	19	KFLYQSNPPSPSGT	22	05	8	13300
REV	LQLPIERL	11	17	PVPLQLPIERLRD	74	04	6	13301
REV	VPLQLPIE	11	17	AEPVPLQLPIERLR	72	04	6	13302
TAT	WNHFGSQPK	15	23	LEPNHFGSQPKTAC	11	11	17	13303
TAT	FLNKGGLIS	14	22	QVCFLNKGGLISYGR	38	04	6	13304
TAT	WKHFGSQPK	13	20	LEFWKHFGSQPKTAC	11	11	17	13305
TAT	YCKKCCFHC	11	17	NNCYCKKCCFHCQVC	26	04	6	13306
TAT	YCKKCCYHC	11	17	TNCYCKKCCYHCQVC	26	02	3	13307
TAT	WNHFGSQPT	10	16	LEPNHFGSQPTTAC	11	07	11	13308
VIF	MIVWQVDRM	46	72	WQVMIVWQVDRMRIR	5	28	44	13309
VIF	WQVMIVWQV	43	67	ENRWQVMIVWQVDRM	2	41	64	13310
VIF	WQVDRMRIR	34	53	MIVWQVDRMRIRTWK	8	14	22	13311

Table XIXa
HIV DR Super Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)	SEQ ID NO.
VIF	LOYLALTAL	33	52	VGSLQYLALTALIKP	147	14	22	13314
VIF	LGHGVSIEW	31	48	DWHLGHGVSIEWRLR	81	11	17	13315
VIF	VDRMRITW	31	48	VWQVDRMRITWNSL	10	15	23	13316
VIF	YDFCFESA	28	44	HLYYDFCFESAIRN	113	08	13	13317
VIF	YWGHTGER	28	44	ITTYWGLHTGERDWH	68	14	22	13318
VIF	IRTNLSLVK	27	42	RMRTITWNSLVKHHM	15	12	19	13319
VIF	LQGVGSIEW	26	41	DWHLQGVGSIEWRKK	81	07	11	13320
VIF	LVKHHMYVS	21	33	WNSLVKHHMYVSKKA	21	05	8	13321
VIF	IPLEGARLV	19	30	EVHPLGEARLVVRT	54	05	8	13322
VIF	LVKHHMYIS	19	30	WKSLLVKKHHMYISOKA	21	05	8	13323
VIF	YLALTALIK	16	25	SLOYLALTALIKPKK	149	11	17	13324
VIF	IRTWKSLVK	15	23	RMRTITWKSLLVKKHHM	15	14	22	13325
VIF	LADQLHLY	15	23	DPDLADQLHLYYFD	104	07	11	13326
VIF	LALTALIKP	15	23	LQYLALTALIKPKKI	100	08	13	13327
VIF	VDPLADQL	14	22	STQVDPGLADQLHIL	111	04	6	13328
VIF	LYYDFCFSE	13	20	LHLYYDFCFESAI	117	10	16	13329
VIF	FSESARKA	13	20	FDCFESAIRKALIG	104	08	14	13330
VIF	WQVDRMKIR	12	19	EPGLADQLHMHYFD	8	05	8	13331
VIF	FDSAIRKA	12	19	FDCFESAIRKALIG	117	12	19	13332
VIF	FSESARKA	12	19	FDCFESAIRNAILG	130	06	9	13333
VIF	IVSPRCYQ	12	19	LGHSVPRCEYOAGH	147	04	6	13334
VIF	LOYLALAAL	12	19	VGSLQYLALAALITP	10	12	13	13335
VIF	VDRMKIRTW	12	19	VWQVDRMKIRTWNSL	68	08	13	13336
VIF	YWGLQTOER	11	17	IKTYWGLQTOERDWH	54	06	9	13337
VIF	IPLGARLV	11	17	EVHPLGDARLVIT	147	08	13	13338
VIF	LQYLALKAL	11	17	VGSLQYLALKALVTP	8	08	13	13339
VIF	IKPKKIKP	10	16	MIVWQVDRMRINTWK	156	09	14	13340
VIF	VDRMRINTW	10	16	TALIKPKKIKPPLPS	71	12	19	13341
VIF	IGCHSRIG	46	72	VWQVDRMRINTWKSLL	15	08	13	13342
VIF	WTELEEL	42	69	HFRIGCQHSRIGTR	60	29	45	13343
VIF	ILQQLLFH	37	58	YNEWTELEELKSE	66	27	42	13344
VIF	FIHFRIGCQ	30	47	IRILQQLLFHFR	31	12	22	13345
VIF	YNEWTELEL	30	47	REPNEWTELEEL	51	14	23	13346
VIF	FPRPWLHGL	24	38	VRHFRPWLHGLGQH	20	15	25	13347
VIF	WEGVEAIR	18	28	GDTWEGVEAIRILQ	51	15	25	13348
VIF	LEELKEAV	16	25	LELEELKEAVRHF	51	15	25	13349
VIF	WAGVEAIR	16	25	GDTWAGVEAIRLQ	47	16	17	13350
VIF	YGDTWAGVE	12	19	YETYGDTWAGVEAIL	71	11	16	13351
VIF	IGCRISRIG	11	17	HFRIGCRHSRIGTR	66	10	16	13352
VIF	FIHFRIGCR	11	17	QLLFHFRIGCRHSR	47	04	6	13353
VIF	YGDTWTGVE	10	16	QLLFVHFRIGCQHSR	31	05	8	13354
VIF	FPRPWLHSL	09	15	YETYGDTWTGVEAIL	47	03	5	13355
VIF	WALELEEL	01	50	VRHFRPWLHSLGQH	15	01	2	13356
VIF	LVTLLSSSK	01	50	YNEWALELEELKNE	87	01	2	13357
VIF	IIAIVVWTI	23	36	EEWLVTLLSSSKLDQ	89	02	3	13358
VIF	VDYRIVIVA	01	33	EWLVTLLSSSKLDQ	20	02	25	13359
VIF				VVAIAIVVWTIVFI	5			13360
VIF				LAKYDYRIVIVAFIV				13361
VIF								13362
VIF								13363

Table XIXa
HIV DR Super Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy(%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy(%)	SEQ ID NO.
VPU	LRQRKIDRL	17	27	RKILRQRKIDRLIDR	44	11	17	13364
VPU	IVVWTVIF	15	23	IIAIVVWTVIFIEYR	27	07	11	13365
VPU	VVWTVIFIE	14	22	IAIVVWTVIFIEYRK	28	06	9	13366
VPU	IEYRKILRQ	13	21	IVFIEYRKILRQKI	36	07	11	13367
VPU	ILAIVALV	11	17	SLYLAIIVALVVAII	3	01	2	13368
VPU	WTVIFIEYR	10	16	IVVWTVIFIEYRKIL	30	05	8	13369
VPU	LAIVALVVA	09	15	LQILAIVALVVAII	4	02	3	13370

[illegible]

5533275321450
Table XIXb
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw53	SEQ ID NO.
VSTQLLNG	KPVVSTQLLLNGSLA						12864
VVSTQLLN	IKPVVSTQLLLNGSL						12865
LTVWGKQL	LLQLTVWGKQLQAR						12866
LLSGIVQQQ	ARQLLSGIVQQQSNL						12867
WATHACVPT	HNWVWATHACVPTDPN						12868
LGAAGSTMG	LGFLGAGSTMGAAS						12869
VRQGSPLS	VNRVRQGSPLSFQT						12870
LLNGSLAE	STQLLLNGSLAEEV						12871
VKLTPLCVT	KPCVKLTPLCVTLNC						12872
LRAIEAQH	NNLRALIEAQQHLQ						12873
VSTVQCTHG	CKNVSTVQCTHGKIP						12874
LGIWGCSGK	QQLGIVGCSGKLC						12875
LWDQSLKPC	IISLWDQSLKPCVKL						12876
LGFLGAAGS	AVFLGFLGAAGSTMG						12877
VWATHACVP	VHNWVWATHACVPTDP						12878
WGKQLQAR	LTVWGKQLQARVLA						12879
WYIKIFIM	TNWLWYIKIFIMIVG						12880
FCASDAKAY	TTLFCASDAKAYDTE						12881
IVGGGLGR	FIMIVGGGLGRIVF						12882
IFIMVGGGL	YKIFIMIVGGGLGL						12883
VYGVVWVK	WTVYGVVWVWKEAT						12884
IKQLQARVL	VWGKQLQARVLAVE						12885
IKIFIMVIG	LWYIKIFIMIVGGGL						12886
MGAASITLT	GSTMGAASITLTVOA						12887
YKIFIMIV	WLWYIKIFIMIVGGGL						12888
ITGLLTTRD	SSNITGLLTTRDGGK						12889
IPHYCAPA	FEPIPHYCAPAGFA						12890
MIVGGLIGL	IFIMIVGGGLIGLRV						12891
VQARQLLSG	TLTVQARQLLSGIVQ						12892
FEPIPHYC	KVSFEPIPHYCAPA						12893
LRSLCLFSY	WDDLRLSLCLFSYHRL						12894
MWKNMVEQ	NFNMWKNMVEQMHE						12895
VHNVWATHA	DTEVHNVWATHACVP						12896
WKNMVEQM	FNMWKNMVEQMHE						12897
YYGVVWKE	VTVYGVVWVWKEATT						12898
LLQLTVWGI	QQHLLQLTVWGKQL						12899
IEPLGVAPT	VVKIEPLGVAPTAK						12900
IKPVVSTQL	THGKIPVSTQLLN						12901
LQARVLAVE	IKQLQARVLAVERYL						12902
WDDLRLSLCL	ALA WDDLRLSLCLFSY						12903
INHTPHR	SRPINHTPHREKR						12904
INHTPHRE	RPINHTPHREKRA						12905
ITQACPKVS	TSVITQACPKVSFEP						12906
IVQQSNLL	LSGIVQQSNLLRAI						12907
LGNNSTNST	NKTLGNNSTNSTLGN						12908
VISTRTHRE	ARPVISTRTHREKRA						12909
WRWGTLFLG	QNLWRWGTLFLGMLM						12910
WRWGTMLLG	QHLWRWGTMLLGMLM						12911
FAVLSIVNR	RIVFAVLSIVNVRQ						12912
LLNGSLAE	TQLLLNGSLAEEVV						12913

Table XIXb

HIV DR Super Motif Peptides with Binding Information

[illegible]

665007-696469

Table XIXb
HIV DR Super Motif Peptides with Binding Information

Cort Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw53	SEQ ID NO.
LTPLCVTLN	CVKLTPLCVTLNCTD						12914
LYKYKVKI	RSELYKYKVKVKIEPL						12915
VPWNSSWSN	TTNVTPWNSSWSNKS						12916
YRLINCNTS	YKEYRLINCNTSAIT						12917
IHYCAPAGF	PIPIHYCAPAGFAIL						12918
LKDDQQLGI	ERYLKDDQQLGIWGC						12919
YKYKVKIE	SELYKYKVKVKIEPLG						12920
IRPVVSTQL	THGIRPVVSTQLLIN						12921
LDKWASLWN	LLALDKWASLWNWFD						12922
LRIVFAVLS	LIGLRIVFAVLSIVN						12923
LNGLAEE	QLLLNGLAEEVVI						12924
YKVKIEPL	LYKYKVKVKIEPLGVA						12925
LKGLRLGWE	RSSLKGLRLGWEGLK						12926
FSYHRLRDL	LCLFSYHRLRDLILI						12927
INCTRPNN	SVENCTRPNNNTRK						12928
VVKIEPLGV	KYKVKVKIEPLGVAPT						12929
WKEATTILF	VPVWKEATTTLCAS						12930
IGLRIVFAV	GGLIGLRIVFAVLSI						12931
FFYCNISGL	GGEFFYCNISGLFNS						12932
FGLGALFLG	RAAFGLGALFLGFLG						12933
FYCNTSGLF	GGEFFYCNISGLFNS						12934
LIGLRIVEA	VGGLIGLRIVFAVLS						12935
VGLGAVFLG	KRAVGLGAVFLGFLG						12936
VGLGMLFLG	KRAYVGLGMLFLGVLS						12937
ICTTAVPWN	GKLICTTAVPWNSSW						12938
ICTTNPWN	GKLICTTNPWNSSW						12939
LGVAFTKAK	IEPLGVAPTAKARRV						12940
LICTTAVPW	SGKLICTTAVPWNSS						12941
LRDQQLGI	ERYLRDQQLGIWGC						12942
VFLGFLGAA	LGA VFLGFLGAA GST						12943
FSYHRLRDF	LCLFSYHRLRDFILI						12944
PIHYCTPA	FEPIPIHYCTPAGFA						12945
IVFAVLSIV	GLRIVFAVLSIVNRV						12946
VFAVLSIVN	LRIVFAVLSIVNRVR						12947
VPWNASWSN	TTAVPWNASWSNKS						12948
IGLRIFAV	GGLIGLRIFAVLSI						12949
IRQAHCNIS	IGDIRQAHCNISRAK						12950
VAPTAKARR	PLGVAPTAKARRVVQ						12951
FNGTGPCKN	DKKFNGTGPCKNVST						12952
IGPGQTFYA	SVRIGPGQTFYATGD						12953
IGSGQAFYV	RYSIGSGQAFYVYTGK						12954
IRYLNLYNQ	QTAIRYLNLYNQTEN						12955
LIGLRIFA	VGGLIGLRIFA VLS						12956
LLQYWSQEL	WWNLLQYWSQELKNS						12957
LRNLCLFSY	WDDLRLNLCLFSYHRL						12958
LVSGFLALA	SIRLVSGFLALAWDDL						12959
VSGFLALAW	IRLVSGFLALAWDDL						12960
FDPIPIHYC	KVTFDPIPIHYCTPA						12961
IIFAVLSIV	GLRIIFAVLSIVNRV						12962
LINCNTSAI	EYRLINCNTSAITQA						12963

HIV DR Super Motif Peptides with Binding Information

[illegible]

6550016521453
 Table XIXb
 HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw53	SEQ ID NO.
LLNATAIAV	AVSLLNATAIAVAEG						12964
LRIFA VLS	LIGLRIEFAVLSIVN						12965
VITQACPKV	NTSVITQACPKVSFE						12966
YVWNLQYW	VLKYVWNLQYWSQE						12967
FAILKCNDK	PAGFAILKCNCKKEN						12968
	LRIFA VLSIVNKR						12969
IFAVLSIVN	YRLNNTSAITOAC						12970
INNTSAIT	VSLNATAIAVAEGT						12971
LNATAIAVA	NYPWNSSWSNKSDE						12972
WNSSWSNKS	NYPWNASWSNKSIED						12973
WNASWSNKS	GKLICTTTVPWNASW						12974
ICTTTVPWN	QQHLLKLTWVGKQL						12975
LLKLTWVGI	RSLEYKYKVVVEIKPL						12976
LYKYKVVEI	LGAMFLGFLGAAGST						12977
MFGLFGAA	EIVMHSFNCGGEFFY						12978
MHSFNCGGE	LLQYWSOELKNSAVS						12979
YWSOELKNS	AVGIGAVFLGFLGAA						12980
IGAVFLGFL	DFILIAARTVELLGH						12981
LYKYKVVEI	SOKLICTTTVPWNAS						12982
MHSFNCGGE	TQLLNGSLAEGEII						12983
YWSOELKNS	LYVYWGQELKNSAIS						12984
IGAVFLGFL	FILIAARTVELLGHIS						12985
LYKYKVVEI	IGALFLGFLGAAGST						12986
MHSFNCGGE	SQELKNSAVSLNAT						12987
YWSOELKNS	KRAVGIGAVFLGFLG						12988
IGAVFLGFL	NSAVSLNATAIAVA						12989
LYKYKVVEI	QTFYATGDHIGDIRQ						12990
MHSFNCGGE	LDIAIAVAEGTDRI						12991
YWSOELKNS	PIPIHYCTPAGFAIL						12992
IGAVFLGFL	GTILGLVICSASN						12993
LYKYKVVEI	VDEIWNNTMTWMEWER						12994
MHSFNCGGE	TLILGLVICSASN						12995
YWSOELKNS	YHRLRDFILIAARTV						12996
IGAVFLGFL	CVKLTPLCVTLDCN						12997
LYKYKVVEI	QQHMLQLTVWGIKQL						12998
MHSFNCGGE	NSVEINCTRPNNNT						12999
YWSOELKNS	TVQVRQLLSGIVQQQ						13000
IGAVFLGFL	WGTLILGLVICSAS						13001
LYKYKVVEI	LNTVGGHQAAMQMLK						13002
MHSFNCGGE	TETLLVQANPDCKT						13003
YWSOELKNS	TLLVQANPDCKTIL						13004
IGAVFLGFL	WHLGLNKIVMYSP						13005
LYKYKVVEI	FSALSEGATPDQNT						13006
MHSFNCGGE	YKRWILGLNKIVRM						13007
YWSOELKNS	GATLEEMMTACQGVG						13008
IGAVFLGFL	GEIYKRWILGLNKI						13009
LYKYKVVEI	VGEIYKRWILGLNK						13010
MHSFNCGGE	SSQVSNQYPIVQNLQ						13011
YWSOELKNS	LDKWEKIRLRPGKK						13012
IGAVFLGFL	GSDIAGTTTLQEQI						13013

identified with

identified with

Table XIXb
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw53	SEQ ID NO.
WASRELERF	HLVVASRELERFALN						13014
IPMFALSE	PEVIPMFALSSEGAT						13015
MFSALSEGA	VIPMFALSSEGATQ						13016
VIPMFALS	SPEVIPMFALSSEGA						13017
MYSVPSILD	IVRMYSVPSILDIRQ						13018
IVRMYSVPS	LNKIVRMYSVPSILD						13019
VRMYSVPSI	NKIVRMYSVPSILDI						13020
YSPVSILDI	VRMYSVPSILDIRQG						13021
MTETLLVQN	KNWMTETLLVQANP						13022
WMETLLVQ	VKNWMTETLLVQAN						13023
ISPRILN	HQAIISPRILN						13024
VKNWMTETL	TQEVKNWMTETLLVQ						13025
IKCFNGKE	QKRIKCFNGCKEGHL						13026
YTAVMQRG	NPPIPVGEIYKRWII						13027
VATLYCVHQ	KGGYTAVFMQRGQNP						13028
FLQSRPEPT	YNTVATLYCVHQRIE						13029
FKTLRAEQA	AAEWDRLLHPVHAGPI						13030
MVHQAIISPR	PGNFQSRPEPTAPP						13031
VHQAIISPR	DRFFKTLRAEQATQE						13032
YKTLRAEQA	OGQMVHQAIISPRILN						13033
VSILDIRQ	QGMVHQAIISPRILN						13034
LAEMSQVT	DRFYKTLRAEQASQE						13035
LGIWFSKH	YSPVSILDIRQGPKE						13036
VKCFNGKE	ARVLAEMSQVTNSA						13037
YNTVATLYC	ANFLGKIWFHSHKGRP						13038
LHPVHAGPI	RKTVKCFNGCKEGHI						13039
LYNTVATLY	RSLYNTVATLYCVHQ						13040
MTDTLLVQN	WDRLLHPVHAGPIAG						13041
WMTDTLLVQ	LRSLYNTVATLYCVH						13042
IEVKDTKEA	KNWMTDTLLVQANP						13043
LOGQMVHQ	VKNWMTDTLLVQAN						13044
MTNNPIP	HQIEVKDTKEALDK						13045
WMTNPPIP	VQNLQGMVHQAIISPR						13046
IAPQMREP	IGWMTNNPIPVPGEI						13047
VHAGPIAPG	QIGWMTNNPIPVPGE						13048
LGFGATLEE	AGPIAPGQMRPEPRGS						13049
VHAGPIPPG	LHPVHAGPIAPGQMR						13050
IPQMREP	LRAALGPGATLEEMMT						13051
LSPRILN	VHPVHAGPIPPGQMR						13052
YRKLHLVWA	AGPIPPGQMRPEPRGS						13053
LGPAAATLEE	HQALSPRILN						13054
LKALGPAAT	KKKYRLKHLVWASRE						13055
LKDEKPLA	KTILKALGPAATLEE						13056
LSGKLD	QEQKDKDEKPLASLR						13057
MTSNPPIP	ASVLSGGKLD						13058
VKNWMTDTL	IGWMTSNPPIPVPGEI						13059
VSILDIKOG	TQDVKNWMTDTLLVQ						13060
WMTSNPPIP	YSPVSILDIKOGPKE						13061
	QIGWMTSNPPIPVGE						13062
							13063

665001-665002-4463 Table XIXb HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w/19	DR7	DR8w2	DR9	DRw53	SEQ ID NO.
FNTVATLYC	KSLFNTVATLYCVHQ						13064
IPMFTALSE	PEVIPMFTALSEGAI						13065
LASLSLFG	LYPLASLSLFGNDP						13066
LERFAVNPFG	SRELERFAVNPGLLE						13067
LFTVATLY	LRSLFNTVATLYCVH						13068
MFTALSEGA	VIPMFTALSEGAIPQ						13069
WDRVHPVHA	AAEWDRVHPVHAGPI						13070
IRMYSPTS	LNKIVRMYSPTSILD						13071
LERFALNPG	SRELERFALNPGLE						13072
LQEQIAWMT	TSTLQEQIAWMTGNP						13073
VHPVHAGPI	WDRVHPVHAGPIPPG						13074
VIPMTALS	SPEVIPMFTALSEGA						13075
VRMYSPTSI	NKIVRMYSPTSILDI						13076
LKIWPSNK	ANFLGIWPSNKGPR						13077
LYPLASLFG	LYPLTSLSLFGNDP						13078
MYSPTSILD	IVRMYSPTSILDIRQ						13079
YKLKHVWA	KKKYKYLKHVWASKE						13080
YSPTSILDI	VRMYSPTSILDIRQ						13081
LTSLSLFG	LYPLTSLSLFGNDP						13082
MLNIVGGH	DLNMLNIVGGHQA						13083
IDVKDTKEA	HQRIDVKDTKEALDK						13084
IGWMTSNPP	QEQIGWMTSNPPIPV						13085
IPVGDITKR	NPPIPVGDITKRWH						13086
LYPLASLS	DKELYPLASLSLFG						13087
VHQAISPT	QMVVHQAISPTLNA						13088
VNPGLETS	REAVNPGLLETS						13089
YPLASLSL	KELYPLASLSLFGN						13090
FLQNRPEPT	PGNFLQNRPEPTAPP						13091
IMMQKSNFK	AAAIMMQKSNFKGPR						13092
LAEAMSQVQ	ARVLAEAMSQVQSQN						13093
LGIWPSK	ANFLGIWPSKGRP						13094
LNPGLLETA	RFALNPGLLETAEGC						13095
YPLASLSL	KELYPLASLSLFGN						13096
WQNYTPGFG	FTDWQNYTPGPGIRY						13097
VRQVPLRP	GPPVRQVPLRPMY						13098
VPLRPMYK	RPQVPLRPMYKGA						13099
LTFGWCFKL	RYPLTFGWCFKLVPV						13100
ILDLWVYHT	RQILDLDWVYHTQGY						13101
WCFKLVPVD	TFGWCFKLVPVDPRE						13102
LWVYHTQGY	ILDLWVYHTQGYFPD						13103
WSKSSIVGW	GGKWSKSSIVGWPAI						13104
ILLWVYNT	RQILDLDWVYNTQGY						13105
LLHPMSQHG	NNCLLHPMSQHGMD						13106
IRYPLTFGW	NNCLLHPICQHGMD						13107
ITSSNTAAT	GGPIRYPLTFGWCHK						13108
LEKHGAITS	HGAITSNTAATNAD						13109
LWYHTQGF	SRDLEKHGAITSNT						13110
MTYKGAIDL	ILDLWVYHTQGFPPD						13111
LVPVDPREV	LRPMYKGAIDLSPF						13112
	CFKLVPVDPREVEEA						13113

Table XIXb

HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR1	DR2wB1	DR2wB2	DR3	DR4w4	DR4w15	DR5w11	DR5w12	SEQ ID NO.
VGWPAIRER	SSIVGWPAIRERMR									13114
WCFKLPVE	TFGWCFKLPVEPEK									13115
FDSRLAFHH	EWREDSRLAFHHVAR									13116
FKLPVDPDR	GWCFKLPVDPREVE									13117
VPLRPMTEK	RPOVPLRPMTEKGF									13118
LLDTGADDT	KEALLDTGADDTVLE									13119
WMGYELHPD	PFLWMGYELHPDKWT									13120
YQYNVLPQG	GIRYQYNVLPQGWKG	0.0001		-0.0015		-0.0023		-0.0010		13121
FRKYTAFTI	DKDFRKYTAFTPSI									13122
WTVNDIQKL	KDSWTVNDIQKLVGK	0.0027		-0.0014		-0.0026		0.1200		13123
LDCTHLEK	IWQLDCTHLEKIL									13124
LDVGDAYFS	VTVLVDGDAYFSYPL	0.0003		-0.0014		-0.0026		-0.0007		13125
MDLYYVGS	YQYMDLYYVGSLEI	0.0006		-0.0014	-0.0160	0.0036		-0.0006		13126
VIPAETGQE	EAEVIPAETGQETAY									13127
WKEGAVVI	KLLWKEGAVVIQDN	0.4600	0.0011	0.0058	-0.0043	0.0750	0.0200	0.0060	-0.0045	13128
WQLDCTHLE	PGIWQLDCTHLEGI									13129
VDRELNR	RKLVDFRELNRKTQD									13130
WPKMIGGI	SPGWPKMIGGIGGF	0.0013		-0.0021		0.0990		-0.0006		13131
IWQLDCTHL	PGIWQLDCTHLEGI									13132
VAVHVASGY	IILVAVHVASGYIEA	0.0010		-0.0014		-0.0026		-0.0007		13133
WKGSPAIQ	PQGWKGSPAIQSSM									13134
IGYSAGER	KGGIGGYSAGERIID									13135
YALGIIQAG	DSQYALGIIQAQPK									13136
FWEVQLGIP	TQDFWEVQLGIPHA									13137
IKKKDSTKW	VFAIKKKDSTKWRL									13138
LGIIQAQPD	QYALGIIQAQPKSE	0.0020	0.0410	0.1300	0.0220	-0.0026	1.9000	-0.0007	0.2200	13139
LGIPHAGL	EVQLGIPHAGLKKK	0.6900		9.5000		0.0065		0.0630		13140
VNTPLVKL	WEFVNTPLVKLWYQ	0.0019		-0.0014	-0.0043	0.0350	0.0095	-0.0007	0.0370	13141
VTVLVDGDA	KKSVTVLVDGDAYFS	0.0190	0.0003	-0.0014	-0.0043	0.0810		-0.0007	0.0460	13142
FPISPIETV	TLNFPISPIETVPVK	0.0480	0.0013	0.0022						13143
ISPIETVPV	NFPISPIETVPVKL									13144
FVNTPLVK	EWEFVNTPLVKLWY	0.0014		-0.0014	0.0920	-0.0026	1.6000	-0.0006	0.0540	13145
LNFPISPIE	GCTLNFPISPIETVP	1.1000	0.0089	1.8000		0.6600		0.0830		13146
WEFVNTPL	PEWEFVNTPLVKL									13147
IQNFRVYR	ITKIQNFRVYRDSR								-0.0045	13148
LVGPTPVI	ITKIQNFRVYRDSR	0.0066	0.0061	-0.0014	-0.0043	-0.0026		0.0043		13149
VQLGIPHA	FWEVQLGIPHAAGL	0.0240		-0.0014		0.0033		-0.0006		13150
WQATWIPEW	TEYWQATWIPEWV									13151
IETVPVKL	ISPIETVPVKLPKM	0.0019		0.0140		-0.0026		-0.0007		13152
IGTVLVGPT	KKAIGTVLVGPTVN									13153
LVAVHVASG	KIILVAVHVASGYIE	0.0120	0.0170	-0.0003		0.0008	0.0030	-0.0004	-0.0045	13154
VLVGPTPVI	IGTVLVGPTPVI	0.0230	-0.0003	-0.0021	-0.0043	0.2300		0.0020		13155
YIEAEVIPA	ASGYIEAEVIPAETG									13156
YVGSDEIG	DDLTVGSDEIGQHR									13157
MDGPKVKQW	KPGMDGPKVKQWPLT									13158
VASGYIEAE	AVIIVASGYIEAEVLP									13159
VGPTPVI	TVLVGPTPVI									13160
VKQWPLTEE	GPKVKQWPLTEEIK									13161
VYRDRSDP	NFRVYRDRSDPIWK									13162
WGFTTPDKK	LLRWGFTTPDKKHQK	0.0010		-0.0014		-0.0026		0.0035		13163

13116	SSIVGWPAIRERMR				
13117	TGWCFLVPVPEK				
13118	EWFRSRLAFHVAR				
13119	GWCFKLPVDPREVE				
13120	RPQVPLRPMTFKGF	-0.0003			
13121	KEALLDTGADDTVLE				
13122	PFLWMGYELHPDKWT				
13123	GIRYQYNVLPQGWKG				
13124	DKDFKRYTAFTPSI				
13125	KDSWTNDIQKLVGK	-0.0005			
13126	IWQLDCTHLEGIIL				
13127	VTVLVDGDAYESVPL	-0.0005			
13128	YQYMDLLYVGSLEI				
13129	EAEPVPAETGOETAY	0.2400	0.0450	0.2100	
13130	KLWKGEGAVVIQDN				
13131	PGIWQLDCTHLEGGI				
13132	RKLVDRELNRKTQD				
13133	PGKWKTGMIGGIGF	-0.0009			
13134	SPGIWQLDCTHLEGG				
13135	IILVAVHVASGYEA	0.0087			
13136	PQGWKGSFAIFQSSM				
13137	KGGIGGYSAGERIID				
13138	DSQYALGHQAQPDK				
13139	TQDFWEVQLGIPHPA				
13140	VFAIKKDKSTKWRKL				
13141	QYALGHQAQPDKSE	-0.0005	0.1400	1.9000	
13142	EVQLGIPHPAGLKKK	1.7000			
13143	WEFVNTPLVKLWYQ	-0.0005	-0.0005	0.0016	
13144	KKSVTVLVDGDAYES	0.0640	-0.0008	0.0046	
13145	TLNFPSIETVPVK	0.1500			
13146	NFPISPIETVPVKLK				
13147	EWFEVNTPLVKLWY	0.0380	0.2600	2.6000	
13148	GCTLNFPISPIETVP	1.4000			
13149	IPEWEFVNTPLVKL				
13150	ITKIQNFRRYYRDSR	0.0820	-0.0005	0.0180	
13151	GTVLVGPTPVNIIGR	0.0024			
13152	FWEVQLGIPHPAGLK				
13153	TEYWQATWPEWFEV				
13154	ISPIETVPVKLPGM	0.0150			
13155	KKAIGTVLVGPTPVN				
13156	KIILVAVHVASGYIE	0.0710	-0.0003	0.0320	
13157	IGTVLVGPTPVNIIG	0.0120	0.0097	0.0480	
13158	ASGYIEAEVIPAETG				
13159	DDLYYGSDLEIGQHR				
13160	KPGMDGPKVKQWPLT				
13161	AVHVASGYIEAEVIP				
13162	TVLVGPTPVNIIGRN				
13163	GPVKVQWPLTEEEKIK				
	NFRVYTRDSRDPWIK				
	LLRWGFTTPDKKHQK	0.0150			
	WGFTTPDKK				
	VYVYRDSRDP				
	VKQWPLTEE				
	VGFTPVNII				
	VASGYIEAE				
	YVGSDELIG				
	MDGPKVKQW				
	VASGYIEAE				
	VGFTPVNII				
	VKQWPLTEE				
	VYVYRDSRDP				
	WGFTTPDKK				
	VYVYRDSRDP				
	VKQWPLTEE				
	VGFTPVNII				
	VASGYIEAE				
	YVGSDELIG				
	MDGPKVKQW				
	VASGYIEAE				
	VGFTPVNII				
	VKQWPLTEE				
	VYVYRDSRDP				
	WGFTTPDKK				
	VYVYRDSRDP				
	VKQWPLTEE				
	VGFTPVNII				
	VASGYIEAE				
	YVGSDELIG				
	MDGPKVKQW				
	VASGYIEAE				
	VGFTPVNII				
	VKQWPLTEE				
	VYVYRDSRDP				
	WGFTTPDKK				
	VYVYRDSRDP				
	VKQWPLTEE				
	VGFTPVNII				
	VASGYIEAE				
	YVGSDELIG				
	MDGPKVKQW				
	VASGYIEAE				
	VGFTPVNII				
	VKQWPLTEE				
	VYVYRDSRDP				
	WGFTTPDKK				
	VYVYRDSRDP				
	VKQWPLTEE			</	

Table XXb

Core Sequence	Exemplary Sequence	DR1	DR2w01	DR2w202	DR3	DR4w4	DR4w15	DR5w11	DR5w12	SEQ ID NO
VIVYQYMDLL	PEIVYQYMDLLYVG									13164
LKKKKSVTV	PAGLKKKKSVTVLDV	0.0060		-0.0014		-0.0026		-0.0006		13165
VPRRAKJII	IKVVPRRKAKIIRDY	0.0003		0.0700		-0.0024		2.5000		13166
FPQITLWQR	SFSFPQITLWQRPV	0.0027				0.0130				13167
VIWGTTPKF	ESIVWGTTPKFERLP									13168
YVDGAANRE	ETFYVDGAANRETKL									13169
FKNLKTGY	QEPFKNLKTGYAKM									13170
IQTKELQKQ	ATDIQTKELQKQITK									13171
YQKQAGDD	IRDYGKQKAGDDCVA									13172
WRAMASDFN	HSNWRAMASDFNLPP	0.1500	0.0004	0.1600	-0.0030	4.7000	2.6000	0.2100	-0.0045	13173
ISKIGPENP	EGKISKIGPENPYNT									13174
LTQIGCTLN	RNLLTQIGCTLNFPI	0.0001		-0.0014		-0.0026		-0.0007		13175
IIOAQPKS	ALGIIIOAQPKSESE									13176
LPEKDSWTV	PIVLPKDSWTVNDI	0.0320	0.0320	0.0200	-0.0043	0.0058	0.6500	0.0660	-0.0045	13177
FQSSMTKIL	PAIFQSSMTKILEPF									13178
FTIPSINNE	YTAFTIPSINNETPG	0.0140	0.0420	0.0300	-0.0043	0.0140	0.3500	0.0270	0.0122	13179
IIEQLIKKE	VSQIIEQLIKKEKVV									13180
LSWVPAHKG	KVYLSWVPAHKGIGG									13181
YLSWVPAHK	EKVYLSWVPAHKGIG	0.0270	0.1300	0.0048	-0.0043	0.1700	0.2800	0.0110	0.0089	13182
YTAFTIPSI	FRKYTAFTIPSIINNE									13183
IATDIQITK	IDIATDIQITKELQ									13184
IWKGPALKL	RDPWKGPALKLLWKG									13185
LQKQITKQ	TKELQKQITKQIONFR	0.0071	0.0210	0.0350		0.0540	0.0200	0.0530		13186
LKEALLDTG	GGQLKEALLDTGADD	0.0001		-0.0021		-0.0024		-0.0005		13187
VYLSWVPAH	KEKVYLSWVPAHKGII									13188
FILKLAGRW	TAYFILKLAGRWTVK									13189
LEGKILVA	CTHILEGKILVAHVH									13190
YFLKLAGR	ETAYFILKLAGRWVPV									13191
IILVAVHVA	BGKILVAVHVASGY									13192
IWGTTPKER	SIVIWGTTPKFRPLPI									13193
LAGRWVPKV	ILKLAGRWVPKVVIHT									13194
VVAKEIVAS	LPVVVAKEIVASCDK	0.0001		-0.0021		0.0043		-0.0010		13195
IDIATDIQ	ERIDIATDIQITKE									13196
IIDIATDI	GERIDIATDIQITK									13197
IIGRNMLTQ	PVNIIGRNMLTQIGC									13198
IKVKQLCKL	YAGIKVKQLCKLLRG									13199
VDKLVSIGI	NEQVDKLVSIGIRKV									13200
IVGAETFYV	KEPVGAETFYVDGA									13201
LPVVAKEI	DFNLPPVVAKEIVAS	0.0042		-0.0021		-0.0024		0.0036		13202
WTVQIQLP	PDKWTVQIQLPEKD									13203
FNLPPVAK	ASDFNLPPVVAKEIV	0.0026		-0.0021		-0.0028		-0.0006		13204
FTSAAVKAA	GSNFTSAAVKAACWV									13205
LALQDSGLE	AHLALQDSGLEVNI									13206
LPPIVAKEI	DFNLPPVVAKEIVAS									13207
LQDSGLEVN	HLALQDSGLEVNIVT									13208
FNLPPVAK	ASDFNLPPVVAKEIV									13209
IGQIRAKIE	DLEIGQIRAKIEELR									13210
IIGRNLLTQ	PVNIIGRNLLTQIGC	0.0059		-0.0014		0.0043		0.0990		13211
IENIVTDSQ	DSGLEVNIVTDSQYA	0.0001		-0.0014		0.0350		-0.0007		13212
										13213

6500 Table XIXb
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw53	SEQ ID NO.
VTYQYMDL	PEIYIYQYMDLTVG		0.0140				13164
LKKKSVTV	PAGLKKKKSQTVLDV		0.0030				13165
VPRKAKII	IKVVPRRKAKIIRDY		0.0006				13166
FPQITLWQR	SESPQITLWQRPV						13167
VIWGTPKF	ESTVIWGTTPKFRLP						13168
YVDGAANRE	ETFYVDGAANRETKL						13169
FKNLTKGY	QEPFKNLTKGYAKM						13170
IQTKELQKQ	ATDIQTKELQKQITK						13171
YGKQMGDD	IRDYGKQMGDDCVA						13172
WRAMASDFN	HSNWRAMASDFNLFP	0.0008	0.0530	0.0250	0.0860		13173
ISKIGPENP	EGKISKIGPENPYNT		-0.0005				13174
LTQIGCTLN	RNLLTQIGCTLNPI						13175
IIQAQPKS	ALGIQAQPKKSESE						13176
LPEKDSWTV	PVLPKDSWTVNDI	0.1100	0.7300	0.0140	0.9100		13177
FQSSMTKIL	PAIFQSSMTKILEPF	0.2800	0.3700	0.0150	2.3000		13178
FTIPSINNE	YTAFTIPSINNETPG						13179
IFQSSMTKI	SPAIQSSMTKILEP						13180
IIQLJKKE	VSQIIEQLJKKEKY						13181
LSWVPAHKG	KVYLSWVPAHKGIG						13182
YLSWVPAHK	EKYLSWVPAHKGIG	-0.0004	0.8400	0.0610	1.9000		13183
YTAFTIPSI	FRKYTAFTIPSINNE						13184
IIATDIQTK	IIIIATDIQTKELQ						13185
IWKGPAKLL	RDPWKGPAKLLWKG	0.0050	0.0055	0.0250	0.0028		13186
LQKQITKIQ	TKELQKQITKIQNFR		-0.0009				13187
LKEALLDTG	GGQLKEALLDTGADD						13188
VYLSWVPAH	KEKYYLSWVPAHKG						13189
FILKLAGRW	TAYFILKLAGRWPKV						13190
LEGKILVA	CTHLEGKILVAHV						13191
YFILKLAGR	ETAYFILKLAGRWTV						13192
IIIVAVHVA	EGKILVAVHVASGY						13193
IWGTIPKFR	SIVIWGTIPKFRPLI						13194
LAGRPVKY	ILKLAGRPVKVVIHT						13195
VVAKEIVAS	LPVVVAKEIVASCDK		-0.0009				13196
IIIIATDIQ	ERIIIIATDIQTK						13197
IIIRNMLTQ	GERIIIIATDIQTK						13198
IKVKQLCKL	PVNIIRNMLTQIGC						13199
VDKLYSSGI	YAGIKVKQLCKLLRG						13200
IVGAETFYV	NEQVDKLYSSGIRKV						13201
LPVVVAKEI	KEPVGAEITYVDGA		0.0530				13202
WTQIQPLP	DFNLPPVVAKEIVAS						13203
FNLPPVAK	PDKWTQIQPLPEKD		0.0840				13204
FTSAAVKAA	ASDFNLPPVVAKEIV						13205
LALQDSGLE	GSNFTSAAVKAAACW						13206
LPPIVAKEI	AHIALQDSGLEVNI						13207
LQDSGLEVN	DFNLPPVVAKEIVAS						13208
FNLPPVAK	IIIALQDSGLEVNI						13209
IGHRAKIE	IIIALQDSGLEVNI						13210
IIIRNMLTQ	ASDFNLPPVVAKEIV						13211
LEVNIIVTDS	DLEIGQHRAKIEELR		-0.0005				13212
	PVNIIRNMLTQIGC		-0.0005				13213
	DSGLEVNIIVTDSQYA						

HIV DR Super Motif Peptides with Binding Information

[illegible]

Table XIXb
HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw53	SEQ ID NO.
LRGAKALTD	CKLLRGAKALTDIVP						13214
LVSSGIRKV	VDKLVSSGIRKVLFL						13215
FLLKLAGRW	TAYFLLKLAGRWTVK						13216
LALQDSGE	AHLALQDSGSEVNI						13217
LQDSGSEVN	HLALQDSGSEVNI						13218
VKVIHTDNG	RWPVKVIHTDNGSNF						13219
WPVKVIHTD	AGRWPVKVIHTDNGS						13220
YELLKLAGR	ETAYFLLKLAGRWTV						13221
ICGKKAIGT	LIEICGKKAIGTVLV						13222
IVAKENVAS	LPPIVAKENIVASC DK						13223
LRWGFTTDP	QHLLRWGFTTDPDKKH						13224
LEGKVLVA	CTHLEKVLVA VHV						13225
LKWGFTTDP	EHLKVGFTTDPDKKH						13226
VILVAHVVA	EGKVILVAHVVASGY						13227
LAWPAHKG	KVYLA WPAHKGIGG						13228
YDQILIEIC	VRQYDQILIEICGKK						13229
YLA WPAHKG	EKVYLA WPAHKGIG						13230
ICGHRKIE	DLEIGQHRKIEELR						13231
IGRNLTIQI	VNIIGRNLTIQIGCT						13232
LWORPLVTI	QITLWORPLVTIKIG						13233
VSLTEITNQ	QKVSLTEITNQKTE						13234
VYLA WPAH	KEKVYLA WPAHKGIG						13235
ICGUKAIGT	LIEICGUKAIGTVLV						13236
LRGKALTE	CKLLRGKALTEVIP						13237
LVNQIEQL	ESELVNQIEQLIKK						13238
LVSQIEQL	ESELVSQIEQLIKK						13239
YFSPDLKD	GDAYFSPDLKDIFRK						13240
IGRNLMTQI	VNIIGRNLMTQIGCT						13241
IKVRQLCKL	YFGKVRQLCKLLRG						13242
LWGPAPKLL	RDPLWGPAPKLLWKG						13243
LWQPLVTI	QITLWQPLVTIKIG						13244
YAGIKVKQL	SQIYAGIKVKQLCKL						13245
IWKTPKFK	SIVIWKTPKFKLPI						13246
LREHLKKG	IEELREHLKKGFTT						13247
VQIQLPEK	KWTVPQIQLPEKDSW						13248
WQPLVTIK	ITLWQPLVTIKIGG						13249
IQAQDPRS	ALGIQAAQDRSESE						13250
LQAIHLAQ	KTELQAIHLALQDSG						13251
LVEICTEME	IKALVEICTEMEKEG						13252
LROHLRWG	IEELRQHLLRWGFTT						13253
LTQLGCTLN	RNMLTQLGCTLNFI						13254
LVSAGIRKV	VDKLVSAGIRKVLFL						13255
VDKLVSAGI	NEQVDKLVSAGIRKV						13256
YPGIKVRQL	SQIYPGIKVRQLCKL						13257
FRKQNPDI	LEPFRKQNPDIYIQ						13258
FSPQITLW	TVSFSFPQITLWQRP						13259
FTSTTVKAA	GSNFTSTTVKAAACW						13260
IIASDIQTK	IIIIASDIQTKELQ						13261
LAGRWPTKT	LLKLAGRWPTKTTH						13262
VQKIATESI	TEAVQKIATESIVW						13263

6650Table XIX 221460 HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR1	DR2wB1	DR2wB2	DR3	DR4w4	DR4w15	DR5w11	DR5w12	SEQ ID NO.
FTIPSTNNE	YTAFTIPSTNNETPG									13264
LEDINLPK	DTVLEDINLPKWKP									13265
LTDIVPLTE	AKALTDIVPLTEAE									13266
LVTIKIGGQ	QRPLVTIKIGGQKE									13267
MRGAHTNDV	YARMRGAHTNDVKQL									13268
VKTIHTDNG	RWPVKTIHTDNGSNF									13269
VQVILPEK	KWTVQVILPEKDSW									13270
WPVKTIHTD	AGRWPVKTIHTDNGS									13271
WORPLVTVK	ITLWQRPLVTVKIGG									13272
WTVQVILP	PDKWTVQVILPEKD									13273
YTAFTIPST	FRKYTAFTIPSTNNE									13274
IDHASDIQ	ERIIDIASDIQIKE									13275
IIDHASDI	GERIIDIASDIQIK									13276
IVDIATDI	GERIVDIATDIQIK									13277
LEEINLPK	DTVLEEINLPKWKP									13278
LQAIYLALQ	KTELQAIYLALQDSG									13279
LQKQIKIQ	TKELQKQIKIQNFR									13280
VDIATDIQ	ERIVDIATDIQIKE									13281
YDQFIEIC	VRQYDQFIEICGKK									13282
FNFPQITLW	VPTFNFPQITLWQRP									13283
IGRNMLTQL	VNIIGRNMLTQLGCT									13284
ISRIGPENP	EGKISRIGPENPYNT									13285
LTEVIPLTE	TKALTEVIPLTEAE									13286
MESIVWGK	KIAMESIVWGKTPK									13287
VPRKVKII	IKVPRKVKIIRDY									13288
VSEFPQIT	QGTVSFSFPQITLWQ									13289
WYQLETEPI	VKLWYQLETEPIVGA									13290
YPGKVKQL	SQIYPGKVKQLCKL									13291
FPOGEAREF	NLAFFPOGEAREFPE									13292
LIEALLDTG	GGQJIEALLDTGADD									13293
VSLDTITNQ	QKVVS�DTITNQKTE									13294
WETWWTDYW	KETWETWWTDYWQAT									13295
YAKMRTAHT	TGKYAKMRTAHTNDV									13296
YKNLKTGKY	QEPYKNLKTGKYARM									13297
LQLPPLERL	PVPLQLPPLERLTLD									13298
VPLQLPPL	AEPVQLPPLERLT									13299
LYQSNPPPS	IKFLYQSNPPPSPEG									13300
YQSNPPSP	LKAVRIKILYQSNP									13301
LQLPIERL	KFLYQSNPPPSPEGT									13302
VPLQPIE	PVPLQLPPIERLRLD									13303
WNHPSQPK	AEPVQLPPIERLR									13304
FLNKGGLIS	LEPNWNHPSQPKTAC									13305
WKHPGSQPK	QVCFNLKGLISYGR									13306
YCKKCCFHC	LEPWKHPGSQPKTAC									13307
YCKKCCYHC	NNCYCKKCCFHCQVC									13308
WNHPSQPT	TNCYCKKCCYHCQVC									13309
MIVWQVDRM	LEPNWNHPSQPTTAC									13310
WQVMIVWQV	WQVMIVWQVDRMRIR									13311
WQVDRMRJR	ENRWQVMIVWQVDRM									13312
	MTVWQVDRMRIRTWK									13313

0.00320

0.0031

-0.0045

0.0032

1.9000

0.0690

-0.0043

0.0036

0.0059

3.3000

HIV DR Super Motif Peptides with Binding Information

[illegible]

663001 6621450
Table XIXb

HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw53	SEQ ID NO.
LOYLALTAL	VGSLQYLALTALIKP						13314
LGHGVSEW	DWHLGHGVSEWRLR						13315
VDRMRITW	VWQVDRMRITWNSL						13316
YDFCFESA	HLYYDFCFESAIRN						13317
YWGHTGER	ITTYWGLHTGERDWH						13318
IRTNLSLVK	RMIRTNWNSLVKHHM						13319
LQQGVSEW	DWHLGGQGVSEWRKK						13320
LVKHHMYVS	WNSLVKHHMYVSKKA						13321
IPLGEARLV	EVHPLGEARLVVRT						13322
LVKHHMYIS	WKSLSVKHHMYISGKA						13323
YLALTALIK	SLQYLALTALIKPKK						13324
IRTWKSLVK	RMIRTNWKSLSVKHHM						13325
LADQLJHLY	DPDLADQLJHLYYFD						13326
LALTALIKP	LQYLALTALIKPKKI						13327
VDPGLADQL	STQVDPGLADQLJHL						13328
LYYDFCFSE	LIHLYYDFCFESAII						13329
FSESARKA	FDGCFESAIRKAILG						13330
LADQLIHHM	EPGLADQLIHHMYFD						13331
WQVDRMKIR	LIVWQVDRMKIRTNW						13332
FSDSAIRKA	FDGCFESAIRKAILG						13333
FSESARINA	LGHVSPRCEYQAGH						13334
IVSPRCEYQ	VGSLQYLALALALITP						13335
LQYLALAL	VWQVDRMKIRTNWNSL						13336
VDRMKIRTW	IKTYWGLQTGERDWH						13337
YWGLQTGER	EVHPLGDARLVIT						13338
IPLDGARLV	VGSLQYLALALALVTP						13339
LQYLALKAL	MIVWQVDRMRINTWK						13340
WQVDRMRIN	TALIKPKKIKPPLPS						13341
IKPKKIKPP	VWQVDRMRINTWKSL						13342
VDRMRINTW	HFRIGCQHSRIGITR						13343
IGCQHSRIG	YNEWTLELEELKSE						13344
WTLLELEEL	IIRILQQLFIHFR						13345
ILQQLFIH	QLLFIHFRIGCQHSR						13346
FIHFRIGCQ	REPYNWTLLELEEL						13347
YNEWTLELL	VRHPPRWLHGLGOH						13348
FPRWLHGL	GDTWEGVEAIRILQ						13349
WEGVEAIRH	LELEELKSEA VRHF						13350
LEELKSEAV	GDTWAGVEAIRILQ						13351
WAGVEAIRH	YETYGDTWAGVEAII						13352
YGDTWAGVE	HFRIGCRHSRIGITR						13353
IGCRHSRIG	QLLFIHFRIGCQHSR						13354
FIHFRIGCR	YETYGDTWTGVEAII						13355
FVHFRIGCQ	VRHPPRWLHSLGOH						13356
YGDTWTGVE	YNEWALELEELKNE						13357
FPRWLHSL	EEWLVTLSSSKLDQ						13358
WALELEEL	EWLVTLSSSKLDQ						13359
LVTLLSSSK	VVAHAIVVWTIVFI						13360
VTLSSSKL	LAKVDYRIVIVAFIV						13361
IAIVVWTI							13362
VDYRIVIVA							13363

0.0084

III.V DR Super_Motif Peptides with Binding Information

[illegible]

665011
 Table XIXb
 HIV DR Super Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR3w2	DR9	DRw53	SEQ ID NO.
LRQRKIDRL	RKILRQRKIDRLIDR						13364
IVVWTVF	IIAIVVWTVFIEYR						13365
VVWTVFIE	IAIVVWTVFIEYRK						13366
IEYRKILRQ	IVFIEYRKILRQRKI						13367
IIAIVLVV	SLYIIAIVLVVAII						13368
WTVFIEYR	IVVWTVFIEYRKIL						13369
LAIVLVVA	LQIIAIVLVVAGII						13370

Table XXa

HIV DR 3a Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)	SEQ ID NO.
ENV	VPTDNPQE	53	83	HACVPTDNPQEVVL	85	12	19	13371
ENV	YLDKQQLLG	31	48	VERYLKQQLLGIWVG	669	18	28	13372
ENV	MHEDIISLW	29	45	VEQMHEIISLWDS	114	17	27	13373
ENV	VSEPIPH	29	45	CPKVSFPIPIHYCA	250	18	28	13374
ENV	LAVERYLKD	26	41	ARVLAVERYLKDQQL	664	15	23	13375
ENV	VKIEPLGVA	23	36	YKVVKIEPLGVAPTK	564	15	23	13376
ENV	VWKEATTL	22	34	GVVWKEATTLFCA	52	22	34	13377
ENV	LAWDDLRL	20	31	FLALAWDDLRLSLCLF	849	19	30	13378
ENV	LIBESQNL	20	31	IYTLIESQNLQEQKN	737	07	11	13379
ENV	LGWGLKYL	09	29	GLRLGWGLKYLWNL	892	07	23	13380
ENV	LELDKWASL	18	28	QELLELDKWASLWNW	753	07	11	13381
ENV	YLRDQQLLG	18	28	VERYLKQQLLGIWVG	669	11	17	13382
ENV	MWQEVGKAM	15	23	IINMWQEVGKAMYAP	492	12	19	13383
ENV	IEEGERD	13	20	PEGIEEGGERDRDR	827	08	13	13384
ENV	MNNENGTN	01	20	INMNNENGTNSTW	212	01	2	13385
ENV	IEEGBEQD	12	19	LGRIEEGBEQDKNR	827	02	3	13386
ENV	LAEEVVR	12	19	NGSLAEEVVRSEN	309	04	8	13387
ENV	LALDKWASL	11	17	QDLLALDKWASLWNW	753	05	6	13388
ENV	LAVERYLRD	11	17	ARVLAVERYLRDQQL	664	10	16	13389
ENV	IRSENLTNN	10	16	EIIRSENLTNNVKT	317	03	5	13390
ENV	MEWEREIDN	10	16	MTWMEWEREIDNYTS	721	03	5	13391
ENV	INEEAAEWD	55	86	KETINEEAAEWDRLH	223	18	28	13392
GAG	FSPEVPMF	34	84	EKAFAFSPEVPMFSAL	182	36	56	13393
GAG	VLAEAMSVQ	33	52	KARVLAEAMSVQVTS	383	09	14	13394
GAG	MLKDTINEE	32	50	AMQMLKDTINEEAAE	218	30	47	13395
GAG	VVEKAFSP	28	44	WVKVVEKAFSPEVI	176	28	44	13396
GAG	LRAEQATQE	27	42	FKTLRAEQATQEVKN	325	09	14	13397
GAG	MLKETINEE	23	36	AMQMLKETINEEAAE	218	22	34	13398
GAG	VTEKAFSP	21	33	WVKVTEKAFSPEVI	176	20	31	13399
GAG	VLAEAMSKA	16	25	KARVLAEAMSKASGA	383	03	5	13400
GAG	IEEEQNSK	15	23	LDKIEEEQNSKSKKA	103	09	14	13401
GAG	LRAEQATQD	14	22	FKTLRAEQATQDVKN	325	10	16	13402
GAG	LRAEQASQE	12	19	YKTLRAEQASQEVKN	325	12	19	13403
GAG	YFPDWQNTY	36	56	TQGYFPDWQNTYTPG	195	33	52	13404
NEF	FLKEGGGLE	30	47	LSHFLKEGGGLEGLI	114	15	23	13405
NEF	FLKEGGGLD	26	41	LSFFLKEGGGLDGLI	114	14	22	13406
NEF	FPDWQNTY	17	27	TQOFFPDWQNTYTPG	195	17	27	13407
NEF	VSRDLEKHG	11	17	VGAVSRDLEKHGAT	46	11	17	13408
NEF	YMDLLVGS	62	97	IYQYMDLLVYGSLE	369	59	92	13409
POL	IGPENPYNT	60	94	ISKIGPENPYNTPVF	236	28	44	13410
POL	LHPDKWTVQ	59	92	GYELHDPDKWTVQPIQ	420	29	45	13411
POL	IPAEQGET	58	91	EVNIVTDSQYALGII	684	58	91	13412
POL	LTEEKIKAL	56	88	AEVPAETGQETAYF	838	55	86	13413
POL	IEAEVPAE	55	86	SGYIEAEVPAETGQ	833	26	41	13414
POL	LFLDGIDKA	55	86	KKVFLFDGIDKAEQE	749	32	50	13415
POL	VAKEIVASC	54	86	PPVVAKEIVASCDKC	781	22	34	13416
POL	LKGEAMHGQ	53	83	KCQLKGEAMHGQVDC	794	47	73	13417
POL	VGSDLEIGQ	53	83	DLYVGSDLEIGQHRA	375	28	44	13418
POL	IIRDYKQKM	50	78	KAKIIRDYKQKMAGD	1017	36	56	13420

IIIV DR 3a Motif Peptides

SEO ID NO.

Exemplary Sequence
Conservancy(%)

Exemplary Sequence	Frequency
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Position

Exemplary Sequence

Core Sequence
Conservancy(%)

Core Sequence	Frequency
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99	1
100	1

Core Sequence

Protein

HIV DR 3a Motif Peptides with Binding Information

[illegible]

655007-0001-160

Table XXb

HIV DR 3a Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw53	SEQ ID NO.
VPTDPNPQE	HACVPTDPNPQEVVL						13371
YLDQQLLG	VERYLKDDQLLGIWG						13372
MIHDIISLW	VEQMHHDIISLWDQS						13373
VSFERPIH	CPKVSFEPIHYCA						13374
LAVERYLKD	ARVLAVERYLKDQQL						13375
VRIEPLGVA	YKVVVKIEPLGVAPTK						13376
VWKEATTL	GVPVWKEATTLFCA						13377
LAWDDLRL	FLALAWDDLRLSLCLF						13378
LGWEGKYL	GLRLGWEGKYLWNL						13379
LELDKWASL	QELLELDKWASLWNW						13380
YLRDQQLLG	VERYLKDDQLLGIWG						13381
MWQEVGKAM	IINMWQEVGKAMYAP						13382
IEEEGERD	PEGIEEGGERDRDR						13383
IEEEGEQD	INEMNENNGTNTSTW						13384
LAEEVVIR	LGRIEEGEGEQDKNR						13385
LALDKWASL	NGSLAEEVVIRSEN						13386
LAVERYLKD	QDLALDKWASLWNW						13387
IRSENLTNN	ARVLAVERYLKDQQL						13388
MEWEREIDN	EIIIRSENLTNNVKT						13389
INEEAEWD	MTWMEWEREIDNYTS						13390
FSPEVTMF	KETINEEAAEWDRJH		0.0023				13391
VLAEMASQV	EKAFSPEVPMFSAL		0.0025				13392
MLKDTNEE	KARVLAEMASQVTS						13393
VVEEKAFSP	AMQMLKDTINEEAAE						13394
LRAEQATQE	WVKVVEEKAFSPFVI		0.0003				13395
MLKETNEE	FKTLRAEQATQEVKN						13396
VIEEKAFSP	AMQMLKETINEEAAE						13397
VLAEMASQA	WVKVIEEKAFSPFVI						13398
IEEQNKSK	KARVLAEMASQAASGA						13399
LRAEQATQD	LDKIEEQNKSKKKA						13400
LRAEQASQE	FKTLRAEQATQDVKN						13401
YFPDWQNTY	YKTLRAEQASQEVKN						13402
FLKEKGGLD	TQGYFPDWQNTYTPG						13403
FPDWQNTY	LSIFLKEKGGLDGLI						13404
YMDLLYVGS	LSFFLKEKGGLDGLI						13405
IGPENPNT	TQGFPPDWQNTYTPG						13406
LHPDKWTQ	VGAVSRLDLEKHGAT						13407
IVTDSQYAL	IYQYMDLLYVGSDDLE						13408
IPAEITQET	ISKIGPENPNTYTPV		-0.0005				13409
LTEEKIKAL	GYELHPDKWTVPPIQ	0.0108	-0.0014				13410
VAKEIVASC	EVNIVTDSQYALGII			-0.0009			13411
VGSLEIGQ	AEVIPAEITQETAYF						13412
IIRYQKQM	QWFLTEEKIKALTEI						13413
	SGYIEAEVIPAEITQ						13414
	RKVLFLDGDIDKAQEE						13415
	PPVVAKEIVASCDC						13416
	KCOLKGEAMHGQVDC		0.0015				13417
	DLYVGSLEIGQHRA						13418
	KAKIIRDYGKQMAGD						13419
							13420

Table XXb

HIV DR 3a Motif Peptides with Binding Information

[illegible]

6550 Table XXb. 2007-1460
HIV DR 3a Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw53	SEQ ID NO.
MASDFNLPP	WRAMASDFNLPPVVA						13421
FYVDGAANR	AETFFYVDGAANRETK	-0.0002	-0.0014	0.0035			13422
IHTDNGSNF	VKVIHTDNGSNFTSA						13423
ILKEPVHGV	NREILKEPVHGVYVD	0.0120	0.0033	0.0010	0.0210		13424
IYQEPFKNL	TYQIYQEPFKNLKTG						13425
VYDFPSKDL	VHGVYDFPSKDLIAE						13426
YVTDGRQK	KAGYVTDGRQKVVVS						13427
LTEEALEL	IVPLTEEALELEAEN						13428
VIQNSDIK	GAVVIQNSDIKVVVP	0.0447	-0.0014	-0.0009			13429
IATDIQKE	IDIAIDTIQKELQK						13430
INNETPGIR	IFSINNETPGIRYQY						13431
LIAEIQKQG	SKDLIAEIQKQGQGG						13432
ICTEMEKEG	LYEICTEMEKEGKIS						13433
VGAETFFVD	ERIVGAETFFYVDGAA						13434
IQKETWEIW	RLPIQKETWEIWWTD						13435
IKQEPGIPY	WAGIKQEPGIPYNPQ	0.0123	-0.0014	-0.0009			13436
MAGDDCVAG	GKQMGDDCVAGRQD				0.0011		13437
IKKEKVYLA	EQLIKKEKVYLAWVP	-0.0003	-0.0005	-0.0015			13438
MAGDDCVAS	GKQMGDDCVASRQD						13439
VPLDKDFRK	YFSVPLDKDFRKYTA						13440
IQKEFGIPY	WAGIQKEFGIPYNPQ						13441
LEKEPIVGA	WYQLEKEPIVGAETF						13442
YQLEKEPIV	KLWYQLEKEPIVGAE						13443
IQKETWEAW	KLPIQKETWEAWWTE						13444
FSSEQTRAN	AREFSSEQTRANSPPT						13445
IASDIQKE	IDIIASDIQKELQK						13446
LATESIIVV	VOKIATESIIVIWGKT						13447
ILIEICGKK	YDQILIEICGKKAIG						13448
VLEENLPG	DDTVLEENLPGKWK						13449
IKKEKVYLS	EOLIKKEKVYLSWVP						13450
VLEDINLPG	DDTVLEDINLPGKWK						13451
VLPKDSWT	QPIVLPKDSWTVND						13452
VIQDNSEIK	GAVVIQDNSEIKVVP						13453
IKDYGKQM	KAKIUDYGKQMAGA						13454
VERETETDP	KEKVERETETDPVAVQ						13455
LTEDRWNKP	VKKLTEDRWNKPKQT						13456
YFFDCFS	IHLYYFFDCFSAIR						13457
LVEDRWNKP	VOKLVEDRWNKPKQT						13458
IDPDLADQL	STQIDPDLADQLIHL						13459
LKNEAVRIIF	LEELKNEAVRHFRP						13460
LKSEAVRHF	LEELKSEAVRHFRP						13461
YIYETGDT	LGQYIYETGDTWAG						13462
LKQEA VRHF	LEELKQEA VRHFRP						13463

665007 "Table XXc" 99827460
 HIV DR 3b Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy (%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy (%)	SEQ ID NO.
ENV	MRDNWRSEL	40	63	GGDMRDNRWSELYKY	550	37	58	13464
ENV	LTVQARQLL	36	56	SITLTQARQLLSGI	620	27	42	13465
ENV	IEAQOHLIQ	35	55	LRAIEAQOHLLOLTV	642	34	53	13466
ENV	IIGDIRQAH	27	44	TGEIIGDIRQAHONI	370	07	11	13467
ENV	VEREKRAVG	23	37	RRVVEREKRAVGIGA	582	11	17	13468
ENV	MVEQMHEDI	23	36	KNNMVEQMHEDISL	110	19	30	13469
ENV	AWDDLRLC	20	31	LALAWDDLRLSLCLS	850	18	28	13470
ENV	LEITTHSFN	20	31	GGDLLEITTHSFNCRG	426	10	16	13471
ENV	YDTEVHNWV	18	28	AKAYDTEVHNWVATH	71	15	23	13472
ENV	AEGTDRIE	17	27	IAVAEGTDRIEVVQ	927	02	3	13473
ENV	VQREKRAVG	17	27	RRVQREKRAVGIGA	582	05	8	13474
ENV	AEGTDRIE	15	23	IAVAEGTDRIEVVQ	927	07	11	13475
ENV	IEAQOHLK	12	19	LRAIEAQOHLKLTIV	642	08	13	13476
ENV	LKCNCKFN	12	19	FAILKCNCKFNFTG	269	05	8	13477
GAG	ANPDCKTIL	45	70	VQANPDCKTILKAL	347	27	42	13478
GAG	FYKTLRAEQ	28	44	VDRFYKTLRAEQASQ	321	19	30	13479
GAG	APGQMREPR	27	42	GPIAPGQMREPRGSD	242	19	30	13480
GAG	FFKTLRAEQ	27	42	VDRFFKTLRAEQATQ	321	26	41	13481
GAG	IWPSHGKRP	23	36	LGKIWPSHGKRPGNF	470	22	34	13482
GAG	LARNCRAPR	20	32	EGHLARNCRAPRKKG	431	19	30	13483
GAG	LAKNCRAPR	18	29	EGHIAKNCRAPRKKG	431	10	16	13484
GAG	ATQEVKNWM	18	28	AEQATQEVKNWMTET	330	14	22	13485
GAG	ATQDVKNWM	15	23	AEQATQDVKNWMTDT	330	11	17	13486
GAG	IARNCRAPR	13	21	EGHIAKNCRAPRKKG	431	13	20	13487
GAG	IWPSNKGPR	13	20	LGKIWPSNKGPRGNF	470	13	20	13488
GAG	ANPDCKSIL	11	17	VQANPDCKSILRAL	347	06	9	13489
GAG	ASQEVKNWM	11	17	AEQASQEVKNWMTET	330	11	17	13490
GAG	IWPSKGRP	10	16	LGKIWPSKGRPNF	470	10	16	13491
NEF	LIYSKKRQE	18	28	LDGLIYSKKRQEILD	171	11	17	13492
NEF	VPDPREVE	11	17	FKLVPDPREVEAN	227	06	9	13493
NEF	MARELHPEY	10	16	FHHMARELHPEYYKD	316	04	6	13494
POL	MGYELHPDK	60	94	FLWMGYELHPDKWTI	416	60	94	13495
POL	FIHFKRKQ	58	91	MAVEIHFKRKQGGIG	930	57	89	13496
POL	MNKLKII	56	89	VESMKNKLKIIQQV	903	45	70	13497
POL	IIGQVRDQA	44	69	LKKIIGQVRDQAHL	910	43	67	13498
POL	YHSNWRAMA	39	61	HEKYIHSNWRAMASDF	764	23	36	13499
POL	MEKEGKISK	36	56	CTEMEKEGKISKIGP	225	22	34	13500
POL	YRDSRDP	34	53	FRVYRDSRDPWKG	975	34	54	13501
POL	ANRETKLQK	30	47	DGAANRETKLQKAGY	635	28	44	13502
POL	IIGQLKEAL	25	39	TIKIGQLKEALLDT	99	17	27	13503
POL	LKDFRXYT	19	30	SVPLDKDFRXYTFT	306	17	27	13504
POL	YRDSRDL	14	22	FRVYRDSRDLWKG	975	13	21	13505
POL	IIGQVREA	13	20	LKKIIGQVREAHL	910	13	20	13506
POL	YHNNWRAMA	10	16	HEKYHNNWRAMASDF	764	06	9	13507
REV	ARNRRRRW	39	61	TROARNRRRRWRAR	38	18	28	13508
REV	ARKNRRRW	18	28	TRQARKNRRRRWRAR	38	13	20	13509
REV	LLKTVRLIK	10	16	DEELKTVRLIKFLY	9	04	6	13510
VIF	ISSEVHIPL	27	42	HPRISSEVHIPLGDA	48	08	13	13511
VIF	VSSEVHIPL	27	42	HPKVSSEVHIPLGEA	48	11	17	13512
VIF	VSIEWRLRR	11	17	GHGVSIEWRLRRYST	85	05	8	13513

Table XXb
HIV DR 3b Motif Peptides

Protein	Core Sequence	Core Sequence Frequency	Core Sequence Conservancy(%)	Exemplary Sequence	Position	Exemplary Sequence Frequency	Exemplary Sequence Conservancy(%)	SEQ ID NO.
VPR	LPSNTRGRG	01	50	IGILPSNTRGRGRN	82	01	2	13514
VPR	LLEELKNEA	17	27	TLELLEELKNEAVRH	19	12	19	13515
VPR	LLEELKSEA	16	25	TLELLEELKSEA VRH	19	15	23	13516
VPU	AKVDYRIVI	01	33	DLLAKVDYRIVTAF	3	01	2	13517
VPU	AKVDYRLGV	01	33	NFLAKVDYRLGVGAL	3	01	2	13518
VPU	ILRQKKIDR	15	23	YRKILRQKKIDRLID	42	12	19	13519

550 Table Xd-332450 HIV DR 3b Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw53	SEQ ID NO.
MRDNWRSEL	GGDMRDNRSELYKY						13464
LTVQARQLL	SITLTVQARQLLSGI						13465
IEAQHLLQ	LRAIEAQHLLQLTV						13466
IIGDIRQAH	TGEIIGDIRQAHNI						13467
VEREKRAVG	RRVVEREKRAVGIG						13468
MVEQMEDI	KNNMVEQMEDIISL						13469
AWDDLRLSLC	LALAWDDLRLSLCLS						13470
LEITTHISFN	GDDLEITTHSFNCRG						13471
YDTEVHNWV	AKAYDTEVHNWVWATH						13472
AEGLDRIE	IAVAEGTDRIEVVQ						13473
VQREKRAVG	RRVQREKRAVGIG						13474
AEGLDRVIE	IAVAEGTDRVIEVQ						13475
IEAQHLLK	LRAIEAQHLLKLTIV						13476
LKCNCKKFN	FAILKCNCKKFNFTG						13477
ANPDKTIL	VQANPDKCKTILKAL						13478
FYKTLRAEQ	VDRFYKTLRAEQASQ						13479
APGQMRPR	GLAPGQMRPRGSD						13480
FFKTLRAEQ	VDRFFKTLRAEQATQ						13481
IWTSKGRP	LGKIWTSKGRPGNF						13482
LARNCRAPR	EGHLARNCRAPRKG						13483
IAKNCRAPR	EGHIAKNCRAPRKG						13484
ATQEVKNWM	AEQATQEVKNWMET						13485
ATQDVKNWM	AEQATQDVKNWMDT						13486
IARNCRAPR	EGHIAARNCRAPRKG						13487
IWTSNKGPR	LGKIWTSNKGPRGNF						13488
ANPDKCSIL	VQANPDKCSILRAL						13489
ASQEVKNWM	AEQASQEVKNWMET						13490
IWTSKGRP	LGKIWTSKGRPGNF						13491
LIYSKKRQE	LDGLIYSKKRQEILD						13492
VPVDPREVE	FKLYVPVDPREVEAN						13493
MARELHPEY	FHHMARELHPEYYKD						13494
MGYELHPDK	FLWMGYELHPDKWTY						13495
FIHFKRKGG	MAVFIHFKRKGGIG						13496
MNKLKXII	VESMNKELKIIQVY						13497
IIGQVRDQA	LKKIIGQVRDQAEHL						13498
YHSNWRAMA	HEKYHSNWRAMASDF						13499
MEKEGKISK	CTEMEKEGKISKIGP						13500
YYRDSRDP	FRVYYRDSRDPWKG						13501
ANRETKLGK	DGAANRETKLGKAGY						13502
IGQLKEAL	TIKIGQLKEALLDT						13503
LDKDFRKYT	SVPLDKDFRKYTAFT						13504
YYRDSRDP	FRVYYRDSRDPWKG						13505
IIGQVRBQA	LKKIIGQVRBQAEHL						13506
YHNNWRAMA	HEKYHNNWRAMASDF						13507
ARNRRRW	TRQARNRRRRWRAR						13508
ARKNRRRW	TRQARNRRRRWRAR						13509
LLKTVRLIK	DEELLKTVRLIKFLY						13510
ISSEVHIPL	HPRISSEVHIPLGDA						13511
VSEVHIPL	HPKYVSEVHIPLGEA						13512
VSIEWRLRR	GHGVSIEWRLRRYST						13513

0.0048

Core Sequence	Exemplary Sequence	DR1	DR2wB1	DR2w2B2	DR3	DR4w4	DR4w15	DR5w11	DR5w12	SEQ ID NO.
LPSNTRGRG	IGILPSNTRGRGRN									13514
LLEELKNEA	TLLELEELKNEAVRH									13515
LLEELKSEA	TLLELEELKSEAVRH									13516
AKVDYRIVT	DLLAKVDYRIVIVAF									13517
AKVDYRLGV	NFLAKVDYRLGVGAL									13518
ILRQRKIDR	YRKILRQRKIDRLID	0.0024	0.0740	0.0410	13.0000	-0.0055		0.1500		13519

Table XXII
HIV DR 3b Motif Peptides with Binding Information

Core Sequence	Exemplary Sequence	DR6w19	DR7	DR8w2	DR9	DRw53	SEQ ID NO.
LPSNTRGRG	IGLPNTRGRGRN						13514
LLEELKNEA	TLELLEELKNEAVRH						13515
LLEELKSEA	TLELLEELKSEAVRH						13516
AKVDYRIMI	DLLAKVDYRIVAF						13517
AKVDYRLGV	NFLAKVDYRLGVGAL						13518
ILQRKIDR	YRKILRQKIDRLID	0.0016	-0.0014	0.0270			13519

TABLE XXI. Population coverage with combined HLA Supertypes

HLA-SUPERTYPES	PHENOTYPIC FREQUENCY					
	Caucasian	North American Black	Japanese	Chinese	Hispanic	Average
<u>a. Individual Supertypes</u>						
A2	45.8	39.0	42.4	45.9	43.0	43.2
A3	37.5	42.1	45.8	52.7	43.1	44.2
B7	38.6	52.7	48.8	35.5	47.1	44.7
A1	47.1	16.1	21.8	14.7	26.3	25.2
A24	23.9	38.9	58.6	40.1	38.3	40.0
B44	43.0	21.2	42.9	39.1	39.0	37.0
B27	28.4	26.1	13.3	13.9	35.3	23.4
B62	12.6	4.8	36.5	25.4	11.1	18.1
B58	10.0	25.1	1.6	9.0	5.9	10.3
<u>b. Combined Supertypes</u>						
A2, A3, B7	83.0	86.1	87.5	88.4	86.3	86.2
A2, A3, B7, A24, B44, A1	99.5	98.1	100.0	99.5	99.4	99.3
A2, A3, B7, A24, B44, A1, B27, B62, B58	99.9	99.6	100.0	99.8	99.9	99.8

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Table XXIII: Immunogenicity of HIV peptides

	Peptide	Sequence	Protein	Immunogenicity	
				patients	transgenic
A2 Supermotif	1261.04	LTFGWCFKL	HIV nef 221	4/12	3/3
	1261.15	MASDFNLPPV	hiv pol 774	1/15	2/6
	1069.32	VLAEMSQV	hiv gag 386	6/19	3/3
	1261.16	CTLNFPISPI	hiv pol 182	0/1	1/6
	1261.02	LLQLTVWGI	HIV env 651	2/8	1/6
	1261.13	KLVGKLNWA	HIV pol 448	3/15	3/3
	1211.04	KLTPLCVTL	HIV env 134	2/12	2/6
	1261.08	ALVEICTEM	HIV pol 220	0/2	1/6
	1261.11	AHRLQQL	HIV vpr 59	5/9	0/6
	1261.09	LVGPTPVNI	HIV pol 163	1/9	1/6
	1261.12	RILQQLFI	HIV vpr 62	6/20	2/6
	1261.05	TLNFPISPI	HIV pol 183	1/7	0/6
	1261.03	MTNNPIPPIV	HIV gag 271	2/17	4/6
	1261.17	KMIGGIGGFI	HIV pol 132	2/7	0/6
	941.03	ILKEPVHGV	HIV pol 498	8/19	3/6
	1261.10	RAMASDFNL	HIV pol 772	2/9	0/6
	1261.07	KAACWWAGI	HIV pol 879	1/8	0/6
A3 Supermotif	1211.32	KIQNFRVYYR	HIV pol 971	4/6	
	1193.03	AVFIHNFKR	HIV pol 931	3/6	
	1069.49	QMAVFIHNFK	HIV pol 929	3/6	
	1150.14	MAVFIHNFK	HIV pol 930	6/6	
	1069.42	KVYLAWVPAHK	HIV pol 722	6/6	
	966.01	AIFQSSMTK	HIV pol 347	5/6	1/6
	940.03	QVPLRPMYK	HIV nef 100	0/6	6/10
	1273.07	TTLFCASDAK	HIV env 61	3/6	
	1273.09	VTIKIGGQLK	HIV pol 98	6/6	
	1069.43	TVYYGVPVWK	HIV env 48		28/33
DR Supermotif	1069.47	VTVYYGVPVWK	HIV env 47	6/6	
	27.0313	KRWILGLNKIVRMY	HIV gag 298	3/13	
	27.0311	GEIYKRWILGLNKI	HIV gag 294	2/13	
	27.0354	WEFVNTPLVLKLYQ	HIV pol 596	2/13	
	27.0377	QKQITKIQNFRVYYR	HIV pol 956	3/13	
	1280.03	KVYLAWVPAHKGIGG	HIV pol 712	3/13	
	27.0361	EKVYLAWVPAHKGIG	HIV pol 711	1/13	
	27.0304	QGQMVHQAI SPRTL N	HIV gag 171	4/13	
	27.0344	SPAIFQSSMTKILEP	HIV pol 335	3/13	
	27.0341	FRKYTAFTIPSINNE	HIV pol 303	3/13	
	27.0364	HSNWRAMASDFNLPP	HIV pol 758	3/13	
	27.0373	KTAVQMAVFIHNFKR	HIV pol 915	4/13	

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Table XXIV. MHC-peptide binding assays: cell lines and radiolabeled ligands.

A. Class I binding assays

Species	Antigen	Allele	Cell line	Radiolabeled peptide	
				Source	Sequence
Human	A1	A*0101	Steinlin	Hu. J chain 102-110	YTAVVPLVY
	A2	A*0201	JY	HBVc 18-27 F6->Y	FLPSDYFPSV
	A2	A*0202	P815 (transfected)	HBVc 18-27 F6->Y	FLPSDYFPSV
	A2	A*0203	FUN	HBVc 18-27 F6->Y	FLPSDYFPSV
	A2	A*0206	CLA	HBVc 18-27 F6->Y	FLPSDYFPSV
	A2	A*0207	21.221 (transfecto)	HBVc 18-27 F6->Y	FLPSDYFPSV
	A3		GM3107	non-natural (A3CON1)	KVFPYALINK
	A11		BVR	non-natural (A3CON1)	KVFPYALINK
	A24	A*2402	KAS116	non-natural (A24CON1)	AYIDNYNKF
	A31	A*3101	SPACH	non-natural (A3CON1)	KVFPYALINK
	A33	A*3301	LWAGS	non-natural (A3CON1)	KVFPYALINK
	A28/68	A*6801	C1R	HBVc 141-151 T7->Y	STLPETYVVR
	A28/68	A*6802	AMAI	HBV pol 646-654 C4->A	FTQAGYPAL
	B7	B*0702	GM3107	A2 sigal seq. 5-13 (L7->Y)	APRTL VYLL
	B8	B*0801	Steinlin	Ngp 586-593 Y1->F, Q5->R 60s	FLKDYQLL
	B27	B*2705	LG2		FRYNGLIHR
	B35	B*3501	C1R, BVR	non-natural (B35CON2)	FPFKYAAAF
	B35	B*3502	TISI	non-natural (B35CON2)	FPFKYAAAF
	B35	B*3503	EHM	non-natural (B35CON2)	FPFKYAAAF
	B44	B*4403	PITOUT	EF-1 G6->Y	AEMGKYSFY
	B51		KAS116	non-natural (B35CON2)	FPFKYAAAF
Mouse	B53	B*5301	AMAI	non-natural (B35CON2)	FPFKYAAAF
	B54	B*5401	KT3	non-natural (B35CON2)	FPFKYAAAF
	Cw4	Cw*0401	C1R	non-natural (C4CON1)	QYDDAVYKL
	Cw6	Cw*0602	21.221 transfecto	non-natural (C6CON1)	YRHDGGNVL
	Cw7	Cw*0702	21.221 transfecto	non-natural (C6CON1)	YRHDGGNVL
	D ^b		EL4	Adenovirus E1A P7->Y	SGPSNTYPEI
	K ^b		EL4	VSV NP 52-59	RGYVFQGL
	D ^d		P815	HIV-IIIIB ENV G4->Y	RGPYRAFTI
	K ^d		P815	non-natural (KdCON1)	KFNPMKTYI
	L ^d		P815	HBVs 28-39	IPQSLDSYWTSL

B. Class II binding assays

Species	Antigen	Allele	Cell line	Radiolabeled peptide	
				Source	Sequence
Human	DR1	DRB1*0101	LG2	HA Y307-319	YPKYVKQNTLKLAT
	DR2	DRB1*1501	L466.1	MBP 88-102Y	VVHFFKNIVTPRTPPY
	DR2	DRB1*1601	L242.5	non-natural (760.16)	YAAFAAAKTAFAAFA
	DR3	DRB1*0301	MAT	MT 65kD Y3-13	YKTIAFDEEARR
	DR4w4	DRB1*0401	Preiss	non-natural (717.01)	YARFQSQTTLKQKT
	DR4w10	DRB1*0402	YAR	non-natural (717.10)	YARFQRQTTLKAAA
	DR4w14	DRB1*0404	BIN 40	non-natural (717.01)	YARFQSQTTLKQKT
	DR4w15	DRB1*0405	KT3	non-natural (717.01)	YARFQSQTTLKQKT
	DR7	DRB1*0701	Pitout	Tet. tox. 830-843	QYIKANSKFIGITE
	DR8	DRB1*0802	OLL	Tet. tox. 830-843	QYIKANSKFIGITE
	DR8	DRB1*0803	LUY	Tet. tox. 830-843	QYIKANSKFIGITE
	DR9	DRB1*0901	HID	Tet. tox. 830-843	QYIKANSKFIGITE
	DR11	DRB1*1101	Sweig	Tet. tox. 830-843	QYIKANSKFIGITE
	DR12	DRB1*1201	Herluf	unknown eluted peptide	EALIHQLKINPYVLS
	DR13	DRB1*1302	H0301	Tet. tox. 830-843 S->A	QYIKANAKFIGITE
	DR51	DRB5*0101	3M3107 or L416.	Tet. tox. 830-843	QYIKANAKFIGITE
	DR51	DRB5*0201	L255.1	HA 307-319	PKYVVKQNTLKLAT
	DR52	DRB3*0101	MAT	Tet. tox. 830-843	NGQIGNDPNRDIL
	DR53	DRB4*0101	L257.6	non-natural (717.01)	YARFQSQTTLKQKT
	DQ3.1	QA1*0301/DQB1*0301	PF	non-natural (ROIV)	AHAHAHAHAHAHAHA
Mouse	IA ^b		DB27.4	non-natural (ROIV)	AHAHAHAHAHAHAHA
	IA ^d		A20	non-natural (ROIV)	AHAHAHAHAHAHAHA
	IA ^k		CH-12	HEL 46-61	YNTDGSTDYGILQINSR
	IA ^s		LS102.9	non-natural (ROIV)	AHAHAHAHAHAHAHA
	IA ^u		91.7	non-natural (ROIV)	AHAHAHAHAHAHAHA
	IE ^d		A20	Lambda repressor 12-26	YLEDARRKKAIYEKKK
	IE ^k		CH-12	Lambda repressor 12-26	YLEDARRKKAIYEKKK

Table XXV. Monoclonal antibodies used in MHC purification.

Monoclonal antibody	Specificity
W6/32	HLA-class I
B123.2	HLA-B and C
IVD12	HLA-DQ
LB3.1	HLA-DR
M1/42	H-2 class I
28-14-8S	H-2 D ^b and L ^d
34-5-8S	H-2 D ^d
B8-24-3	H-2 K ^b
SF1-1.1.1	H-2 K ^d
Y-3	H-2 K ^b
10.3.6	H-2 IA ^k
14.4.4	H-2 IE ^d , IE ^K
MKD6	H-2 IA ^d
Y3JP	H-2 IA ^b , IA ^s , IA ^u

Table XXVI. The table lists the 64 fully represented aligned amino acid sequences that were identified for Motif analysis. Included are the aligned amino acid sequence ID number, the complete nucleotide sequence name it was derived from, the accession numbers for the sequence, the subtype, country and the total length of all nine sequences.

	ID Number	Name	Accession Numbers	Subtype	Country	Length
1	A.KE.Q23-CxC-CG	HIVQ2317	AF004885	A	KE	3584
2	A.SE.UGSE8891	AUGSE8891	AF069673	A	SE	3584
3	A.UG.92UG037	H92UG037	U51190	A	UG	3584
4	A.UG.U455	HIVU455A	M62320	A	UG	3584
5	AC.IN.21301	21301	AF067156	AC	IN	3584
6	AC.RW.92RW009	92RW009	U88823	AC	RW	3584
7	AC.ZM.ZAM184	ZAM184	U86780	AC	ZM	3584
8	ADI.ZR.MAL	HIVMALCG	K03456, X04415	ADI	ZR	3584
9	AE.CF.90CR402	HIV90CF402	U51188	AE	CF	3584
10	AE.TH.93TH253	H93TH253	U51 189	AE	TH	3584
11	AE.TH.CM240	HIV1CM240	U54771	AE	TH	3584
12	AG.DJ.DJ263	DJ263	AF063223	AG	DJ	3584
13	AG.DJ.DJ264	HDJ264	AF063224	AG	DJ	3584
14	AG.NG.92NG003	92NG003	U88825	AG	NG	3584
15	AG.NG.92NG083	H92NG083	U88826	AG	NG	3584
16	AG.NG.IBNG	HIVIBNG	L39106	AG	NG	3584
17	AGI.CY.94CY0323	94CY032-3	AF049337	AGI	CY	3584
18	AGI.ZR.Z321	HIVU76035, Z321B	U76035	AGI	ZR	3584
19	AGJ.AU.BFP90	HIVBFP90	AF064699	AGJ	AU	3584
20	B.CN.RL42	HCHRL42CG	U71182	B	CN	3584
21	B.DE.D31	HIV1D31	U43096	B	DE	3584
22	B.DE.HAN	HIVHAN2	U43141	B	DE	3584
23	B.FR.HXB2R	HIVHXB2	AF033819, K03455, M38432	B	FR	3584
24	B.GA.OYI	HIVOYI	M26727	B	GA	3584
25	B.GB.CAM1	HIVCAM1	D00917, D10112	B	GB	3584
26	B.GB.MANC	HIV1MANC	U23487	B	GB	3584
27	B.NL.ACH32OA	HIV1ACH32OA	U34604	B	NL	3584
28	B.US.ADA	HIV1AD8	AF004394	B	US	3584
29	B.US.DH123	HIV1DH123	AF069140	B	US	3584
30	B.US.JRCSF	HIVJRCSF	M38429	B	US	3584
31	B.US.JRFL	HIVJRFL	U63632	B	US	3584
32	B.US.MN	HIVMN	M17449	B	US	3584
33	B.US.P896	HIV1896	M96155, U39362	B	US	3584
34	B.US.RF	HIVRF	M12508	B	US	3584
35	B.US.SF2	HIVSF2CG	K02007	B	US	3584
36	B.US.WEAU16O	HIVWEAU160	U21135	B	US	3584
37	B.US.WR27	HIV1WR27	U26546	B	US	3584
38	B.US.YU2	HIVYU2	M93258	B	US	3584
39	BF.BR.93BR029.4	93BR029	AF005495	BF	BR	3584
40	C.BR.92BR025	H92BR025	U52953	C	BR	3584
41	C.BW.BW96BW0502	96BW0502	AF110967	C	BW	3584
42	C.ET.ETH2220	HIVETH2220	U46016	C	ET	3584
43	C.IN.11246	1N11246	AF067159	C	IN	3584
44	C.IN.21068	C1N21068	AF067155	C	IN	3584
45	C.IN.301904	301904	AF067157	C	IN	3584
46	C.IN.301905	CIN301905	AF067158	C	IN	3584
47	C.IN.301999	CIN301999	AF067154	C	IN	3584
48	D.UG.94UG1141	94UG114	U88824	D	UG	3584
49	D.ZR.84ZR085	84ZR085	U88822	D	ZR	3584
50	D.ZR.ELI	HIVELICG	K03454, X04414	D	ZR	3584
51	D.ZR.NDK	HIVNDK	M27323	D	ZR	3584
52	F.BR.93BR0201	93BR020	AF005494	F	BR	3584
53	F.FN.FIN9363	FIN9363	AF075703	F	FN	3584
54	G.BE.DRCBL	DRCBL	AF084936	G	BE	3584
55	G.FI.HH87931	HH8793	AF061640, AF061641	G	FI	3584
56	G.SE.SE6165	SE6165	AF061642	G	SE	3584
57	H.BE.VI991	VI991	VI991	H	BE	3584
58	H.BE.VI997	VI997	VI997	H	BE	3584

TABLE XXVII

in vitro binding of conserved HIV derived peptides to HLA-A2 supertype alleles

peptide	AA	protein	1st Position	sequence	Conservation (%)		A2-supertype binding capacity (IC50 nM)					alleles bound
					total	B	A*0201	A*0202	A*0203	A*0206	A*6802	
1261.14	10	NEF	221	LTFGWCFKL	55	74	294.1	48.9	185.2	57.8	6.2	5
1261.04	9	NEF	221	LTFGWCFKL	61	74	35.7	33.1	4545.5	205.6	5.6	4
1261.06	9	POL	316	YTAFTPSI	58	68	26.3	6.1	9.1	7	16.7	5
1261.15	10	POL	744	MASDFNLPPV	39	68	62.5	22.6	55.6	33.6	18.2	5
1069.32	9	GAG	386	VLAEMSQV	52	74	66.6	82.7	15.2	145.6	363.6	5
1261.16	10	POL	182	CTLNFPISPI	94	100	147	23.9	30.3	8.4	100	5
1261.02	9	ENV	651	LDQLTVWGI	53	63	9.8	215	43.5	24.7	645.2	4
1261.13	9	POL	448	KLVGKLNWA	95	95	59.5	12.6	5.9	39.8	3076.9	4
1211.04	9	ENV	134	KLTPLCVTL	81	95	102	126.5	66.7	185	20000	4
1261.08	9	POL	220	ALVEICTEM	23	79	217.3	187	140.8	264.3	2857.1	4
1261.11	9	VPR	59	AIRILQQL	61	74	333.3	22.6	41.7	38.5	547.9	4
1261.09	9	POL	163	LVGPTPVNI	84	100	454.8	153.6	19.2	2846.2	67.8	4
1261.12	9	VPR	62	RILQQLFI	56	74	19.2	1535.7	125	37	1818.2	3
1261.05	9	POL	183	TLNFPISPI	97	100	75.7	1482.8	1.1	1947.4	57.1	3
1261.03	9	GAG	271	MTNNPPIPV	31	89	166.6	7166.7	33.3	1608.7	12.1	3
1261.17	10	POL	132	KMIGGIGGFI	97	95	172.4	54.4	4.8	770.8	3333.3	3
941.03	9	POL	498	ILKEPVHGV	64	79	192.3	2388.9	6.7	37000	363.6	3
1260.10	9	POL	772	RAMASDFNL	64	79	217.3	116.2	25000	52.1	3076.9	3
1261.07	9	POL	879	KAACWVWAGI	49	79	277.7	1075	83.3	160.9	2666.7	3
1211.09	10	ENV	814	SLLNMTDIAV	22	68	9.8	1303	238.1	28.5	5479.4	3
1211.05	9	ENV	608	FLGAAGSTM	86	100	73.5	3583.3	1.5	4111.1	66666.7	2
25.0053	9	VPR	66	QLLFHFR	69	89	94.3	21500	25000	1608.7	476.2	2
25.0139	10	GAG	270	WMTNNPPIPV	31	89	98	3671.4	16.9	18500	2222.2	2
1069.33	10	POL	993	LLWKGEAVV	95	100	111.1	632.4	25	770.8	3636.4	2
25.0142	10	NEF	219	PLTFGWCFKL	61	74	142.8	741.4	4761.9	3700	47.6	2
1069.34	9	POL	993	LLWKGEAV	97	100	172.4	10750	21.7	1608.7	2666.7	2
25.0161	10	POL	452	KLNWASQIYA	42	84	217.3	3909.1	400	6166.7	3076.9	2
1211.082	9	GAG	79	SLYNTVATL	34	58	277.7	3583.3	50	37000	100000	2
25.0037	9	GAG	486	FLQSRPEPT	44	68	454.5	10750	32.3	18500	3076.9	2
25.0046	9	POL	91	TLWQRPLVT	61	68	270.2	21500	2500	18500	2857.1	1

TABLE XXVIII

in vitro binding of conserved HIV derived peptides to HLA-A3 supertype alleles

peptide	AA	protein	1st Position	sequence	Conservation (%)		A3-supertype binding capacity (IC50 nM)					alleles	
					total	B	A*0301	A*1101	A*3101	A*3301	A*6801	bound	bound
1273.01	9	GAG	163	MVHQAI SPR	42	58	61.1	89.6	18.0	13.8	9.5	5	5
1193.0200	9	POL	572	IVTWGKTPK	75	79	129.4	16.2	18.2	96.7	242.4	5	5
1193.03	9	POL	931	AVFIHFKR	97	100	64.7	3.3	5.1	107.4	4.2	5	5
1193.01	9	POL	724	YLAWVPAHK	34	95	142.9	105.3	327.3	33.0	2.0	5	5
1211.32	10	POL	971	KIQNFRVYYR	81	95	343.8	28.6	2.7	341.2	210.5	5	5
1069.49	10	POL	929	QMAVFIHFK	94	100	9.2	8.5	268.7	432.8	400.0	4	4
1273.03	10	GAG	162	QMVHQAI SPR	42	58	42.3	6000.0	243.2	290.0	186.0	4	4
1193.09	9	POL	353	MTKILE PER	67	84	13750.0	375.0	81.8	69.0	25.8	4	4
966.01	9	POL	347	AIFQSSMTK	56	79	10.0	10.0	12000.0	96666.7	242.4	3	3
940.03	10	NEF	100	QVPLRPMTYK	72	79	18.0	9.5	1836.7	2230.8	133.3	3	3
1069.43	10	ENV	48	TVYYGV PVWK	64	95	11.0	3.5	1636.4	10357.1	14.5	3	3
1069.48	10	POL	931	AVFIHFKRK	91	100	114.6	20.7	1125.0	5000.0	307.7	3	3
1273.05	9	POL	99	TIKIGGQLK	27	63	40.7	181.8	18000.0	36250.0	72.7	3	3
1273.06	9	ENV	64	TLFCASDAK	81	84	118.3	11.3	10588.2	22307.7	190.5	3	3
1273.07	10	ENV	61	TTLFCASDAK	78	84	119.6	27.3	9473.7	14500.0	140.4	3	3
1273.04	9	ENV	878	RIVELLGRR	34	89	200.0	600.0	138.5	13809.5	444.4	3	3
1273.09	10	POL	98	VTIKIGGQLK	27	63	297.3	28.6	10588.2	11600.0	125.0	3	3
1273.02	9	POL	246	NTPVFAIKK	58	94.7	333.3	100.0	30000.0	48333.3	4.7	3	3
1150.14	9	POL	930	MAVFIHFK	94	100	647.1	20.0	375.0	517.9	2.5	3	3
1273.08	9	VIF	7	VMIVWQVDR	69	95	3235.3	272.7	3.8	5.3	2424.2	3	3
1069.47	11	ENV	47	VTVYYGV PVWK	64	94	84.6	11.3	4615.4	36250.0	170.2	3	3
1069.42	11	POL	722	KVYLAWVPAHK	32	89	3.5	7.6	163.6	3580.2	8000.0	3	3
1069.44	9	POL	855	KLGRWPVK	78	68	8.5	133.3	500.0	72500.0	80000.0	3	3

TABLE XXIX

in vitro binding of conserved HIV derived peptides to HLA-B7 supertype alleles

peptide	AA	protein	1st Position	sequence	Conservation (%)		B7-supertype binding capacity (IC50 nM)					alleles bound	
					total	B	B*0702	B*3501	B*5101	B*5301	B*5401		
1146.01	9	NEF	94	FPVRPQVPL	75	74	15.7	43.0	11.6	481.9	71.4	5	
1296.01	9	ENV	259	IPHYCAPA	56	42	423	343	153	-	3.7	4	
15.0268	10	GAG	545	YPLASLRSLF	15	32	392.9	480.0	39.3	150.0	714.3	4	
1261.01	9	POL	186	FPISPIETV	88	95	3437.5	1043.5	148.6	251.4	9.1	3	
1296.02	9	ENV	250	CPKVSFEPI	47	79	100.0	5142.9	161.8	2447.4	100.0	3	
1296.03	11	POL	893	IPYNPQSQGVV	92	89	458.3	72000.0	119.6	46500.0	66.7	3	
29.0028	8	REV	75	VPLQLPPL	56	68	112.2	6000.0	0.8	46500.0	270.3	3	
1292.13	9	GAG	237	HPVHAGPIA	30	74	50.0	11.6	13750.0	4428.6	4.3	3	

Table XXX: A1-motif peptides

Peptide	Sequence	Protein	Conservancy		IC50 nM
			Total	Clade B	
1.0431	EVNIVTDSQY	HIV pol 1187	83	93	472
1.0014	FRDYVDRFY	HIV gag 298	51	96	278
2.0129	IYQYMDDLY	HIV pol 359	78	87	391
1069.27	VIYQYMDDLY	HIV pol 358	78	87	446
1069.26	VTVLDVGDAY	HIV pol 265	96	93	439

Table XXXI: A24-motif peptides

Peptide	Sequence	Protein	Conservancy		IC50 nM
			Total	Clade B	
25.0113	IWGCSGKLI	HIV env 69	69	91	444
25.0127	IYETYGDTW	HIV vpr 92	92	100	207
1069.60	IYQEPFKNL	HIV pol 1036	74	87	444
25.0128	PYNEWTLEL	HIV vpr 56	56	71	86
25.0123	PYNTPVFAI	HIV pol 74	74	100	387
1069.57	RYLKDQQLL	HIV env 2778	40	53	43
1069.58	RYLRDQQLL	HIV env 2778	23	32	52
1069.59	TYQIQEPPF	HIV pol 1033	78	93	67
25.0115	VWKEATTIL	HIV env 47	47	85	400
25.0218	VWKEATTILF	HIV env 47	47	85	44
25.0219	YWQATWIPEW	HIV pol 96	96	93	182

Table XXXII: Immunogenicity of A2-supertype cross-reactive binding peptides

Peptide	Sequence	Protein	Conservancy		Immunogenicity		
			Total	Clade B	XRN	patients	transgenic
1261.14	LTFGWCFKLV	HIV nef 221	55	74	5	0/1	0/6
1261.04	LTFGWCFKL	HIV nef 221	61	74	4	4/12	3/3
1261.06	YFAFTPSI	HIV pol 316	58	68	5	0/1	0/6
1261.15	MASDFNLPV	HIV pol 774	39	68	5	1/15	2/6
1069.32	VLAEAMSQV	HIV gag 386	52	74	5	6/19	3/3
1261.16	CTLNFPISPI	HIV pol 182	94	100	5	0/1	1/6
1261.02	LLQLTVWGI	HIV env 651	53	63	4	2/8	1/6
1261.13	KLVGKLNWA	HIV pol 448	95	95	4	3/15	3/3
1211.04	KLTPLCVTL	HIV env 134	85	95	4	2/12	2/6
1261.08	ALVEICTEM	HIV pol 220	23	79	4	0/2	1/6
1261.11	AIIRILQQL	HIV vpr 59	61	74	4	5/9	0/6
1261.09	LVGPTPVNI	HIV pol 163	84	100	4	1/9	1/6
1261.12	RILQQLLFI	HIV vpr 62	56	74	3	6/20	2/6
1261.05	TLNFPISPI	HIV pol 183	97	100	3	1/7	0/6
1261.03	MTNNPPIPV	HIV gag 271	31	89	3	2/17	4/6
1261.17	KMIGGIGGFI	HIV pol 132	97	95	3	2/7	0/6
941.03	ILKEPVHGV	HIV pol 498	64	79	3	8/19	3/6
1261.10	RAMASDFNL	HIV pol 772	64	79	3	2/9	0/6
1261.07	KAACWWAGI	HIV pol 879	49	79	3	1/8	0/6
1211.09	SLLNATDIAV	HIV env 814	22	68	3		

Table XXXIII: Immunogenicity of HIV-derived A3-supertype peptides

Peptide	Sequence	Protein	Conservancy			Immunogenicity	
			Total	Clade B	XRN	transgenic	patients
1211.32	KIQNFRVYYR	HIV pol 971	81	95	5	4/6	
1193.02	IVIWGKTPK	HIV pol 572	75	79	5	0/6	
1193.03	AVFIHNEKR	HIV pol 931	97	100	5	3/6	
1069.49	QMAVFIHNEFK	HIV pol 929	94	100	4	3/6	
1150.14	MAVFIHNEFK	HIV pol 930	94	100	3	6/6	
1069.48	AVFIHNEKRR	HIV pol 931	91	100	3	0/6	
1273.01	MVHQAI SPR	HIV gag 163	42	58	5	0/6	
1273.03	QMVHQAI SPR	HIV gag 162	42	58	4	0/6	
1193.01	YLA WVP AHK	HIV pol 724	34	95	5	0/6	
1069.42	KVYLA WVP AHK	HIV pol 722	32	89	3	6/6	
1193.09	MTKILEPFR	HIV pol 353	67	84	4	0/8	
966.01	AIFQSSMTK	HIV pol 347	56	79	3	5/6	1/6
940.03	QVPLRPMTYK	HIV nef 100	72	79	3	0/6	6/10
1069.44	KLAGR WPVK	HIV pol 855	78	68	3		
1273.02	NTPVFAIKK	HIV pol 246	58	95	3	0/6	
1273.08	VMIVWQVDR	HIV vif 7	69	95	3	0/6	
1273.04	RIVELLGRR	HIV env 878	34	89	3		
1273.07	TTLFCASDAK	HIV env 61	78	84	3	3/6	
1273.06	TLFCASDAK	HIV env 62	81	84	3	0/6	
1273.09	VTIKIGGQLK	HIV pol 98	27	63	3	6/6	
1273.05	TIKIGGQLK	HIV pol 99	27	63	3	0/6	
1069.43	TVYYGVPVWK	HIV env 48	64	95	3	28/33	
1069.47	VTVYYGVPVWK	HIV env 47	64	94	3	6/6	

Table XXXIV. HLA-DR screening panels

Screening Panel	Antigen	Alleles	Representative Assay		Phenotypic Frequencies					
			Allele	Alias	Cauc.	Blk.	Jpn.	Chn.	Hisp.	Avg.
Primary	DR1	DRB1*0101-03	DRB1*0101	(DR1)	18.5	8.4	10.7	4.5	10.1	10.4
	DR4	DRB1*0401-12	DRB1*0401	(DR4w4)	23.6	6.1	40.4	21.9	29.8	24.4
	DR7	DRB1*0701-02	DRB1*0701	(DR7)	26.2	11.1	1.0	15.0	16.6	14.0
	Panel total				59.6	24.5	49.3	38.7	51.1	44.6
Secondary	DR2	DRB1*1501-03	DRB1*1501	(DR2w2 β1)	19.9	14.8	30.9	22.0	15.0	20.5
	DR2	DRB5*0101	DRB5*0101	(DR2w2 β2)	-	-	-	-	-	-
	DR9	DRB1*09011,09012	DRB1*0901	(DR9)	3.6	4.7	24.5	19.9	6.7	11.9
	DR13	DRB1*1301-06	DRB1*1302	(DR6w19)	21.7	16.5	14.6	12.2	10.5	15.1
	Panel total				42.0	33.9	61.0	48.9	30.5	43.2
Tertiary	DR4	DRB1*0405	DRB1*0405	(DR4w15)	-	-	-	-	-	-
	DR8	DRB1*0801-5	DRB1*0802	(DR8w2)	5.5	10.9	25.0	10.7	23.3	15.1
	DR11	DRB1*1101-05	DRB1*1101	(DR5w11)	17.0	18.0	4.9	19.4	18.1	15.5
	Panel total				22.0	27.8	29.2	29.0	39.0	29.4
Quarternary	DR3	DRB1*0301-2	DRB1*0301	(DR3w17)	17.7	19.5	0.4	7.3	14.4	11.9
	DR12	DRB1*1201-02	DRB1*1201	(DR5w12)	2.8	5.5	13.1	17.6	5.7	8.9
	Panel total				20.2	24.4	13.5	24.2	19.7	20.4

Table XXXV: cross-reactive HLA-DR binding peptides

Peptide	Sequence	Protein	Binding capacity (IC50-nM)												DR Alleles	
			DR1	DR2w2B1	DR2w2B2	DR3	DR4w4	DR4w15	DR5w11	DR5w12	DR6w19	DR7	DR8w2	DR9	DR53	bound
27.0313	KRWIIIGLNKIVRMV	HIV gag 298	4.2	5.1	24	188	633	404	54	124	0.36	379	49	58		12
27.0354	WEFVNTPLVKLWYQ	HIV pol 596	7.2	222	2.1	13636	28	20	317	1355	90	15	350	39		10
27.0377	QKQITKIQNFRVYYR	HIV pol 956	2.9	3.4	80	-	357	49	53	124	25	25	75	577		11
1280.03	KVYLAWVPAHKGIGG	HIV pol 712	8.3	25	24	-	156	165	71	12598	2500	179	196	250		9
27.0311	GEYKRWIILGNKI	HIV gag 294	82	138	225	-	1667	380	213	1656	98	192	63	536		9
27.0361	EKVYLAWVPAHKGIG	HIV pol 711	3.6	21	4.9	3226	9.3	27	37	6478	3500	18	31	144		9
27.0297	QHLLQLTVWGKQLQ	HIV env 729	6.1	21	690	-	1316	345	2128	1064	350	44	907	375		8
27.0304	QQQMVHQASPRTLN	HIV gag 171	72	65	17647	-	60	400	-	-	412	455	7313	117		8
27.0344	SPAFQSSMTKILEP	HIV pol 335	357	217	667	-	3571	109	741	-	13	68	3267	33		8
F091.15	IKQFINMWQEVGKAMY	HIV env 566	128	217	206	-	417	271	4878	-	1000	-	350	5769	104	8
27.0341	FRKYTAFTIPSINNE	HIV pol 303	185	70	4167	-	294	136	1818	-	-	30	803	39		7
27.0364	HSNWRAMASDFNLPP	HIV pol 758	33	-	125	-	11	15	95	-	4375	472	1960	872		7
27.0373	KTAVQMAVFHFNEKR	HIV pol 915	161	650	690	-	909	452	182	18625	125	1786	1441	2586		7

A dash indicates IC50>20µM

654097 0002450

Table XXXVI: DR3 binding peptides

Peptide	Sequence	Protein	DR3
35.0135	YRKILRQRKIDRLID	HIV vpu 31	23
35.0131	WAGIKQEFGIPYNPQ	HIV pol 874	300
35.0127	EVNIVTDSQYALGI	HIV pol 674	732
35.0125	AETFYVDGAANRETK	HIV pol 619	769
35.0133	GAVVIQDNSDIKVP	HIV pol 989	1000

TABLE XXXVII
Immunogenicity of HIV-derived DR-supermotif peptides

Peptide	Sequence	Protein	conservation (%)		DR Alleles bound	Patient Immunogenicity
			total	clade B		
27.0313	KRWILGLNKRIRMY	HIV gag 298	85 [89] ¹	94 [95]	12	3/13
27.0311	GEIYKRWILGLNKL	HIV gag 294	58 [86]	95 [95]	9	2/13
27.0354	WEFVNTPLVLKWLWYQ	HIV pol 596	79 [89]	84 [95]	10	2/13
27.0377	QKQITKIQNFRVYYR	HIV pol 956	56 [67]	95 [95]	11	3/13
1280.03	KVYLAWVPAHKGIGG	HIV pol 712	32 [34]	89 [95]	9	3/13
27.0361	EKVYLAWVPAHKGIG	HIV pol 711	32 [34]	94 [95]	9	1/13
27.0304	QGQMVHQAIISPTLN	HIV gag 171	44 [42]	52 [58]	8	4/13
27.0344	SPAIFQSSMTKILEP	HIV pol 335	52 [59]	79 [78]	8	3/13
27.0341	FRKYTAFTIPSINNE	HIV pol 303	59 [58]	68 [68]	7	3/13
27.0364	HSNWRAMASDENLPP	HIV pol 758	48 [67]	68 [79]	7	3/13
27.0373	KTAVQMAVFIHNFKR	HIV pol 915	87 [95]	94 [100]	7	4/13

1: conservation of core region

Table XXXVIII. Candidate CTL Epitopes

Restriction	Peptide	Protein	Sequence
HLA-A2	1069.32	HIV gag 386	VLAEAMSQV
"	1261.03	HIV gag 271	MTNNPPIPV
"	1261.15	HIV pol 774	MASDFNLPPV
"	1261.13	HIV pol 448	KLVGKLNWA
"	1261.09	HIV pol 163	LVGPTPVNI
"	941.03	HIV pol 498	ILKEPVHGV
"	1261.07	HIV pol 879	KAACWWAGI
"	1261.17	HIV pol 132	KMIGGIGGFI
"	1261.10	HIV pol 772	RAMASDFNL
"	1261.05	HIV pol 183	TLNFPISPI
"	1211.04	HIV env 134	KLTPLCVTL
"	1261.02	HIV env 651	LLQLTVWGI
"	1211.09	HIV env 163	SLLNATDIAV
"	1261.04	HIV nef 221	LTFGWCFKL
"	1261.11	HIV vpr 59	AIRILQQL
"	1261.12	HIV vpr 62	RILQQLLFI
HLA-A3	1069.49	HIV pol 929	QMAVFIHNFK
"	1069.42	HIV pol 722	KVYLAWVPAHK
"	1211.32	HIV pol 971	KIQNFRVYYR
"	1193.09	HIV pol 353	MTKILEPFR
"	966.01	HIV pol 347	AIFQSSMTK
"	1273.09	HIV pol 98	VTIKIGGQLK
"	1273.07	HIV env 61	TTLFCASDAK
"	1069.47	HIV env 47	VTVYYGVVPWK
"	940.03	HIV nef 100	QVPLRPMTYK
"	1273.08	HIV vif 7	VMIVWQVDR
"	1273.03	HIV gag 162	QMVHQAISPR
HLA-B7	15.0268	HIV gag 545	YPLASLRSLF
"	1292.13	HIV gag 237	HPVHAGPIA
"	1261.01	HIV pol 186	FPISPIETV
"	1296.03	HIV pol 893	IPYNPQSQGVV
"	1296.01	HIV env 259	IPHYCAPA
"	1296.02	HIV env 250	CPKVSFEPI
"	1146.01	HIV nef 94	FPVRPQVPL
"	29.0028	HIV rev 75	VPLQLPPL
HLA-A1	1.0431	HIV pol 684	EVNIVTDSQY
"	1.0014	HIV gag 317	FRDYVDRFY
"	1069.27	HIV pol 368	VIYQYMDDLY
"	1069.26	HIV pol 295	VTVLDVGDAY
HLA-A24	1069.60	HIV pol 533	IYQEPFKNL
"	25.0123	HIV pol 244	PYNTPVFAI
"	1069.59	HIV pol 530	TYQIQEPF
"	25.0219	HIV pol 597	YWQATWIPEW
"	25.0113	HIV env 681	IWGCSGKLI
"	1069.57	HIV env 671	RYLKDQQLL
"	25.0115	HIV env 55	VWKEATTTLF
"	25.0127	HIV vpr 46	IYETYGDTW
"	25.0128	HIV vpr 14	PYNEWTLEL

Selection Criteria	Peptide	Sequence	Protein
DR	27.0313	KRWILGLNKIVRM	HIV gag 298
	27.0354	WEFVNTPLVLWYQ	HIV pol 596
	27.0377	QKQITKIQNFVYYR	HIV pol 956
	1280.03	KVYLAWVPAHKGIGG	HIV pol 712
	27.0311	GEIYKRWILGLNKI	HIV gag 294
	27.0361	EKVYLAWVPAHKGIG	HIV pol 711
	27.0297	QHLLQLTVWGKQLQ	HIV env 729
	27.0304	QGQMVHQAI SPRTL N	HIV gag 171
	27.0344	SPAIFQSSMTKILEP	HIV pol 335
	F091.15	IKQFINMWQEVGKAMY	HIV env 566
	27.0341	FRKYTAFTIPSINNE	HIV pol 303
	27.0364	HSNWRAMASDFNLPP	HIV pol 758
27.0373	KTAVQMAVFIHNFKR	HIV pol 915	
DR3	35.0135	YRKILRQRKIDRLID	HIV vpu 31
	35.0131	WAGIKQEFGIPYNPQ	HIV pol 874
	35.0127	EYNIVTDSQYALGII	HIV pol 674
	35.0125	AETFYVDGAANRETK	HIV pol 619
	35.0133	GAVVIQDNSDIK VVP	HIV pol 989

TABLE XL
Estimated population coverage by a panel of HIV derived HTL epitopes

Antigen	Alleles	Representative assay	No. of epitopes ²	Population coverage (phenotypic frequency)				
				Cauc.	Blk.	Jpn.	Chn.	Hisp.
DR1	DRB1*0101-03	DR1	13	18.5	8.4	10.7	4.5	10.1
DR2	DRB1*1501-03	DR2w2 B1	12	19.9	14.8	30.9	22.0	15.0
DR2	DRB5*0101	DR2w2 B2	12	-	-	-	-	-
DR3	DRB1*0301-2	DR3	5	17.7	19.5	0.40	7.3	14.4
DR4	DRB1*0401-12	DR4w4	10	23.6	6.1	40.4	21.9	29.8
DR4	DRB1*0401-12	DR4w15	13	-	-	-	-	-
DR7	DRB1*0701-02	DR7	11	26.2	11.1	1.0	15.0	16.6
DR8	DRB1*0801-5	DR8w2	9	5.5	10.9	25.0	10.7	23.3
DR9	DRB1*09011,09012	DR9	11	3.6	4.7	24.5	19.9	6.7
DR11	DRB1*1101-05	DR5w11	9	17.0	18.0	4.9	19.4	18.1
DR13	DRB1*1301-06	DR6w19	8	21.7	16.5	14.6	12.2	10.5
Total ¹				98.5	95.1	97.1	91.3	94.3
								95.1

1. Total opulation coverage has been adjusted to account for the presence of DRX in many ethnic populations. It has been assumed that the range of specificities represented by DRX alleles will mirror those of previously characterized HLA-DR alleles. The proportion of DRX incorporated under each motif is representative of the frequency of the motif in the remainder of the population. Total coverage has not been adjusted to account for unknown gene types.

2. Number of epitopes represents a minimal estimate, considering only the epitopes shown in Table 13. Additional alleles possibly bound by nested epitopes have not been accounted.